

Figure 1. Multiple sequence alignment of the deduced amino acid sequences of Atf1, Atf2, Atf8, AtfA, and tDGAT from *Arabidopsis thaliana*. The alignment is shown in blocks of 100 residues, with positions 1 to 470 indicated at the top. Conserved regions are highlighted with red and blue boxes. Arrows indicate the positions of the stop codons in the tDGAT sequence. The sequences are as follows:

Atf1: MTDVSTTNQRYMTQTD FMSWRMEEDPILRSTIVAVALLDRSPD...QSRFVDMRRAVDLVPLFRRTAIEAPMGFAPPRWADDHDFDLWSHLRRRYTLP
Atf2:MPVTDSDIFLLGESREHPMHVGSLELFTTPEADAGPDYVKSMHETLLKHTD...VDPTFRKKPAGPVGSLGNLWWDDESDDVDLEYHVRHSAALPA
Atf8:MPLPMSPPLDSMFLFLLGESREHPMHVGGVEIFQLPEGADTYDMRAMLDRLALADGDGIVTPRLAKRAHRSFSTLGQWSWETVDIDLDLGHHIRHDAALPA
AtfA:MRPLHSPIDFIFLLSLERKQQLPMHVGGGLFQIPDNADPTFYIQDLVNDIRISKSIPVPPFNKK.....LNGLFWDDEDEEDLDLGHHRHIALPA
tDGAT:MRQLTAVDANFLNVETGTTAAHIIAGLGLILDPVACPGGRLTAEDLIEVIRERAHLPAPRLMRRLAAVPLGLIDRPYWEDDPDFDPAHVFEVGLPAL

Atf1: PRTWDGVLDFARTAEMTAFDKRRPLWEFTVLDGLHDSGRSALVLMKVHHSLT DGVSGMQIAREIVDFTRDGGPRPDRTDHRTAA PNGESPTPPGRLSWYRNT
Atf2: PYRVRELLTTLTSRLHGTLLDRHRPLWEMYLIBGLSDGRFAIYTKLHHS LMDGVSGLRLLMRTLSTDPDV RDAPPPWN...LPRRASANGAAPAPDLWSV
Atf8: PGGEAE LMALCSRLHGSLLDRSRPLWEMH LIEGLGDGRFAVYTKIHHA VADGV TAMKMLRNA LSENSED RDVPAPWQPRGPRPQRTPSKAFSLSGLAGST
AtfA: PGRIRELLIYISQEHSTLLDRAKPLWT CNII BGI EGNRFAMVFKIHHA VADGV AMRLIEKSLSHDVTEKSI VPPWCVE...GKRAKRLREPKTGKIKKI
tDGAT: PGNAAQ LAADVAM LHERPLDRA RPLWEAVVIQGLEGRITAVYIKVHHA VADGV LATETILAALLDLSPQPRELP PDDTVPQQA PALAERVRTGLLRALAHF

Atf1: A TDVARRASNTLGRNS...VRLVLRTPRA TWRDAAALAGSTLRLTRPVVSTLSPVMKKKSTR RHC AVL DV PVEALAQAAAAGAG SINDAFLAA VLLGMAK
Atf2: VNGVRRTVGEVAGL.....APASLRIRARTAMGQH.DMRFP.YEAPRTMLNVP IGGARRF AAQSW PLE RVHVRKAAGV SVNDVVMAMCAGALRG
Atf8: FRAARDTVGEVAGL.....VPA LAGTVSRAFRDQ.GGPLA.LSAPKTPFNVPITGARQFAAQSW PLE RLRLVAKLSDT TINDVVLAMSSGALRS
AtfA: MSGIKSQQLQATPTV.....IQELSQTVFKD IGRNPDHVSS.FQAPCSILNQRVSSRRFAAAQSF DLD RFRNIAKSLNVT TINDVVVLAMVCSGALRA
tDGAT: VRGARMLAARTAPYLYDEIPGLAQLPGVQPLARAIQGRDGVVPLPRTVAPPTPFNGTISARRAVAFGELPLAEIRRIRELGG SVNDVVMALVATALHR

Atf1: YHRLHGA EIS.EILRMTLPISLRAETDPVGG..NRITLARFALPADID DPAAELMHRVHATVDAWR...HEP AIPLSPTIAGALN...LPASTLG
Atf2: YLEEQKALPDEPLIAMVPVSLRDEQKADAGG.NAVGVVILCNLATDVPDPAERLTAISASM SQGKELFGSLTSMQALAWSAFNMSPIA...LTPVPGFVR
Atf8: YLEDQNALPAEPLIAMVPVSLKSQR.EASNG..NNIGVLMCNLGTLPDPAERLTAIRTSMREGKEAYETMSATQILAMSALGAAPIG...ASMLFGHNS
AtfA: YLMSHNSLP SKPLIAMVPASIRND.DSDVS..NRITMILANLATHKDDPLQRLEIIRTSVQNSKQRFKMTSDATILNYSVAVVGYPAG...LNIISGMPP
tDGAT: WLDKRGSLPDRPLVAAPVSLRRGRDGDAAAGGNRMSAMVTF LATHLADPAERFAA IRGDIAAAKRRFARS SGAWLEGLSELVPA PLAGPLLRLALQARPG

Atf1: NMLKHVDFVASNVVGVSPVPLFIAGSEV LHY YAF SPT LGS A F . NVTLTMSYTTTCCVGINADTD AIPDLATLTDSITADGFRAVLGLCTKTITDTRVVAS
Atf2: FTTPPPF NVIISNVPGPRKTM YWNGSRLDGIYPTSVVLDGQA.LNITLT TNGGNLDFGVIGCRRSVPSLQRLILFYLETALGELEAALL.....
Atf8: RVRPPF NVIISNVPGPSSPLYWNGARLDAIYPLSVVDGQG.LNITCTSNDDIISFVGTCRRSVPDLQRIIPARLLEELRALERAVGI.....
AtfA: .KRQAF NVIISNVPGPREPLYWNGAKLDALYFASIVLDGQA.LNITMTSYLDKLEVG LIA CRNALPDMKNSLLTHLGH EELIQLFEGVIAKQEDIKTAN..
tDGAT: EYLRPV NLLVSNVPGPFDPLYLRGARVLGYFPTISVSDLTGG L NITVTLSYDGKLDVGIVTCRQMIPDPWEIMDHLDDALGELRG LIDG.....