```
Hsap ABCD1 aligned with Dmel cg2316:

Dmel cg2316   1    MS-VLSKYVDRIAEKCEHNGFTKHAFSYALVTSAILALTIKVTIPYVKNVNTTSSVRTQKGKTNGQLSPSTRDSSEEDFK   79
Hsap ABCD1    1    MTHMLNAAADRV--KWTRSSAAKRA---ACLVAAAYAL--KTLYPIIGKRLKQSG----HGKKKAAAYPAAENT------   63

Dmel cg2316   80   LAEAEKLLVAQQLKKKATNNLVEPGLNKEFLKHLQMLAKIMIPQAFCYETGLLSVHTFCLISRTFLSIYVAALEGALVKF   159
Hsap ABCD1    64   ----EILHCTETICEKPS-----PGVNADFFKQLLELRKILFPKLVTTETGWLCLHSVALISRTFLSIYVAGLDGKIVKS   134

Dmel cg2316   160  IVRKDIKQFALVLLKWFGIAIPATFVNSMIRFLESKLSLAFRTRLVRHSYRLYFKNQNYYRVSNLDGRIENADHRLTEDI   239
Hsap ABCD1    135  IVEKKPRTFIIKLIKWLMIAIPATFVNSAIRYLECKLALAFRTRLVDHAYETYFTNQTYYKVINMDGRLANPDQSLTEDI   214

Dmel cg2316   240  SVFANSVAHLYSSLTKPCFDLMLIGLALMRSSKKMKANIITGPALSIGVIALTAHILRIVSPKFGQLVSEEANRYGYLRH   319
Hsap ABCD1    215  MMFSQSVAHLYSNLTKPILDVMLTSYTLIQTATSRGASPIGPTLLAGLVVYATAKVLKACSPKFGKLVAEEAHRKGYLRY   294

Dmel cg2316   320  IHSRIITNAEEIAFYGGHKVEMQQLRQAYNRLVNQMTTIFNQKLWFIMLEQFFMKYVWSGTGMIMVSLPILTGSDVGLGT   399
Hsap ABCD1    295  VHSRIIANVEEIAFYRGHKVEMKQLQKSYKALADQMNLILSKRLWYIMIEQFLMKYVWSSSGLIMVAIPIITATGFADG-   373

Dmel cg2316   400  VPNTAISESRVSERTQYLTTARNLLISAADAIERLMSSYKEIVSLAGYTFRVAGMMDVFEETALGVYCKTSVM---ESNQ   476
Hsap ABCD1    374  --EDGQKQVMVSERTEAFTTARNLLASGADAIERIMSSYKEVTELAGYTARVYNMFWFVFDEVKRGIYKRTAVIQESESHS   451

Dmel cg2316   477  SNGI-IEFRNGKPIA-KGRIIYSDDPKNMSISLRAVPVVTPNCDIVVPKLTLCIEPGVHLLITGPNGCGKSSLFRILSGL   554
Hsap ABCD1    452  KNGAKVELPLSDTLAIKGKVIDVDH----GIICENVPIITPAGEVVASRLNFKVEEGMHLLITGPNGCGKSSLFRILSGL   527

Dmel cg2316   555  WPIYAGELHIPRPVKDVPCMFYIPQRPYMSIGSLCDQIIYPDTREDMKRKHITENELRSILKMVSLEHIAQRDS-FDVVR   633
Hsap ABCD1    528  WPVYEGVLYKPPPQH----MFYIPQRPYMSLGSLRDQVIYPDSVDDMHDKGYTDQDLERILHNVHLYHIVQREGGWDAVM   603

Dmel cg2316   634  DWKDILSGGEKQRMAIARLFYHRPRYALLDECTSAVSIDVESSIYEIAKGMGITLLTITHRPTLWKYHTHILEFDGLGNW   713
Hsap ABCD1    604  DWKDVLSGGEKQRMGMARMFYHKPKYALLDECTSAVSIDVEGKIFQAAKGAGISLLSITHRPSLWKYHTHLLQFDGEGGW   683

Dmel cg2316   714  QFRKMN-------SDEEQK-----------GQFLS---------------------   730
Hsap ABCD1    684  RFEQLDTAIRLTLSEEKQKLESQLAGIPKMQQRLNELCKILGEDSVLKTIKNEDETS   740


RED = identical residues
BLUE = conserved residues
```

Figure S1. Amino acid alignment of human ABCD1 and Drosophila CG2316 shows high levels of conservation. Sequences were aligned using COBALT software through NCBI.

```
Dmel cg2781 aligned with Hsap ELOVL7, ELOVL1, and ELOVL4:

Dmel cg27811    MDYLTM-----------------FYDGWRDLMDnkSDPRTRDYPLMSSPF--PTIAISLTYaYIVKVLGPKLMENRKPF    60
Hsap ELOVL71    MAFSD------------LTSRTVHLYDNWI--KD--ADPRVEDWLLMSSPL-PQTILLGFYV-YFVTSLGPKLMENRKPF    62
Hsap ELOVL11    M-----------------EAVVNLYQEVM--KH--ADPRIQGYPLMGSPLlMTSILLT-YV-YFVLSLGPRIMANRKPF    56
Hsap ELOVL41    MGLLDSepgsvlnvvstALNDTVEFYRWTWSI----ADKRVENWPLMQSPW--PTLSISTLY-LLFVWLGPKWMKDREPF    73

Dmel cg278161   ELRKVLIVYNAAQVIFSAWLFYESCIGGWLNGYNLRCEPVNYSYSPKAIRTAEGCWWYYFSKFTEFFDTFFFVMRKRYDQ   140
Hsap ELOVL763   ELKKAMITYNFFIVLFSVYMCYEFVMSGWGIGYSFRCDIVDYSRSPTALRMARTCWLYYFSKFIELLDTIFFVLRKKNSQ   142
Hsap ELOVL157   QLRGFMIVYNFSLVALSLHIVYEFLMSGWLSTYTWRCDPVDYSNSPEALRMVRVAWLFLFSKFIELMDTVIFILRKKDGQ   136
Hsap ELOVL474   QMRLVLIIYNFGMVLLNLFIFRELFMGSYNAGYSYICQSVDYSNNVHEVRIAAALWWYFVSKGVEYLDTVFFILRKKNNQ   153

Dmel cg2781141  VSTLHVIHHGIMPVSVWWGVKFTPGGHSTFFGFLNTFVHIFMYAYYMLAAMGPKVQKYLWWKKYLTVMQMIQFVLVMVHS   220
Hsap ELOVL7143  VTFLHVFHHTIMPWTWWFGVKFAAGGLGTFHALLNTAVHVVMYSYYGLSALGPAYQKYLWWKKYLTSLQLVQFVIVAIHI   222
Hsap ELOVL1137  VTFLHVFHHSVLPWSWWWGVKIAPGGMGSFHAMINSSVHVIMYLYYGLSAFGPVAQPYLWWKKHMTAIQLIQFVLVSLHI   216
Hsap ELOVL4154  VSFLHVYHHCTMFTLWWIGIKWVAGGQAFFGAQLNSFIHVIMYSYYGLTAFGPWIQKYLWWKRYLTMLQLIQFHVTIGHT   233

Dmel cg2781221  FQLFFKNDCNYPI-GFAYFIGAHAVMFYFLFSNFYKRAYV--KRDGKDKASVKANGhANGHVKALKDGDVA---PTSNGQ   294
Hsap ELOVL7223  SQFFFMEDCKYQFPVFACIIMSYSFMFPLLFLHFWYRAYT--KGQRLPKT-VKN-----GTCKNKDN-------------   281
Hsap ELOVL1217  SQYYFMSSCNYQYPVIIHLIWMYGTIFFMLFSNFWYHSYT--KGKRLPRA-LQQNG-APGIAKVKAN-------------   279
Hsap ELOVL4234  ALSLY-TDCPFPK-WMHWALIAYAISFIFLFLNFYIRTYKepKKPKAGKTAMNGIS-ANGVSKSEKQLMIEngkKQKNGK   310

Dmel cg2781295  ANGFhntfskfttdmcnpalnsstrqrvlvnagnk    329
Hsap ELOVL7       ---------------------------------
Hsap ELOVL1       ---------------------------------
Hsap ELOVL4311  AKGD-----------------------------    314
```

RED = identical residues
BLUE = conserved residues

Figure S2. Amino acid alignments of *Drosophila* elongase CG2781 and three human elongases (ELOVL1,4,and 7). Sequences were aligned using COBALT software through NCBI.