## SUPPLEMENTS

Α

118 114 243 239 366 364 104 684 109 614 726 739 851 864 967 686 1088 1114 1213 -SOKSHA BOTLINKEOVILPSSKAPPHRCLPGCOICOOLVRCFCGRLVWCHAJOTDA: AN W SOUTH BOSH ROAL BENSALSENHIEGSPIDAVGVINFOGGSHSVHARVENEN Target MHSHFILSDIGTVGKYGNEMKLARNLEKYLSLOKIHCKSRQGVPVVGLVVEGGPNVLLSVAETVKDKDFV--VVCEGTGRAADLLAFTHKHLADEGMLRPQVKEZITCM1QNTFNFSLKOSKHLF 2x5.1.A.LHSHFILVDDGTVGKYGARVERSIEWII)00 HIMARIGOGVFW/DJTVUBSVD0 BSFV(WVVO BGTGRAADLLAVIHKOT BGANEPGANEFFILISTIKKIFNFOOS BAUNE 2x5.1.4 HIJROV KOONDEPCY HILLDIGIVIE 106011K CAUNERSONNERSONNESSTEOLKESMENEN SMETER STEUREN MENNEN MENNEN MENNEN SMETER STEUREN MENNEN SMETER SME Target I GELY PYNDILLWAVLMKKOKMAMFFMOHGEEATVKAVIACILYRAMAHEAKESHWYDDASEBLKNYSKOFGOLALDLLEKAFKONGORAMAMILTYELRMSNSICLKLAVSGGLRPFVSHITTO ----DPPFHIAGRLIYCIDIIFWFSRLLDFFAVNOHAGPYV Target|ThiaRmiannfyllingivilsfona**r**ailsf**xa**bfshsla**Ra**ivferfwhiygetovagetovs----cppgsfliffloavylfvoavylfvoavilfafennvyl**dme**sisnnim<u>R</u>ynR zx5.1.a MMIGKWDANKFIVVIMAUVLSFGVFRKALDYP EN PSMSLA "DIVE PYMMIFGEVYAYELPVCAN" 511P710 0FGTMLTFFLQAVYLFVQVIIMVNLLAFINVYLQV AISNIVMKYDR Target KRYINTYARKPULPPPLILLSHVGLLLRANGLCHARPPUGEGGVGLKLYLSKEDIKKLHDFEGOVEKYFHEKNEDVNCSCEERIRVFOLKENTENYFGLKENNEKVSFIKDSLSLDSCVEKHEK QWSVENHTTNSPIDIFGTINFODGEHTHHANYIRISYDT zx5.1. Å K = IILOLLLKERONELFRLVISVEGGMONTEL NULVOUNE SELENE SE CHORDON SELENE SE SECTOTIGIA PAGUIEN NULVGENE VOILUNE SECTOTIGIA PAGUIEN NULVGENE VOILUNE SECTOTIGIA PAGUIEN S Target OILMECWVHRUCTITFDADSEEOODILEIAILTALLKGTNISASRQLNLAMAMDRVDIAKHILLIYGOHRKEDALEOAMSDALWDRVDFVLLIZYGVNLHRFLLIFKLEELYNTKGGFUNTLA --GNRNESAESTLHSOFIRTAQPYWFKENSIVIHNSRNNSKEONVS-DDPES ZX5.1.4 M F 2 F F N IL WA LINNROUMME F MONGEES NEWANDAN SEN SE VOD SEEDK VSN FGOLAN ILLESSF G E MAM ILLTE NNSNSTCLKLAVSSF REFY MICTO zx5.1.ÅQTHMECK<mark>ENTE</mark>LIVENISSENHOD (DVALITALLKGTNASAE OLILILÄMDRVDIK)HUFVYSOOMHVOSLEOAMIDALVMDRVSEVKLIID)GVSHHKELDICRAS Target FIMLFTYTVLVEMOPOPSVOEMLVSIYIFINAIEVVREICISEPGKFTOKVEVUUSEYMNLTEIVAIGLFSAGFVLRMG----Target MKZQPVLZRLQSQKSWIKGVFDKRZCSTIIPSSKNPHRCTPVCQVCQNLIRCYCGRLIGDHAGIDYSWTISAAKGKESZ Target HIVQDVKQHTLLSGYRITLIDIGLVVZ; LIGRAYRSNYTRKHFR, LYNNL---YRKYKHQRHSS---ZX5.1.A

1229

2x5.1.ÅYÄETMÄÄHEKPVLPPP---LIIISHLVSLFCCVCKRRKKENTETS

**S1. Alignment of TRPM6 with TRPM7.** The TRPM6 and TRPM7 amino acid sequences alignment. The alignment was performed according to TRPM7 part which has been assigned to structure by CryoEM. (A) The hydrophobic and (B) the polar character of TRPM6/TRPM7 alignments. Specific TRPM6np binding epitope aligned with TRPM7 region is labelled in yellow frame. TRPM6 sequence corresponds to human; TRPM7 sequence corresponds to part of CryoEM assigned structure (PDB: 5ZX5).