

hAChE	1	MRPPQCLL-----HTPS-----LASPLLLLLLWLLGGGVGAEG--REDAELLVTVRGGRLRGIRL----KTPGGP-VSA
Ppa-UAR-1	1	MKRRDRNDHIQMSLPKCFSLPTCPYHWLYASISTENMRLLVLSVSL-FFITASYSTSDYYFPVISTGYGSIRGYAF---TAHDGTE-AQI
CEST-1.1	1	MLKPATV-----L-----L-LIQ-----MYVCKRVQLSSGTIEGKILNISYSPLGNQSATV
CEST-2.2	1	MFFRFFI-----L-----WAILQ-----NVRSTKVKLSTGTIEGRLLTASYSPLGNQTGIV
CEST-4	1	MLLLPGL-----MNNLLLFLS---FLLLF---SITKSAIVSTSLGQIDGDQI-----GS-FHL
hAChE	63	FLGIPFAEPPMGPRRFLPPEPKQPWSGVVDATTFQSVCYQYVDTLYPGFEGTEMWNPNRELSIEDCLYLNWVTPYPRP-T-SPTPVLVWIIY
Ppa-UAR-1	86	FKKIPFASAPIGDLRWKPKPHRPWNGTLDGTFFGPACTQRTNKYDG-----PVTGFSEDCLHVNVTSERCRESNSTCPVAFIIH
CEST-1.1	46	FLGIPFVEPPIGDLRYRKPRPPKSWEGVLVTNEYKSACMSNATKTYKNK-----FGGPISEDCLYLNVLVTNEYCLEN-KNCSVMMIVH
CEST-2.2	47	FFGVPYVEPPVGNLRFKPRPPKPWDGVLEAKEYKAACMSDQKKTYKNG-----VGGPVSEDCLYANVFTNQYCLEH-KNCSVMLTIH
CEST-4	47	FKHIPLAKPPIGKLRFAQPEPEKWTGVRNAKAYGPACISNSSVSTS-----PQKWIDEDCLHINIFTSDKCLKS-KDCAVVTFYFH
hAChE	151	GGGFYSGASS-L--DVYDGRFLVQAERTVLVSMNYRVGAFGFLALPGSREAPGNVGLLDQRLALQWVQENVAAFGGDPTSVTLFGESAGA
Ppa-UAR-1	167	GGAGLYESTMKFPDEKLVRFVSQ--GIVVVTTAYRLSAFGAMDLDENALPANLGLHDIVAALNFTTRNEIGHFGGSKKITLLGQSEGG
CEST-1.1	128	GGGYLTESASTFNPEILINNFVGQGRNIVVVTFNRYRLGLFSFGQFNGDR-GDKNFGLYDMIESVNWVRREIENFGGNKNRITLAGHSAGA
CEST-2.2	129	GGRFVIESASAYDPEIIINNFVGQGRNIVVVTFNRYRLGLFGLGMLNGDN-QDTNFGLYDILEVVRWTRKEIKNFGGDKDRITMQGHSAGA
CEST-4	127	GGGLMYDSAVMFNDTYLLGTFTVNQ--DVIIAIPAFRLGIFSHFVVEDQSIAPTNLALYDILLGVFEFVKNEIHNFGGNNQKNTIMGHSYGG
hAChE	238	ASVGMHLLSPP-----SRGLFHRAVLQSGAPNGPWATVGMGEARRRATQLAHLVGCPPGGTGGND-----T-ELVACLRTRPAQVLVNH
Ppa-UAR-1	255	HYALMIAFSPGISKPGEKRLIDGIIIVMSGNGGL---EFREKAVERSHSVAKQLNCTGTA-----R-EIVECMRLHDTESIVAA
CEST-1.1	218	SMIVAFTSSPL-----TKGLVHQIIMSAPMTN---MSKKS NFKGMTVMAQMVGC LSEEIGFNKLSEEQVE-NTYSCLRKKS AQQILDA
CEST-2.2	218	VFTAAFSTSP L-----SKGLIHQIIMSASMSN---LSKKS NVKELTVVARIVGCLPDEHGF PKLSNVEVE-KAYTCLRSKSAQQILDA
CEST-4	215	SIVNILTFSSKIN--HDLSLFQQSICMSSGHDF---ETLEIQIQKTNRFAKHAGACTVPSIIIEKKMTTRQSDLYRMKCLQNKD ALELLRV
hAChE	316	EW H-----VLPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLVGVVKDEGSYFLVYGAPGFSKD NESLISRAEFLAGVRVGVPQ
Ppa-UAR-1	329	SYKVNGPHILSQKAPFGI----TMSGELFPITNEKEL-REDPNPIRLMIGTTIEEIGGGVAGVD-----
CEST-1.1	297	QLW-----LLQNSTYFL--GAPPIDEHFLTDPENLYASKSIYPINTLIGTTTLEVEESSYIIDPAFADKKVELLEN-----
CEST-2.2	298	QLY-----MLRNTTYII--GQGHIDGIYQVDYDPDNLATNSIYPINTMIGTTTAE LMDSPYIYDPKNTGKKEILLQN-----
CEST-4	299	QRL-----LE-DEGYPTY-GYLVQREPLIQEIPYQEF-MKSPKKIPMLTGCTRYEMDHSPAP-----
hAChE	411	VSDLAAEAVVLH-YTDWLHPEDPAR-L----RE-ALS-DVV-----G-D-HNVVCPVAQLAGRLAAQGARVYAYVFEHRASTLSWPLW--
Ppa-UAR-1	388	-----KINRILGIENGEECY---DKYLN DVES-GAFNPGYIEAS-QEMIMTAHIYAKYVAQIGGEAYLYEYDYP-----
CEST-1.1	367	---L---CDHIG-YVLYEEPETFSKKCKQYMNGNSS-MNL-----SNE-MEFYTPAIDFADSHTSNGTKVFLYSYDYRGAGPAYDRYLE
CEST-2.2	368	---L---CEHIG-YELYKEPEEFSQKCRNFYKNGEDA-KSL-----GDD-MEFYYGAIQLANVHSSKDTNVFVYSFDYKEAGNAYKKYDK
CEST-4	353	-----KPIGQALGFENPEEVYMKFRKDWDDVEYEFGNH----SDETQAIMVQVRVRVNNLLSKNVPAYLYEYTP-----
hAChE	474	-MGVPHGYEIEFIFGIPLDPSRNYTAAE-KIFAQRLMRYWANFARTGDPNEPRDPKAPQWPPYTAGAQQYVS LDLRPL-E----VRRGLR
Ppa-UAR-1	452	-VHGHTDDAYHVLGIHE---YEMDENE-RWLSRAYPRYFSNFIKGERLAK-----DWSKVTPLLMNYYSVNRSRTDGVFPHTKYGYK
CEST-1.1	443	VRSPHSEDLIYVFGTHR---GIFAPKD-YIIEKIYSGMFADFVNFNENPLPSGD---QKWNQYTKENREHFLINF DKN-FITPGMRDNY
CEST-2.2	444	SLSPKHGEDFAYAFGTNR---GNFSTKD-YVIEYIYSGMFADFVNFGDPSPLED---QEW AQYTP EKREYFLIDF DKN-FTMPGMKDHY
CEST-4	419	-KHARHTDDL FYLMGVHR---FEKDENE-IELGKVYETIFMNF AKFGDPKE-----GFELANAENESYEVYWDGETGERPQMKT KFE
hAChE	567	AQACAFWN RFLPK-----LLSA---T-----DTLDEAERQWKAEFHRWSSYMVHWKN-----
Ppa-UAR-1	530	NNLVKYYD-ELVK-YDQ-----VLSAAKMQAAN-----API-E---
CEST-1.1	525	TEAYEFWSTVGKKSFKKEWSPSLDTFTCALVISPLVSHMKQTTTAFDKTFEQT ELLYKEEVNFLKREKLERTQELKMETKRRDKALRIQN
CEST-2.2	526	PKALEFWSTCGSKSFKEHFSPSVDIFIIGNLLNPIMSHLNHNETGPDKTFEQFDKLYNEREEFLKLLKAVRKLEI-----QKKMWRGRS
CEST-4	497	EKIINYWLKDMVE-YDK-----HITELKNQKIS-----I-----RKPVVRF--
hAChE	601	-----QFDHYSKQ-----DRCSDL-----
Ppa-UAR-1	560	-----YK-SLNFDAGFQGFLSLSI--FD-----AIIF--VC-----VVLG-VLSLLCCLCNCFTSL-C-CCCCRGGY--SSI-
CEST-1.1	615	RKNGLANK---EITEGDEEDES KLD--IL-----LIIS--AG-----TLFGGILYV-----TLPNVIL-QKRARDGY--EL--
CEST-2.2	610	SKDLM-LKELVDLEKINEEEQETGAN--FL-----LIIF--GG-----TLLGGILYV-----SISHFCL-HHRSRDGY--QL--
CEST-4	532	-----Y-----EESKYYHQYSYMTISIL-----LIF--T-----IFLTGYLFG-----RCCCV-GNQDRNLY--IQLD
hAChE	-	-----
Ppa-UAR-1	-	-----
CEST-1.1	672	----LS-----
CEST-2.2	669	----LK-----
CEST-4	580	GSNIPTGHIVKNF

\* =Catalytic triad (in AChE)

^ =Disulfide bond (in AChE)