

### Figure S2: Alignment of the synthetic stabilized human *ATP7A* cDNA sequence

(Synth\_hATP7A) with the native *ATP7A* cDNA sequence (hATP7A). Only the altered bases in the synthetic sequence are shown. Alignments were generated using MUltiple Sequence Comparison by Log Expectation software (<http://www.ebi.ac.uk/Tools/msa/muscle/>) with output using Boxshade software ([http://embnet.vital-it.ch/software/BOX\\_form.html](http://embnet.vital-it.ch/software/BOX_form.html)).

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hATP7A          1 ATGGATCCAAGTATGGGTGTGAATTCTGTTACCATTTCTGTTGAGGGTATGACTTGCAAT
Synth_hATP7A    1 .....C..TTCA.....A.....CAGC..C..T..CAGC..C..A..A.....C.....C

hATP7A          61 TCCTGTGTTTGGACCATTGAGCAGCAGATTGAAAAGTGAATGGTGTGCATCACATTAAG
Synth_hATP7A    61 AGT..C..G.....T..C..A..A..A..C..T..G..C..C..A..A..C..T..C..A

hATP7A          121 GTATCACTGGAAGAAAAAATGCAACTATTATTTATGACCCTAAACTACAGACTCCAAG
Synth_hATP7A    121 ..CAGTT...G..G..G..C..C..A..C..C..C..T..A..GT..G..A..C..T..A

hATP7A          181 ACCCTACAGGAAGCTATTGATGACATGGGCTTTGATGCTGTTATCCATAATCCTGACCCT
Synth_hATP7A    181 ..AT...A..G..A..C..C..T.....A..C..C..A..C..A..C..C..A..T..A

hATP7A          241 CTCCCTGTTTTAACTGACACCTTGTCTGACTGTTACGGCGTCACTGACTTTGCCATGG
Synth_hATP7A    241 T.G..A..AC.C..A.....AC....C.....A..A..A..AAGC.....AC.....

hATP7A          301 GACCATATCCAAAGCACATTGCTGAAGACCAAGGGTGTGACAGACATTAATAATTTACCT
Synth_hATP7A    301 ..T..C..A..G.....TC.....A..A..A..C..T.....C..G..C.....A

hATP7A          361 CAGAAAAGAAGTGTAGCAGTGACAATAATCCCTTCTATAGTGAATGCCAATCAGATAAAA
Synth_hATP7A    361 .....GC.T..A..G.....A..C..C.....AAGC..C..A..C..A..C..A..C..G

hATP7A          421 GAGCTGGTTCCAGAAGTCAAGTTTAGATACTGGGACACTGGAGAAAAAGTCAGGAGCTTGT
Synth_hATP7A    421 ..A.....A.....G..GTCAC....C..C..A..C..A.....G...AGC..G..A..C

hATP7A          481 GAAGATCATAGTATGGCTCAAGCTGGTGAAGTCGTGCTGAAGATGAAAGTGGAAAGGGATG
Synth_hATP7A    481 ..G.....CTCA.....C..G.....G..G..C.....G..C.....A...

hATP7A          541 ACCTGCCATTTCATGTACTAGCACTATTGAAGGAAAAATTGGGAAACTGCAAGGTGTTTCAG
Synth_hATP7A    541 ..A..T..CAGC..C..ATCA..A..A..G..G..G..A..A..GT...G..A..G..A

hATP7A          601 CGAATTAAGTCTCCCTGGACAATCAAGAAGCTACTATTGTTTATCAACCTCATCTTATC
Synth_hATP7A    601 A.G..C..G..AAG.....T..C..G..G..A..G..A..C..C..G..A..C..G..A

hATP7A          661 TCAGTAGAGGAAATGAAAAGCAGATTGAAGCTATGGGCTTTCCAGCATTTGTCAAAAAG
Synth_hATP7A    661 AGC..T..A..G.....G..A.....C..G..A.....T..C..T.....C..G..G..A

hATP7A          721 CAGCCCAAGTACCTCAAATTGGGAGCTATTGATGTAGAACGTCTAAAGAACACACCAGTT
Synth_hATP7A    721 ..A.....T.G..GC....C..G..A..C..T..GA..AT.....C..T..A

hATP7A          781 AAATCCTCAGAAGGGTCCACAGCAAAGGAGTCCATCATATACCAATGATTCAACAGCCACT
Synth_hATP7A    781 ..GAGTAGC..G..AAGC..A..GC..TCA..TAGT..C..A..C..CAGC..T..A..A
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hATP7A 841 TTCATCATTGATGGCATGCATTGTAAATCATGTGTGTCAAATATTGAAAGTACTTTATCT  
Synth\_hATP7A 841 .....C..A....C..C..GAGC..C..AAGT..C..A..GTCA..AC..AGC

hATP7A 901 GCACTCCAATATGTAAGCAGCATAGTAGTTTCTTTAGAGAATAGGTCTGCCATTGTGAAG  
Synth\_hATP7A 901 ..TT.G..G..C..GTCATC...T..G..GAGCC...A..CC..AGC..G..A..C...

hATP7A 961 TATAATGCAAGCTCAGTCACTCCAGAATCCCTGAGAAAAGCAATAGAGGCTGTATCACCG  
Synth\_hATP7A 961 ..C..C..TTCAAGT..G..A..T..GAGTT..C...G..T..T..A..A..TAGT..A

hATP7A 1021 GGGCTATATAGAGTTAGTATCACAAGTGAAGTTGAGAGTACCTCAAACCTCCCTCCAGC  
Synth\_hATP7A 1021 ..A..G..CC...CTCA....CTCA..G..G..ATCA..T..C..TAGC..G..ATCT

hATP7A 1081 TCATCTCTTCAGAAGATTCCTTTGAATGTAGTTAGCCAGCCTCTGACACAAGAACTGTG  
Synth\_hATP7A 1081 AGT..CT.G..A....A..AC....C..T..ATCA..A..A....T..G..G..A..C

hATP7A 1141 ATAAACATTGATGGCATGACTTGTAATTCCTGTGTGCAGTCTATTGAGGGTGTTCATATCA  
Synth\_hATP7A 1141 ..C.....C..C..G.....A..C..CAG...C..A..AAGC..A..A..A..G..T..C

hATP7A 1201 AAAAAGCCAGGTGTAATCCATACGAGTCTCCCTTGCAAATAGCAATGGGACTGTTGAG  
Synth\_hATP7A 1201 ..G..A..G..A..G..GAG...TA...GAGTT.G..T..CTC...C..A..A..G..A

hATP7A 1261 TATGATCCTCTACTAACCTCTCCAGAAACGTTGAGAGGAGCAATAGAAGACATGGGATTT  
Synth\_hATP7A 1261 ..C..C..AT....G..AAGC..G..G..AC..C....C..T..C..G..T.....T..C

hATP7A 1321 GATGCTACCTTGTCAGACACGAATGAGCCGTTGGTAGTAATAGCTCAGCCTTCATCGGAA  
Synth\_hATP7A 1321 ..C..A..AC..AGT..T..A..C..A..AC....G..G..T..A..A..AAGTAGC..G

hATP7A 1381 ATGCCGCTTTTGACTTCAACTAATGAATTTTATACTAAAGGGATGACACCAGTTCAAGAC  
Synth\_hATP7A 1381 .....AT.GC...AAGT..A..C..G..C..C..A..G..C.....C..G..G..G..T

hATP7A 1441 AAGGAGGAAGGAAAGAATTCATCTAAGTGTACATACAGGTCCTGGCATGACTTGCGCT  
Synth\_hATP7A 1441 ..A..A..G..T..A..C...AG...A..C.....C..A..G..A..A....A..T..A

hATP7A 1501 TCCTGTGTAGCAAACATTGAACGGAATTTAAGGCGGGAAGAAGGAATATATTCTATACTT  
Synth\_hATP7A 1501 AGT..C..G..G.....C..GA....CC..C.AA.A..G..G..T..C..CAG...T..G

hATP7A 1561 GTGGCCCTGATGGCTGGCAAGGCAGAAGTAAGGTATAATCCTGCTGTTATACAACCCCA  
Synth\_hATP7A 1561 ..T..TT.....A....A..T..G..GC....C..C..A..A..G..C..G..A..G

hATP7A 1621 ATGATAGCAGAGTTCATCCGAGAACTTGGATTTGGAGCCACTGTGATAGAAAATGCTGAT  
Synth\_hATP7A 1621 .....C..T.....A.G..G..G..G..C..T..A..C.....C..G..C..C..C

hATP7A 1681 GAAGGAGATGGTGTGTTTGGAACTTGTGAGGGGAATGACGTGTGCCTCCTGCGTACAT  
Synth\_hATP7A 1681 ..G..G..C..A..GC.A..G..A..G..AC.T..G.....C..C..A..G.....C

hATP7A 1741 AAAATAGAGTCTAGTCTCACAAAACACAGAGGGATCCTATACTGCTCCGTGGCCCTGGCA  
Synth\_hATP7A 1741 ..G..C...AG.TCGT.A....G..TC....C.....G.....AGT..A..TT....C

hATP7A 1801 ACCAACAAAGCACATATTAATATGACCCAGAAATTATTGGTCTAGAGATATTATCCAT  
Synth\_hATP7A 1801 ..G.....G..T..C..C..G..C..T..T..G..C..C..A..AC.T..C..C.....C

hATP7A 1861 ACAATTGAAAGCTTAGGTTTTGAAGCTTCTTTGGTCAAGAAGGATCGGTCAGCAAGTCAC

Synth\_hATP7A 1861 ..C..C..GTCAC...C..C.....CAG.C.A..G.....CA.AAGT..TTCA..T  
 hATP7A 1921 TTAGATCATAAACGAGAAATAAGACAATGGAGACGGTCTTTTCTTGTGAGTCTGTTTTTC  
 Synth\_hATP7A 1921 C.C..C..C..GA.G..G..TC.G..G...C....AGC..CT.G..CTCAT...C...  
 hATP7A 1981 TGTATTCTCTGTAATGGGGCTGATGATATATATGATGGTTATGGACCACCACCTTTGCAACT  
 Synth\_hATP7A 1981 ..C..A..G..C.....T.....C..C.....G.....T....C..T..A  
 hATP7A 2041 CTTACACATAATCAAACATGAGTAAAGAAGAAATGATCAACCTTCATTCTTCTATGTTC  
 Synth\_hATP7A 2041 ..A..T..C..C..G.....TCA..G..G..G.....G..CAG...G.....T  
 hATP7A 2101 CTGGAGCGCCAGATTCTTCCAGGATTGTCTGTTATGAATTTGCTGTCTTTTTATTGTGT  
 Synth\_hATP7A 2101 ..C...A.A....C..G.....TC.AAG...G....CC....T....CC..C....C  
 hATP7A 2161 GTACCTGTACAGTTTTTCGGAGGCTGGTACTTCTACATTCAGGCTTATAAAGCACTGAAG  
 Synth\_hATP7A 2161 .....G.....A..C..T..C..A.....C..A..A..C..G..CT....A  
 hATP7A 2221 CATAAGACAGCAAATATGGACGTACTGATTGTGCTGGCAACCACCATTGCATTTGCCCTAC  
 Synth\_hATP7A 2221 ..C..A..C..T..C.....T..GT...C..A....C..A..A..C..C..C..A...  
 hATP7A 2281 TCTTTGATTATTCTTCTAGTTGCAATGTATGAGAGAGCCAAAGTGAACCCTATTACTTTC  
 Synth\_hATP7A 2281 AG.C....C..CT.G....G.....C..AC....A..G..C....A..A..C...  
 hATP7A 2341 TTTGACACACCCCCTATGCTGTTTGTGTTTATTGCACTAGGCCGATGGCTGGAACATATA  
 Synth\_hATP7A 2341 ..C..T..T..A..A.....C.....C..A..C..G..GA.G...T....G..C..C  
 hATP7A 2401 GCAAAGGGCAAACATCAGAGGCTCTTGCAAAGTTAATTTCACTACAAGCTACAGAAGCA  
 Synth\_hATP7A 2401 .....A..G..CAGT..A..A..G..T...C.G..CAGTT.G..G..A..C..G..C  
 hATP7A 2461 ACTATTGTAACTCTTGATTCTGATAATATCCTCCTCAGTGAAGAACAAGTGGATGTGGAA  
 Synth\_hATP7A 2461 ..A..A..G..C..A..CAG...C..C.....G..GTCA..G..G..G..A..C..A..G  
 hATP7A 2521 CTTGTACAACGTGGAGATATCATTAAAGTAGTTCCAGGAGGCAAATTTCCAGTGGATGGT  
 Synth\_hATP7A 2521 ..G..G..GA.A..C..C.....C..G..G..G..G.....A..G..C..T..A..C..A  
 hATP7A 2581 CGTGTATTGAAGGACATTCTATGGTAGATGAGTCCCTCATCACAGGGGAGGCAATGCCT  
 Synth\_hATP7A 2581 A.A..G..C..G..T..CAGC.....C..C..AAGT..G.....T..A.....  
 hATP7A 2641 GTGGCTAAGAAACCTGGCAGCACAGTGATTGCTGGTTCCATTAACCAGAACGGGTCCTG  
 Synth\_hATP7A 2641 .....C..A..G..A..ATC...T..C..C..C..CAG...C.....A....AAGT..C  
 hATP7A 2701 CTTATCTGCGCAACACATGTTGGAGCAGACACAACCCTTTCTCAAATTGTCAAACCTTGTG  
 Synth\_hATP7A 2701 ..G.....T..T..T....A.....T..T..C..TT.GAG...G..C.....GT.G...  
 hATP7A 2761 GAAGAGGCACAAACATCAAAGGCTCCTATCCAGCAGTTTGCAGACAAACTCAGTGGCTAT  
 Synth\_hATP7A 2761 .....A..T....CAGC..A..G..A.....A.....C..C.....G..GTCA..A..C  
 hATP7A 2821 TTTGTTCTTTTATTGTTTTTGTTCATTGCCACCCTCTGGTATGGATTGTAATTGGA  
 Synth\_hATP7A 2821 ..C..A..A..C..C..G..C..GAG...A..A..AT.GC.A..G.....C..G..A..C  
 hATP7A 2881 TTTCTGAATTTGAAATTGTGGAAACCTACTTTCCTGGCTACAATAGAAGTATCTCCCGA  
 Synth\_hATP7A 2881 ..CT....C.....C..A..G..A.....C..A..A.....CC..TCG....G...

hATP7A 2941 ACAGAAACGATAATACGATTTGCTTTCCAAGCCTCTATCACAGTTCTGTGTATTGCATGT  
Synth\_hATP7A 2941 ..C..G..A..C..CA.G..C.....G..T..C..A..C..GT....C..C..C...

hATP7A 3001 CCCTGTTCACTGGGACTGGCCACTCCAAGTCTGTGTATGGTGGGTACAGGAGTAGGTGCT  
Synth\_hATP7A 3001 .....AGTT....CT....T..C..C..A..A..C.....A..C..T..C..G..A..A

hATP7A 3061 CAAAATGGCATACTAATAAAAGGTGGAGAGCCATTGGAGATGGCTCATAAGGTAAAGGTA  
Synth\_hATP7A 3061 ..G..C..A..C..G..C..G..C..T..A..TC.....A..C..A..G..A..G

hATP7A 3121 GTGGTATTTGATAAGACTGGAACCATTACTCACGGAACCCAGTGGTGAATCAAGTAAAG  
Synth\_hATP7A 3121 ..A..G..C.....C.....T..C..A..C..A..A..C..G..G..A

hATP7A 3181 GTTCTAACTGAAAGTAACAGAATATCACACCATAAAATCTTGGCCATTGTGGGAACTGCT  
Synth\_hATP7A 3181 ..G..G..A..GTCA..TC.G..CAGT..T..C..G..AC....G..A..A..C..A..C

hATP7A 3241 GAAAGTAACAGTGAACACCCTCTAGGAACAGCCATAACCAAATATTGCAAACAGGAGCTG  
Synth\_hATP7A 3241 ..GTCA..T..C..G..T..AT....C..C..T..C..T..G..C..T..G..A..AT..

hATP7A 3301 GACACTGAAACCTTGGGTACCTGCATAGATTTCCAGGTTGTGCCAGGCTGTGGTATTAGC  
Synth\_hATP7A 3301 ..T..C..G..AC....A..A.....C..C..T..A..G..T..T..A..C..A.CATCA

hATP7A 3361 TGTAAGTCAACCAATATTGAAGGCTTGCTACATAAGAATAACTGGAATATAGAGGACAAT  
Synth\_hATP7A 3361 ..C..G..G..A..C..A..G..AC.CT....C.....C..T.....C..C..A.....C

hATP7A 3421 AATATTAATAAATGCATCCCTGGTTCAAATTGATGCCAGTAATGAACAGTCATCAACTTCG  
Synth\_hATP7A 3421 ..C..C..G..C..TAGTT....G..G..A..C..ATCA..C..G..AAGTAGT..AAGT

hATP7A 3481 TCTTCCATGATTATTGATGCCAGATCTCAAATGCTCTTAATGCTCAGCAGTATAAAGTC  
Synth\_hATP7A 3481 AG.AGT....C..C..C..A..A..TAGC..C..CT.G..C..C..A..A..C..G..G

hATP7A 3541 CTCATTGGTAACCGGGAGTGGATGATTAGAAATGGTCTTGTTCATTAATAACGATGTAAT  
Synth\_hATP7A 3541 T.G..A..G..TA....A.....CC....C..AT.G..G..C..C..T..C..G..C

hATP7A 3601 GATTTTCATGACTGAACATGAGAGAAAAGGTCGGACTGCTGTATTAGTAGCAGTTGATGAT  
Synth\_hATP7A 3601 ..C.....A..G..C..AC....G..AA.A..A..C..GC.G..G..C..G..C..C

hATP7A 3661 GAGCTGTGTGGCTTGATAGCCATTGCAGACACAGTGAAGCCTGAAGCAGAAGTGGCTATC  
Synth\_hATP7A 3661 ..AT....C..AC....C..G..C.....T..C.....A..A..G..T..GT....C..A

hATP7A 3721 CATATTCTGAAATCTATGGGCTTAGAAGTAGTTCTGATGACTGGAGACAACAGTAAAACA  
Synth\_hATP7A 3721 ..C..CT....GAG.....AC....G..G..GT.....A..T..T...TCA..G..C

hATP7A 3781 GCTAGATCTATTGCTTCTCAGGTTGGCATTACTAAGGTGTTTGTGTAAGTTCTACCTTCT  
Synth\_hATP7A 3781 ..AC....G..A..CAG...A..G..A..C..A..A..C..C..A..G..GT.G..AAG.

hATP7A 3841 CACAAGGTTGCTAAAGTGAAGCAACTTCAAGAGGAGGGGAAACGGGTAGCAATGGTGGGA  
Synth\_hATP7A 3841 ..T..A..G..A..G..T..A..GT.G..G..A..A..A..GA....G..G.....C...

hATP7A 3901 GATGGAATCAATGACTCCCCAGCTCTGGCAATGGCTAATGTGGGAATTGCTATTGGCACA  
Synth\_hATP7A 3901 .....AGT..C..AT....C.....A..C..C..T..C..A..C..T..T

hATP7A 3961 GGCACAGATGTAGCCATTGAAGCAGCTGATGTGGTTTTGATAAGGAATGATCTTCTGGAT  
Synth\_hATP7A 3961 ..A..C..C..G..A..A..G..C..A..C..A..AC....CC....C..CT.GT....C

hATP7A 4021 GTAGTGGCAAGTATTGACTTATCAAGAGAGACAGTCAAGAGGATTCGGATAAAATTTTGTC  
Synth\_hATP7A 4021 ..G..A..CTCA..A..TC.GAGTC....A..C..G..AC....CA....C..C..G

hATP7A 4081 TTTGCTCTAATTTATAATCTGGTTGGAATTCATAGCTGCTGGAGTTTTTATGCCATT  
Synth\_hATP7A 4081 ..C..AT.G..C..C..CT....G....C..A..C..C..C..T..G..C....A..A

hATP7A 4141 GGTTTGGTTTTGCAGCCCTGGATGGGATCTGCAGCAATGGCTGCTTCATCTGTTTCTGTA  
Synth\_hATP7A 4141 ..AC....GC....A..A.....TAG...T.....A..AAGTAG...GAG...G

hATP7A 4201 GTACTTTCTTCTCTCTTCTTAACTTTACAGGAAACCAACTTACGAGAGTTATGAACTG  
Synth\_hATP7A 4201 ..GT.GAG.AG.T.G....G..GT.G...C....G..T..C....ATCA..C..GT..

hATP7A 4261 CCTGCCCGGAGCCAGATAGGACAGAAGAGTCCTTCAGAAATCAGCGTTCATGTTGGAATA  
Synth\_hATP7A 4261 ..A..AA..TCA..A..C..T..A..ATCA..CAGT..G..TTCA..G..C..G..C..C

hATP7A 4321 GATGATACCTCAAGGAATTCTCCTAAACTGGGTTTGCTGGACCGGATTGTTAATTATAGC  
Synth\_hATP7A 4321 ..C..C..T..TC.....A..GT....AC..T....TA....C..G..C..CTCA

hATP7A 4381 AGAGCCTCTATAAACTCACTACTGTCTGATAAACGCTCCCTAACAGTGTTGTTACCAGT  
Synth\_hATP7A 4381 C....T..A..C...AGTT.GT..AG...C..GA.GAGTT.G...TCC..G..G..ATCA

hATP7A 4441 GAACCTGACAAGCACTCACTCCTGGTGGGAGACTTCAGGGAAGATGATGACACTGCATTA  
Synth\_hATP7A 4441 ..G..A..T..A..TAGTT.GT....A..T..T...C....G..C..C..T..A..TC.G

hATP7A 4501 TAA  
Synth\_hATP7A 4501 ..G