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          *           20           *           40           *
arabidC : -----MALALRRLSSSVKK---PISLLSS-----NGGSLRFMWIKQLNA : 36
peaM : ---MAMAMALRKLSSSVNKSSRPLFSASSLYYKSSLPDEAVYDKENPRVTWPKQLNS : 54
humanC : -----MTMPVNGAHK-----DADLWSSHDK---MLAQP-- : 25
humanM : MLYFSLFWAARPLQRCGQLVRMAIRAQHS-----NAAQTQTGEANRGWTGQES- : 48
yeastC : -----MPYTLSDAHHKLITS : 15
yeastM : -----MFPRASALAK---CMATVHRRGLLTSGAQLSVSK : 31
PfSHMTc : -----MFNNDP-- : 6
PfSHTMm : -----MLKEFVKNVNVR : 12

          60           *           80           *           100           *
arabidC : SLDEIDPEVADIIE---LEKARQWKGFELIPSENFTSLSVMQAVGSMVTNKYSEGYP : 90
peaM : PLEVIDPEIADIIE---LEKARQWKGLELIPSENFTSLSVMQAVGSMVTNKYSEGYP : 108
humanC : -LKDS DVEVYNIK---KESNRQRVGLELIAENFASRAVLEALGSC LNNKYSEGYP : 78
humanM : -LSDSDPEMWELLQ---REKDRQCRGLELIAENFCSRAALEALGSC LNNKYSEGYP : 101
yeastC : HLVDTDPEVDSTIK---DEIERQKHSIDLIAENFTSTSVFDALGTPLSNKYSEGYP : 69
yeastM : PVSEGDPPEMFDILQ---QERHRQKHSITLIPSENFTSKAVMDLLGSELQNKYSEGYP : 85
PfSHMTc : -LQKYDKELFDLLE---KEKNRQIETINLIAENLTNTAVRECLGDRISNKYSEGYP : 59
PfSHTMm : N-HRYIS--FYSLRNQSR LNDIDDETYNMLKSYKNKND-INLSLVHNIIMPTYMKEYL : 65
                                     &                                     & #

          120           *           140           *           160           *
arabidC : GARYYGGNEYVVCILLTRYIDMAETLCQKRALEAFQLDPSKMGVNVQSLSGSPANFQ : 147
peaM : GARYYGGNE-----YIDMAETLCQKRALEAFRLDPAKMGVNVQPLSGSPSNFQ : 156
humanC : GQRYYGGTE-----FIDELETLCQKRALQAYKLDPPQCGVNVQPYSGSPANFA : 126
humanM : GKRYYGGAE-----VVEIEIELLCQRRALEAFDLDPAQMGVNVQPYSGSPANLA : 149
yeastC : GARYYGGNE-----HIDRMEILCQQRALKAFHVTPDKMGVNVQTLGSPANLQ : 117
yeastM : GERYYGGNE-----IIDKSESLCQARALELYGLDPAKMGVNVQPLSGAPANLY : 133
PfSHMTc : HKRYYGGND-----YVDKIEELCYKRALEAFNVSEEEWGVNVQPLSGSAANVQ : 107
PfSHTMm : SIDLNRNIF-----VNNKNIENLEYIALNSFN LQKKYWGCLISNVSLNNNKS I : 113
      ##                                     ##

          180           *           200           *           220
arabidC : VYTALLKPHERIMALDLP HGGHLSHG YQTD T---KKISAVS IFFETMPYRLDENTGY : 201
peaM : VYTALLKPHDRIMALDLP HGGHLSHG YQTD T---KKISAVS IFFETMPYRLDESTGY : 210
humanC : VYTALVEPHGRIMGLDLP DGGH LTHGFM TDK---KKISATS IFFESMPYKVNPD TGY : 180
humanM : VYTALLQPHDRIMGLDLP DGGH LTHGYMS DV---KRISATS IFFESMPYKLNPK TGL : 203
yeastC : VYQAIMKPHERIMGLYLP DGGHLSHG YATEN---RKISAVS TYFESFPYRVNPETGI : 171
yeastM : VYSAIMNVGERIMGLDLP DGGHLSHG YQLKSG--TPISFI SKYFQSMPYHVDHTTGL : 188
PfSHMTc : ALYALVGVGKIMGMHLCSGGH LTHGFE DEK---KKVSITS DLFESKLYKCNSE-GY : 160
PfSHTMm : DDYFFIKLYGHFLKKE-CKI--LRIN YCLEQNIENNVSNDIMQNL YNINIINKNRN-E : 166
      #   ##&                                     #

          *           240           *           260           *           280
arabidC : IDYDQLEKSAVLEFRPKLI VAGASAYARLYDYARIRKVCN-KQK-----AVMLADMAH : 252
peaM : IDYDQLEKSATLEFRPKLI VAGASAYARLYDYARIRKVCD-KQK-----AVLLADMAH : 261
humanC : INYDQLEENARLEFRPKLI IAGTSCYSRNLEYARLRKIAD-ENG-----AYLMADMAH : 231
humanM : IDYNQLALTARLEFRPLI IAGTSAYARLI DYARMREVCD-EVK-----AHLADMAH : 254
yeastC : IDYDTLEKNAILYRPKVLVAGTSAYCRLIDYKRMREIAD-KCG-----AYLMVDMAH : 222
yeastM : IDYDNLQVLAKAFRPKVI VAGTSAYSRLIDYARFKEISQ-GCG-----AYLMSDMAH : 239
PfSHMTc : VDMESVRNLALSFQPKVII CGYTSYPRDIDYKGFREICD-EVN-----AYLFADISH : 211
PfSHTMm : PNYDEIQKISNDENPDII YFDESNNPYNI DYDRFIKGLKNKNKNIHNKPIIITNMNN : 223
                                     &                                     (#) #

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Supp. Fig. 2 part (i)

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      *           300           *           320           *           340
arabidC : ISGLVAAGVIPSPFEYADVTTTTHKSLRGPRGAMIFFRKGLKEIN-KQGKEVMYDY : 308
peaM    : ISGLVAAGVIPSPFDYADVTTTTHKSLRGPRGAMIFFRKGLKEVN-KQGKEVFYDY : 317
humanC  : ISGLVAAGVVPSPFEHCHVTTTTHKTLRGCRAGMIFYRKGVKSVDPKTGKEILYNL : 288
humanM  : ISGLVAAKVIPSPFKHADIVTTTTHKTLRGARGLIFYRKGVKAVDPKTGREIPYTF : 311
yeastC  : ISGLIAAGVIPSPFEYADIVTTTTHKSLRGPRGAMIFFRRGVRSINPKTGKEVLYDL : 279
yeastM  : ISGLVAANVVPSPFEHSDIVTTTTHKSLRGPRGAMIFFRKGIKSWTKK-GKEIPYEL : 295
PfSHMTc : ISSFVACNLLNPNFTYADVTTTTHKILRGPRSALIFFNK-----K--RNP--GI : 257
PfSHTMm : KANLISQNLINSPFTHSDIVFTYFNENFRAHNSFVIFYKKGYKCVNTD-GHIIEYDY : 279
      #   ##

      *           360           *           380           *           400
arabidC : EDRINQAVFPGLQGGPHNHTITGLAVALKQARTPEYKAYQDOVLRNCSKFAELDIRP : 365
peaM    : EDKINQAVFPGLQGGPHNHTITGLAVALKQATTPEYRAYQEOVLSNSSKFAK----- : 369
humanC  : ESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTLEFKVYQHVVANCRALSE----- : 340
humanM  : EDRINFVFPGLQGGPHNHAIAAVAVALKQACTPMFREYSLOVLKNARAMAD----- : 363
yeastC  : ENPINFSVFPGLQGGPHNHTIAALATAKQAAATPEFKEYQTQVLKNAKALES----- : 331
yeastM  : EKKINFSVFPGLQGGPHNHTIGAMAVALKQAMSPEFKEYQQKIVDNSKWFAQ----- : 347
PfSHMTc : DQKINSSVFPGLQGGPHNKKIAAVACQLKEVNTPEFFKEYTKQVLLNSKALAE----- : 309
PfSHTMm : EKKLKY-AEDDIYL---NNIFFSFTSFKLMKNEEFKEYVKQIKENTYILYK----- : 327
      #

      0           *           420           *           440           *
arabidC : TVIIISYGLSMQTL LAKGYDLVSGGTDNHLVIVNLKNKGIDGSRVEKVLELVHIAANK : 422
peaM    : -ALS-----EKG YDLVSGGTE NHLVIVNLKNKGIDGSRVEKVLELVHIAANK : 415
humanC  : -ALT-----ELG YKIVTGGSDNHLIIVDLRSKGT DGGRAEKVLEACSIACNK : 386
humanM  : -ALL-----ERG YSLVSGGTDNHLVIVDLRPKGLDGARAEKVLELV SITANK : 409
yeastC  : -EFK-----NLG YRLVSNGTDSH MVIVSLREKGV D GARVEYICEKINIALNK : 377
yeastM  : -ELT-----KMG YKLVSGGTDNHLVIVDLSGTQVDGARVETILSALNIAANK : 393
PfSHMTc : -CLL-----KRNL D LVTNGTDNHLIIVDLRKYNITGSKLQETCNAI NIALNK : 355
PfSHTMm : --YI-----NRKY FHIQYSQNN SFFNLN P SSCTFNIQEFYLLCNKLNIYFD- : 371

      460           *           480           *           500           *
arabidC : NTVPGDVSAMVPGGIRMGTPALTSRGFI EDEFAKVAEYFDLAVKIALKIKAESQGIY : 479
peaM    : NTVPGDVSAMVPGGIRMGTPALTSRGFVE EDFVKVAEYFDAAVSLALKVKAES---- : 468
humanC  : NTCPGDRSALRPSGLRLGTPALTSRG LLEKDFQKVAFIHRGIELTLQIQSDTG--- : 440
humanM  : NTCPGDRSAITPGGLRLGAPALTSRQFR EDDFRRVVD FIDEGVNI GLEVKSKT--- : 462
yeastC  : NSIPGDKSALVPGGVRIGAPAMTTRGMGE EDFHRIVQYINKAVEFAQQVQQSLP--- : 431
yeastM  : NTIPGDKSALFPSGLRIGTPAMTTRGFGREEFSQVAKYIDS AVKLAENLKTLEPTT- : 449
PfSHMTc : NTIPSDVDCVSPSGIRIGTPALTTRGCKE KDMEFIADMLLKAILLTDELQQKYG--- : 409
PfSHTMm : --ILKDKSSNQKS-FNIGTNNLTS LGLLTHDIKNVAEFFNESVVLIFYLKEKSK--- : 422
      #           #

      520           *           540           *           560
arabidC : KKSFGTKLKDE VATMQSNEKLQSEMSK LREMVEEYAKQFPTIGFEKETMRYKE- : 532
peaM    : K---G TKLKDEVEALQTSSYVQSEISK LHDVEEFAKQFPTIGFEKATMKYNK- : 518
humanC  : ---VRATLKEFKERLAGD-KYQA AVQALREEVESFASLEPLPGLPDF----- : 483
humanM  : -----AKLQDFKSFL LK DSETSQRLANLRQRVEQFARAFPM PGFDEH----- : 504
yeastC  : --KDACRLKDFKAKVDEG---SDVLNTW KKEIYDWAGEYPLAV----- : 469
yeastM  : KLDARSRLNEFKKLCNES---S-EVAALSGEISKWVGQYPVPGDI----- : 490
PfSHMTc : -----KKLVDFKKGLVNN---PKIDELKKEVVQWAKNLPFA----- : 442
PfSHTMm : -----LTNMSFIQYIEDN-SSASDIYS LAVDISSFISSYPSPYTNE----- : 462

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Supp. Fig. 2 part (ii)

Supplementary Figure 2 – Sequence alignments of the PfSHMT isoforms.

Alignment of PfSHMTc and PfSHMTm with cytoplasmic (C) and mitochondrial (M) SHMTs from other organisms, showing the absence in PfSHMTm of most of the highly conserved residues associated with the active site {Franca, 2005 #1015}. Ampersands (&) under the sequences indicate such residues that are conserved in PfSHMTm (4 in total), hashes (#) indicate such residues that are not conserved in PfSHMTc (16 in total) and ((#)) indicates the one conservative replacement.