```
                    10        20        30        40        50        60        70        80
ACD-1/1-629   1 MEPTLSPNYRNEAFEHDDSYLVNFVAGSSSGESSTPPPSFVPKCNFRYNQSRSQMIIEVPVAQLKKLRKLEGTVSIKRETQHF 83
ASIC1a/1-574  1 ----------------------------------------------------------MELKAEEEEVGGVQPVS-------IQAF 21

                90       100       110       120       130       140       150       160
ACD-1/1-629  84 CETTTMHGPKRIFQGKRWAT--LFWLIMVSCSLGLLITQVFILASEYLSKPTVSDVSFLINEDGMDFPLITICNLNPIRKTYV 164
ASIC1a/1-574 22 ASSSTLHGLAHIFSYERLSLKRALWALCFLGSLAVLLCVCTERVQYYFHYHHVTKLDEVAAS-QLTFPAVTLCNLNEFRFSQV 103

               170       180       190       200       210       220       230       240
ACD-1/1-629 165 NEINKTGEVSPPMINYMMKWFTEIPTLIGGADRPTLHEGNEELKLYMKNHLNFTVDSFFMNSGFSCPDIFKLCSFQGEIFDCC 247
ASIC1a/1-574 104 SKNDLYHAG--ELLALLNNRYEIPDTQMADEKQLEILQDKANFRSFKP--KPFNMREFYDRAGHDIRDMLLSCHFRGEVCSAE 182

                 250       260       270       280       290       300       310       320       330
ACD-1/1-629 248 TLSTEVLTPLGKCFTLDLSSSTKASMHKQTEPGIQAGLAITLDAHLEEQFDGSNGMDALFTNSFVNGFRYFVHPPNTIPHLSS 330
ASIC1a/1-574 183 DFK-VVFTRYGKCYTFNSGRDGRPRLKTMKD-GTGNGLEIMLDIQQDEYLPVWGETD---ETSFEAGIKVQIHSQDEPPFIDQ 260

                340       350       360       370       380       390       400       410
ACD-1/1-629 331 DEFTVSPNTVAFSAISSDRYVLLPTHQWGNCTEN-FPDGIQSNLSYSSGNCLSLCKAKFYMENCGCTPALYNIENNLKECTPY 412
ASIC1a/1-574 261 LGFGVAPGFQTFVACQEQRLIYLP-PPWGTCKAVTMDSDLDFFDSYSITACRIDCETRYLVENCNCR--MVHMPGDAPYCTPE 340

                420       430       440       450       460       470       480       490
ACD-1/1-629 413 ETTTCLDNILAKPNKETGKIEFQTPNCKACAQQCNSLVYRAYNSYGSQFSAGAFHYLKSINPEWTDGHMRANFQMINIFYRDM 495
ASIC1a/1-574 341 QYKECADPALDFLVEKD-------QEYCVCEMPCNLTRYGKELSMVKIPSKASAKYLAKKFNKSEQ-YIGENILVLDIFFEVL 415

                500       510       520       530       540       550       560       570
ACD-1/1-629 496 SYTEYNQVQDASVTQLLSDIGGNMGMF----LGMSVITITEICLFFSK----------------------MFWLGFSKKRRDY 552
ASIC1a/1-574 416 NYETIEQKKAYEIAGLLGELLMTPVPFSCHGHGVAPYHPKAGCSLLSHEGPPPQRPFPKPCCLGDIGGQMGLFIGASILTVLE 498

                590       600       610       620       630       640       650
ACD-1/1-629 553 MYSKRVNEKTHEREVCETVEKMKAIASQGNLSNLSILKINKLKNYSEILNGSLVILSSKFTYPEHYFYIFNENILDF        629
ASIC1a/1-574 499 LFDYAYEVIKHKLCRRGKCQKEAKRSSADKGVALSLDDVKRHNPCESLRGHPAGMTYAANILPHHPARGTFEDFTC-        574
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Supplementary Figure 3, Wang et al.