

SLC26A8_H.sapiens	334	TLIDMIFYSFLLPVTFDFSLLPKIILOAFSLSTVSSFLLIFLGGKIIASLHNYSVNSNODLIATGLCNVVSFFRSCVFTGAIARTIIQDKSGGRQOFA
SLC26A8_M.musculus	334	TLIDMIFYSFLLPVTFDFSLLPKIILOAFSLSTVSSFLLIFLGGKIIASLHNYSVNSNODLIATGLCNVVSFFRSCVFTGAIARTIIQDKSGGRQOFA
SLC26A3_M.musculus	309	AVVGNMSICFQPPITPVEVFQDTIGDSFGIATVGFVAVAFSVASVYSLKYDYPIDGNOELIATGLCVSNIFTGAEKGFAGSTALSRSVQESTGGKTOVA
SLC26A3_R.norvegicus	309	AVVGNMSICFQPPITPVEVFQDTIGDCFGIATVGFVAVAFSVASVYSLKYDYPIDGNOELIATGLCVSNIFTGAEKGFAGSTALSRSVQESTGGKTOVA
SLC26A3_O.cuniculus	308	SVIGKMEKGFQAPAAPDTQVFDAGIDCFITIAIVGFVAVAFSVASVYSLKYDYPIDGSOELIATGLGNIVTGSFKGFAGSTALSRSVQESTGGKTOVA
SLC26A3_H.sapiens	316	AVVCDMNECFQPPITPVEVFQNTVGDVCFIATVAVAFVAVAFSVASVYSLKYDYPIDGNOELIATGLGNIVCVVGRGFAGSTALSRSVQESTGGKTOIA
SLC26A4_M.musculus	326	GIVKSIPTSCFLPPVLPVSLVGLFSDMLAASFIAVVAIAIIVSVGKQVYATKHDYVIDGNOEFTAFGICSNVFSGFSCFVATTALSRVAVQESTGGKTOVA
SLC26A4_R.norvegicus	326	GIVKSIPTSCFLPPVLPVSLVGLFSDMLAASFIAVVAIAIIVSVGKQVYATKHDYVIDGNOEFTAFGICSNVFSGFSCFVATTALSRVAVQESTGGKTOVA
SLC26A4_H.sapiens	326	GIVKSIPTSCFLPPVLPVSLVGLFSDMLAASFIAVVAIAIIVSVGKQVYATKHDYVIDGNOEFTAFGICSNVFSGFSCFVATTALSRVAVQESTGGKTOVA
SLC26A4_X.leavis	310	GIKTIPTSCFIPAMSPDVSLFSSLISSAFSTGTIVAYAVIIVSVGKQVYATKNNYRVDGNOEFTAFGICSNMFGGTFSCFCASTALSRVAVQESTGGKSOIA
SLC26A3_X.leavis	330	GTVKNIPSCFIPPMMPDVSMFPQIISSAISIGIVAYAVAVSLGKVEATKKNYVAIDGNOEFTAFGICSNVFSGFSCFVATTALSRVAVQESTGGKTOIA
SLC26A5_M.unguiculatus	316	DVVGTIPICLLPPANEDTSLFHLVYVDAIAIAIIVGFVSVTISMAKTLANKHGYQVDGNOELIATGLCNSIGSLFQTFESISCSLSRSLVQESTGGKTOIA
SLC26A5_M.musculus	316	DVVGTIPICLLPPANEDTSLFHLVYVDAIAIAIIVGFVSVTISMAKTLANKHGYQVDGNOELIATGLCNSIGSLFQTFESISCSLSRSLVQESTGGKTOIA
SLC26A5_H.sapiens	316	DVVGTIPICLLPPANEDTSLFHLVYVDAIAIAIIVGFVSVTISMAKTLANKHGYQVDGNOELIATGLCNSIGSLFQTFESISCSLSRSLVQESTGGKTOIA
SLC26A5_D.rerio	319	DVVGKIPTICLLPPKVEDFVFPNLFADAVPIAVVGFVSVTISLAKTFALKYGYVSDGNOELIATGLCNFVVSFFHTEFVVATASMSRSLVQESTGGHTETA
SLC26A6_H.sapiens	300	DVVGNIPACLVPVPAENTQLFSKLVGSAFTIIVVGFVAVAIISLGIKIFALRHGYRVDGNOELIATGLSNLIGGTFQCFPVVSCMSRSLVQESTGGNSOVA
SLC26A6_S.scrofa	322	DVVGRIPACLVPVPAEPQFLFARLVGNFAFAIIVVGFVAVAIISLGIKIFALRHGYRVDGNOELIATGLSNFIGGTFQCFPVVSCMSRSLVQESTGGNSOVA
SLC26A6_M.musculus	299	DVVGNITTCGLIPPVVAKTELFAITLVGNFAFAIIVVGFVAVAIISLGIKIFALRHGYRVDGNOELIATGLSNLIGGTFQCFPVVSCMSRSLVQESTGGNTOVA
SLC26A6_X.laervis	318	DIVGEIPTCMKAPMLENTNIFARVVGNAFAIIVVYAFTISLAKMFGVKHGYNDGNOELIATGLSNISIGSFFQCFITIGTAMSRSLVQESTGGHSOVA
SLC26A6_A.japonica	310	DVVGDIPTSGLNPEPTTETDISIFTEVIGDAFAMAVGYAINISLGTFAKHKGYKVDGNOELIATGLSNVVGFFQCYCVTSSMSRSLVQESTGGKTOVA
SLC26A9_H.sapiens	310	QIVGEIPTQRCFPTPVSPVVSQWKDMIGTAFSLAVVYVINLAMGRTLANKHGYDVDGNOEMIALGCNSFFGFFFKIHVICCALSVTLAVDAGGKSOVA
SLC26A9_M.musculus	310	QIVGEIPTQRCFPTPVSPVVSQWKDMIGTAFSLAVVYVINLAMGRTLANKHGYDVDGNOEMIALGCNSFFGFFFKIHVICCALSVTLAVDAGGKSOVA
SLC26A2_H.sapiens	359	SIACHIPITCFMPPKVPENLIPSAVDAIAIAISIIICFAITVSLSEMFAKKHGYTVKANOEYAI GFCNIIIPSFHCFITTSAAIAKTLVKESTGCQTOLS
SLC26A2_E.caballus	361	SIACHIPITCFMPPKAPDWNLIPSAVDAIAIAISIIICFAITVSLSEMFAKKHGYTVKANOEYAI GFCNIIIPSFHCFITTSAAIAKTLVKESTGCQSOLS
SLC26A2_B.bubalis	354	SIACHIPITCFMPPKAPDWNLIPRVAIDAIAIAIICFAITVSLSEMFAKKHGYTVKANOEYAI GFCNIIIPSFHCFITTSAAIAKTLVKESTGCQTOVS
SLC26A2_B.taurus	354	SIACHIPITCFMPPKAPDWNLIPRVAIDAIAIAIICFAITVSLSEMFAKKHGYTVKANOEYAI GFCNIIIPSFHCFITTSAAIAKTLVKESTGCQTOVS
SLC26A2_M.musculus	359	SIACHIPITCFMPPKAPDWSLIPNVAIDAIAIAISIIICFAITVSLSEMFAKKHGYTVKANOEYAI GFCNIIIPSFHCFITTSAAIAKTLVKESTGCQTOVS
SLC26A2_R.norvegicus	359	SIACQIPTCFMPPKAPDWSLIPNVAIDAIAIAISIIICFAITVSLSEMFAKKHGYTVKANOEYAI GFCNIIIPSFHCFITTSAAIAKTLVKESTGCQTOVS
SLC26A2_C.intestinalis	350	RVVGPIPTCFPAPMLEDFSIMGSIIGDGFALAVVGFVAVSVLSKMYAKYGYSDGNOELIATGLCVSNVAFSFFRSCFPNAAALARCIVQENTGGNTOLV
SLC26A10_H.sapiens	256	QIVGLIPGCFPPQELLENLAELPRILADSLPIATVSVFVAVSASLAIHADKYSYTDGNOEFTAFHAGSNLISLFSFCFPNSATLATTNLLVDAGGKTOIA
SLC26A10_D.rerio	239	QIVGHIPTACFPPEPRIPALETVPEIAGDTVAITTVAYAVSVSLAMIYADKHYSDGNOEFTAFHAGSNLISLFSFCFPNSATLATTNLLVDAGGKTOIA
SLC26A7_H.sapiens	285	EVVGHIPQCIPSPRAPPMNLSAVITEAFGVAVVAVASLALAQSAKKFKYSIDDGNOEFTAFHAGSNLISLFSFCIPSAAMGRTAGLYSTGAKTOVA
SLC26A7_M.musculus	285	EVVGHIPNCPSPRAPPMNLSAVLTEAFGVAVVAVASLALAQSAKKFKYSVDGNOEFTAFHAGSNLISLFSFCIPSAAMGRTAGLYSTGAKTOVA
SLC26A5_C.intestinalis	325	KIICEIPTSCFLPVTFPPVDFKFTSIIIGHAIPITAVGYVAVSIAKIFANFNGYKIRPNOELIATVAFASNLVVSFFFCFPAPFMSRSCVQVDSGGKTOVA

Supplementary Fig. S2: Sequence alignment of the SLC26 transporters region encompassing TMD7 and TMD8.

Multiple sequence alignment of SLC26a2-10 shows high conservation of the Gly367 and Pro371 (red) residues. F368 (blue) is conserved in many SLC26 transporters. The pore Glu417 (pink) is highly conserved among the SLC26 transporters.