

	10	20	30	40	50	60
Rat	-MELKTEEEVGGVQPVSIQAFASSSTLHGLAHIFSYERLSLKRALWALCFLGSLAVLLC					
Xenopus1.1	-MDVK-EAEELSSPQPLAIQAFASGSTLHGLAHIFTYERFSCRRLIWILCFLGSLSLLLF					
Xenopus1.2	-MDVK-EAEELGSPQPLAVQAFASGSTLHGLAHIFTYERFSCRRLIWILCFLGSLSLLLF					
EFS	-MDLKPPAEDGVSNHPASVEAFAKTSTLHGISHIFTYERFSFKRIIWTLAFLGSLSFVLVH					
	70	80	90	100	110	120
Rat	VCTERVQYYFCYHHVTKLDEVAASQLTFPAVTLCNLNEFRFSQVSKNDLYHAGELLALLN					
Xenopus1.1	VCTERIYYFEYPHVTKLDEISTPKMIFPAVTFCNLNEFRFSRVTKNDLYHAGELLSLLN					
Xenopus1.2	VCTERIYYFEYPHVTKLDEIATPNMIFPAVTFCNLNEFRFSRVTKNDLYHAGELLSLLN					
EFS	TCTORIQQYYFQYPHVTKLDEISAANMTFPAITICNLNEFRFSKITKNDLYHAGELLTLLN					
	130	140	150	160	170	180
Rat	NRYEIPDTQMADEKQLEILQDKANFRSFKPKPFNMREFYDRAGHDIRDMLLSCHFRGEAC					
Xenopus1.1	NRYELPDSQLADEKVMEILQDKANFRNFKPKPFNMREFYDRTGHDIRDMLLNCKFRGEEC					
Xenopus1.2	NRYELPDSQLADENVMEILQDKANFRNFKPKPFNMREFYDRTGHDIREMLLGCKFRGEEC					
EFS	NRYEIPDPHLAERHILEALVEKANFRNFKPKPFNMREFYARAGHDMKDMLLHCIFKGEFC					
	190	200	210	220	230	240
Rat	SAEDFKVVFTRYGKCYTFNSGQDGR-PRLKTMKGGTGNGLEIMLDIQQDEYLPVWGETDE					
Xenopus1.1	SADNFVPVFTRYGKCYTFNSGRNG--PPLVTTKGGTGNGLELMLDIQQDEYLPVWGETDE					
Xenopus1.2	SAEDFVPVFTRYGKCYTFNSGRNGR-SPFVTTKGGTGNGLELMMDIQQDEYLPVWGETDE					
EFS	TAQDFKIVFTRYGKCYTFNSGQIKDQPIILTLEGGTGNGLELMLDIQQDEYLPVWGETDE					
	250	260	270	280	290	300
rat	TSFEAGIKVQIHSQDEPPFIDQLGFGVAPGFQTFVSCQEQRLLIYLPSPWGTTCNAVMTMSD					
Xenopus1.1	TSFEAGIKVQIHSQDEPPFIDQLGFGVAPGFQTFVSCQEQRLLTYLPPPWGDKSSAMDSE					
Xenopus1.2	TSFEAGIKVQIHSQDEPPFIDQLGFGVAPGFQTFVSCQEQRLLTYLPPPWGDKSSAMDSE					
EFS	TSFEAGIKVQIHSQSEPPFIDQLGFGVPPGFQTFVACQEQRLLRYLPPPWGDKSTPMSD					
	310	320	330	340	350	360
Rat	FFDSYSITACRIDCETRYLVENCNCRMVHMPGDAPYCTPEQYKECADPALDFLVEKDQEY					
Xenopus1.1	FFDTYSISACRIDCETRYLVENCNCRMVHMPGDAAAYCTPELYKECADPALDFLVEKDNDF					
Xenopus1.2	FFDTYSITACRIDCETRYLVENCNCRMVHMPGDAAAYCTPELYKECADPALDFLVEKDNDF					
EFS	FFDTYSITACRIDCETRYLVENCNCRMVHMPGDAPYCTPEQYKECADPALDFLVEKDSVF					
	370	380	390	400	410	420
Rat	CVCEMPCNLTRYGKELSMVKIPSKASAKYLAKKFNKSEQYIGENILVLDIFFEVLNYETI					
Xenopus1.1	CVCETPCNMTRYGKELSMVKIPSKASARYLAKKYNKSEQYIADNILVLDIFFEALNYETI					
Xenopus1.2	CVCETPCNMTRYGKELSMVKIPSKASARYLAKKYNKSEQYIAENILVLDIFFEALNYETI					
EFS	CTCETPCNMTRYGKELSMVKIPSKASAKYLAKKYNKSEDIYIGENILVLDIFFEALNYETI					
	430	440	450	460	470	480
Rat	EQKKAYEIVAGLLGDIGGQMGFLFIGASILTVLELFDYAYEVIKHRLCRRGKCKQKEAKRSSA					
Xenopus1.1	EQKKAYEVAGLLGDIGGQMGFLFIGASILTVLELFDYAYEVLRYKLCGGAKCGKDSKRNNN					
Xenopus1.2	EQKKAYEVAGLLGDIGGQMGFLFIGASILTVLELFDYAYEVLRYKLCGGAKCRKDSKRNNN					
EFS	EQKKAYEVAGLLGDIGGQMGFLFIGASLLTILELFDYVYEVVKHKMCGVLRMGKQQRNNN					
	490	500	510	520		
Rat	DKGVALSLDDVKRHNPCESLRGHPAGMTYAANILPHHPARGTFEDFTC					
Xenopus1.1	DKGVTLSLDDVKRHAPIEGVRGHPAGMSYTANILPHHAVRGAFEDFTC					
Xenopus1.2	DKGVTLSLDDVKRHAPCEGVRGHPAGMSYTANILPHHAVRGAFEDFTC					
EFS	DKGVTLSLDDIKRHNPCESLRGHPTGMSYTANMLPHHPPRNTFEDFTC					

Supplemental Figure 1. Alignment of ASIC1 proteins. Transmembrane domains TM1 and TM2 are underlined. The three residues in the $\beta 1$ - $\beta 2$ linker are highlighted in yellow. Identical residues are in red, similar in green and blue, and non-conserved in black. EFS=elephant shark. EFS=elephant shark.