

B

MLSPVCFLPLLDTSFCGFLAIWSSHSLTPKKLWEQHTAVEEYEQEFIAKWR
 SLDDLVDLLVLPVLGSAFYIGSSSLASESQSYVTLYNLLDFPAGVVPVTIVT
 LQDEEELAFYKGCYGDSSDKNFSEAVRGSVGLLVTVQCIALPWEELCLR
 FMKEVDTLVKNQRGPK

C

69% homology

FAAH	438	SRSAGKLWELQHEIEVYRKTVIAQWRALDDLVDVLTPLAPALDLNAPGRATGAVSYTMLY S + KLWE +E Y + IA+WR+LDDLVD+L P+L A + + A+ + SY LY
FAAH-OUT	25	SLTPKKLWEQHTAVEEYEQEFIAKWRSLDDLVDLLVLPVLGSAFYIGSSSLASESQSYVTLY
FAAH	498	NCLDFPAGVVPVTTVTAEDEAQMEHYRGYFGDIWDKMLQKGMKKS VGLPVAVQCVALPWQ N LDFPAGVVPVT VT +DE ++ Y+G +GD DK + ++ SVGL V VQC+ALPW+
FAAH-OUT	85	NLLDFPAGVVPVTIVTTLQDEEELAFYKGCYGDSSDKNFSEAVRGSVGLLVTVQCIALPWE
FAAH	558	EELCLRFMREVERLMTPEK EELCLRFM+EV+ L+ ++
FAAH-OUT	145	EELCLRFMKEVDTLVKNQR