

1 10 20 30 40 50 60
Acetylcholinesterase MARFITSSSLSPSTTFSFASATASPAIASSLPRSKSTKATKARKTILSANSFKTSSLSL
ache2_
1DX4_ACETYLCHOLINEST
consensus>70

70 80 90 100 110 120
Acetylcholinesterase SSSASSPSLSSSPSFFKSSSSSKSRYSSSHLFNAFASLIPSSLAFSSLSFSLSLTSTNDLY
ache2_
1DX4_ACETYLCHOLINEST
consensus>70

130 140 150 160 170 180
Acetylcholinesterase RGFFATLVILLRMSSVAYGITDRLIVQTTSGPVRGRAVTVQGREVHVETGIPYAKPPVDD
ache2_ITDRLIVQTTSGPVRGRAVTVQGREVHVETGIPYAKPPVDD
1DX4_ACETYLCHOLINESTVIDRLIVQTTSGPVRGRSVTVQGREVHVETGIPYAKPPVED
consensus>70!DRLIVQTTSGPVRGRAVTVQGREVHVETGIPYAKPPV#D

190 200 210 220 230 240
Acetylcholinesterase LRFRKPVPAEPWHGVLDATRLPATCVQERYEYFPGFSGEEIWNPNNTNVSSEDCLYNNIWAP
ache2_LRFRKPVPAEPWHGVLDATRLPATCVQERYEYFPGFSGEEIWNPNNTNVSSEDCLYNNIWAP
1DX4_ACETYLCHOLINESTLRFRKPVPAEPWHGVLDATGLPATCVQERYEYFPGFSGEEIWNPNNTNVSSEDCLYNNIWAP
consensus>70LRFRKPVPAEPWHGVLDAT.LATCVQERYEYFPGFSGEEIWNPNNTNVSSEDCLY.NIWAP

250 260 270 280 290
Acetylcholinesterase SKARLRHGRGANGVEH..AAKTDEDHLIHSATPQNTTNGLPILIIWIYGGGFMTGSATLDI
ache2_SKARLRHGRGANGVEH..AAKTDEDHLIHSATPQNTTNGLPILIIWIYGGGFMTGSATLDI
1DX4_ACETYLCHOLINESTAKARLRHGRGANGVEH..AAKTDEDHLIHSATPQNTTNGLPILIIWIYGGGFMTGSATLDI
consensus>70SKARLRHGRGANGVEH..AAKTDEDHLIHSATPQNTTNGLPILIIWIYGGGFMTGSATLDI

300 310 320 330 340 350
Acetylcholinesterase YNADIMSAVGNVIVASFQYRVGAFGFLHLSFVMPG.FEEAPGNVGLWDQALALRWLKEN
ache2_YNADIMSAVGNVIVASFQYRVGAFGFLHLSFVMPG.FEEAPGNVGLWDQALALRWLKEN
1DX4_ACETYLCHOLINESTYNADIMSAVGNVIVASFQYRVGAFGFLHLSFVMPG.FEEAPGNVGLWDQALALRWLKEN
consensus>70YNADIM.SAVGNVIVASFQYRVGAFGFLHLSFVMPG.FEEAPGNVGLWDQALALRWLKEN

360 370 380 390 400 410
Acetylcholinesterase ARAFGGNPEWMTLFGESAGSSSVNAQLVSPVTRGLVKRGMMSQSGTMNAPWSHMTSEKAVE
ache2_ARAFGGNPEWMTLFGESAGSSSVNAQLVSPVTRGLVKRGMMSQSGTMNAPWSHMTSEKAVE
1DX4_ACETYLCHOLINESTARAFGGNPEWMTLFGESAGSSSVNAQLVSPVTRGLVKRGMMSQSGTMNAPWSHMTSEKAVE
consensus>70A.AFGGNPEWMTLFGESAGSSSVNAQLVSPVTRGLVKRGMMSQSGTMNAPWSHMTSEKAVE

420 430 440 450 460 470
Acetylcholinesterase IGKALINDCNCNASLSENQSVMA CMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAF
ache2_IGKALINDCNCNASLSENQSVMA CMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAF
1DX4_ACETYLCHOLINESTIGKALINDCNCNASLSENQSVMA CMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAF
consensus>70IGKALINDCNCNASLSENQSVMA CMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAF

480 490 500 510 520 530
Acetylcholinesterase TADPMTLMKTADMTG YDIMIGNV DEGTYFLLYDFIDYFDKDEATSLPRDKYLEIMNNIF
ache2_TADPMTLMKTADMTG YDIMIGNV DEGTYFLLYDFIDYFDKDEATSLPRDKYLEIMNNIF
1DX4_ACETYLCHOLINESTTADPMTLMKTADMTG YDIMIGNV DEGTYFLLYDFIDYFDKDEATSLPRDKYLEIMNNIF
consensus>70TADPMTLMKTADMTG YDIMIGNV DEGTYFLLYDFIDYFDKDEATSLPRDKYLEIMNNIF

540 550 560 570 580 590
Acetylcholinesterase NKATQAEAREAIIFQYTSWEGNPGYQNOQOIGRAVGDHFFTCPT NEYAQALAERGAQVHYY
ache2_NKATQAEAREAIIFQYTSWEGNPGYQNOQOIGRAVGDHFFTCPT NEYAQALAERGAQVHYY
1DX4_ACETYLCHOLINESTGKATQAEAREAIIFQYTSWEGNPGYQNOQOIGRAVGDHFFTCPT NEYAQALAERGAQVHYY
consensus>70NKATQAEAREAIIFQYTSWEGNPGYQNOQOIGRAVGDHFFTCPT NEYAQALAERGAQVHYY

600 610 620 630 640 650
Acetylcholinesterase YFTHRTSTSLWGEWMGVVLHGDEIEYFFGQPLNLSLOYRPVERELGKRMLNSVIEFAKTGN
ache2_YFTHRTSTSLWGEWMGVVLHGDEIEYFFGQPLNLSLOYRPVERELGKRMLNSVIEFAKTGN
1DX4_ACETYLCHOLINESTYFTHRTSTSLWGEWMGVVLHGDEIEYFFGQPLNLSLOYRPVERELGKRMLNSVIEFAKTGN
consensus>70YFTHRTSTSLWGEWMGVVLHGDEIEYFFGQPLNLSLOYRPVERELGKRMLNSVIEFAKTGN

	660	670	680	690	700	710
Acetylcholinesterase	PAV DGE EWP N FSKEDPVYYVFSTDEKTEKLQ RGPLAK RCSFWNDYLPKVRSWVGS ECEN N					
ache2_	PAV DGE EWP N FSKEDPVYYVFSTDEKTEKLQ RGPLAK RCSFWNDYLPKVRSWVGS ECEN N					
1DX4_ACETYLCHOLINEST	PAQ DGE EWP N FSKEDPVYYVFSTDDKIEKLARGPLAA RCSFWNDYLPKVRSWAGT CDGDS					
consensus>70	PA.DGEEWP N FSKEDPVYY!FSTD#K.EKL.RGPLA.RCSFWNDYLPKVRSW.G...#.					

	720	730	740
Acetylcholinesterase	NAASAAVN NINGQQYLLKQVIMLTIMVTCIFQ		
ache2_	NAAS.....		
1DX4_ACETYLCHOLINEST	GSAS.....		
consensus>70	..AS.....		