Figure S1

A

```
   ScAVT3 1    [255]GEDLSEEEEEEEETEEEPEE-------EALETESTQLVSREHGRHP-----HKSSTVKAVLLLLKSFVGTGVLFL  318
MmQ8BHK3 1         MSVTKSARSPQVATPLNLDL---PESAKKLQSQDPSPANGSSSESS--KKTKGITGFQTLVHLVKGNMGTGILGL  70
HsSLC36A2 1        MSVTKSTEGPQGAVAIKLDLmspPESAKKLENKDSTFLDESPSESAglKKTKGITVFQALIHLVKGNMGTGILGL  75
CeSKAT-1 1         ---MSEEEGRERAVTVEGDA-------ESMN-DGRALV-QPPARSG-----DVITPTRAVLTLSKSMFNAGCFSL  58

   ScAVT3 319  PKAFHNGGWGFSALCLLSCALISYGCFVSLITTKDKV-----------------GVDGYGDMGRILYGPKMKFAILSSIA  381
MmQ8BHK3 71   PLAVKNAGILMGPLSLLVMGLIACHCMHILVRCAQRFCHRLNKPFMDYGDTVMHGLAFSPNAWLQNHAHWGRRVVSFFLI  150
HsSLC36A2 76  PLAVKNAGILMGPLSLLVMGFIACHCMHILVKCAQRFCKRLNKPFMDYGDTVMHGLEANPNAWLQNHAHWGRHIVSFFLI  155
CeSKAT-1 59   PYAWKLGGLWVSFVMSFVIAGLNWYGNHILVRASQHLAKKSDRSALDYGHFAKKVCDYSDIRFLRNNSKAVMYFVNVTIL  138

   ScAVT3 382  LSQIGFSAAYTVFTATNLQVFSENFFH-----------LKPGSISLATYIFAQVLIFVPLS-LTRNIAKLSGTALIADLF  449
MmQ8BHK3 151  VTQLGFCCVYIVFLADNLKQVVEAVNSTTISCHKNETVVLTPTMDSRLYMLSFLPVLGLLV-FVRNLRVLTIFSLLANIS  229
HsSLC36A2 156 ITQLGFCCVYIVFLADNLKQVVEAVNSTTNNCYSNETVILTPTMDSRLYMLSFLPFLVLLV-LIRNLRILTIFSMLANIS  234
CeSKAT-1 139  FYQLGMCSVAILFISDNLVNLVGD--H-----------LGGTRHQQMILMATVSLFFILLTnMFTEMRIVSFFALVSSVF  205

   ScAVT3 450  ILLGLVYVYVYsiYYIAVNGVASDTMLMFNKADWSLFIGTAIFTFEGIGLLIPIQESMKHPKHFRP---SLSAVMCIVAV  526
MmQ8BHK3 230  MLVSL-VIIAQ--YIIQEIPDASQLPLVASWKTYPLFFGTAIFSFESIGVVLPLENKMKDARGFPT---ILSLGMSIITT  303
HsSLC36A2 235 MLVSL-VIIIQ--YITQEIPDPSRLPLVASWKTYPLFFGTAIFSFESIGVVLPLENKMKNARHFPA---ILSLGMSIVTS  308
CeSKAT-1 206  FVIG-AAVIMQ--YTVQQPNQWDKLPAATNFTGTITMIGMSMYAFEGQTMILPIENKLDNPAAFLApfgVLSTTMIICTA  282

   ScAVT3 527  IFISCGLLCYAAFGSDVKTVVLLNFPQdTSYTLTVQLLYALAILLSTPLQLFPAIRILENWTFPSNASGKYNPKVKWLKN  606
MmQ8BHK3 304  LYIAIGALGYLRFGDDIKASITLNLPN-CWLYQSVKLLYVVGILCTYALQFYVPAEII----IPLAVSQVSKRWALPVDL  378
HsSLC36A2 309 LYIGMAALGYLRFGDDIKASISLNLPN-CWLYQSVKLLYIAGILCTYALQFYVPAEII----IPFAISRVSTRWALPLDL  383
CeSKAT-1 283  FMTALGFFGYTGFGDSIAPTITTNVPK-EGLYSTVNVFLMLQSLLGNSIAMYVVYDMFFNGFRRKFGARFPNVPKWLSDK  361

   ScAVT3 607  YFRCAIVVLTSILAwVGANDLDKFVSLVGSFACIPLIYIYPPLLHYKASILSGTSRARLLLD----LIVIVFGVAVMAYT  682
MmQ8BHK3 379  SIRLALVCLTCMLA-ILIPRLDLVLSLVGSVSSSALALIIPPLLEVVTYYGEGISPLTVTKD-ALISILGFMGFVVGTYQ  456
HsSLC36A2 384 SIRLVMVCLTCLLA-ILIPRLDLVISLVGSVSGTALALIIPPLLEVTTFYSEGMSPLTIFKD-ALISILGFVGFVVGTYQ  461
CeSKAT-1 362  GFRVFWVLVTYLMA-VLIPKLEIMIPLVGVTSGALCALIFPPFFEMITFWTDWKGLLTYRQRmTKIFINLVVMAIGVFAI  440

   ScAVT3 683  SWQT   -IKMWSQ------------  692
MmQ8BHK3 457  ALDE   LIKSGNSP-ALSNSTMFIQ  478
HsSLC36A2 462 ALDE   LLKSEDSH-PFSNSTTFVR  483
CeSKAT-1 441  IAGV[6]IIQSFSQPdP---------  460
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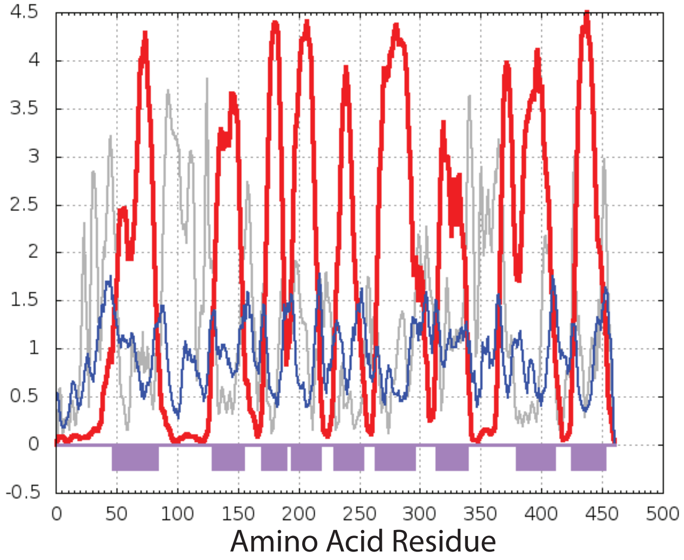
B



http://split.pmfst.hr/split/4/

Red line: Transmembrane helix preference. (THM index)
Blue line: Beta preference. (BET index)
Gray line: Modified hydrophobic moment index. (INDA index)
Violet boxes (below abscisa): Predicted transmembrane helix position. (DIG index)

C