

Appendix V

Annotated protein sequence alignments of human NCBT variants (see Section V)

In this appendix we present ClustalW (1) sequence alignments of the variants of each of the five NCBTs, color coded per their diagrammatic representation in the Figures of the review. TM1 and TM14 of each variant are shown as gray boxes to mark the Nt/TMD and TMD/Ct boundaries. Sequence accessions are provided in Appendix IV.

Alignment 1: NBCe1 variants. An alignment of human NBCe1-A, NBCe1-B, NBCe1-C, NBCe1-D, and NBCe1-E as depicted in Figure 18 of the review. Shown are the **41-aa autostimulatory domain**, the **85-aa auto inhibitory domain**, the **9-aa cassette I**, and the **61-aa alternative Ct that includes a PDZ-binding sequence**.

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NBCe1-A -----MSTENVEGKPSNLGER 16
NBCe1-D -----MSTENVEGKPSNLGER 16
NBCe1-B MEDEAVLDRGASFLKHVCDEEEVEGHHTIYIGVHVPKSYRRRRRHKRKTGHKKEKKEKERI 60
NBCe1-E MEDEAVLDRGASFLKHVCDEEEVEGHHTIYIGVHVPKSYRRRRRHKRKTGHKKEKKEKERI 60
NBCe1-C MEDEAVLDRGASFLKHVCDEEEVEGHHTIYIGVHVPKSYRRRRRHKRKTGHKKEKKEKERI 60
                                     . : . . : . : .

NBCe1-A GRARSSTFLRVVQPMFNHSIFTSAVSPAERIRFILGEEDDSPAPPQLFTELDELLAVDG 76
NBCe1-D GRARSSTFLRVVQPMFNHSIFTSAVSPAERIRFILGEEDDSPAPPQLFTELDELLAVDG 76
NBCe1-B SENYSDKSDIENADESSSSILKPLISPAERIRFILGEEDDSPAPPQLFTELDELLAVDG 120
NBCe1-E SENYSDKSDIENADESSSSILKPLISPAERIRFILGEEDDSPAPPQLFTELDELLAVDG 120
NBCe1-C SENYSDKSDIENADESSSSILKPLISPAERIRFILGEEDDSPAPPQLFTELDELLAVDG 120
.. *.. . **:. :*****

NBCe1-A QEMEWKETARWIKFEEKVEQGERWSKPHVATLSLHSLFELRTCMEKGSIMLDREASSLP 136
NBCe1-D QEMEWKETARWIKFEEKVEQGERWSKPHVATLSLHSLFELRTCMEKGSIMLDREASSLP 136
NBCe1-B QEMEWKETARWIKFEEKVEQGERWSKPHVATLSLHSLFELRTCMEKGSIMLDREASSLP 180
NBCe1-E QEMEWKETARWIKFEEKVEQGERWSKPHVATLSLHSLFELRTCMEKGSIMLDREASSLP 180
NBCe1-C QEMEWKETARWIKFEEKVEQGERWSKPHVATLSLHSLFELRTCMEKGSIMLDREASSLP 180
*****

NBCe1-A QLVEMIVDHIQIETGLLKPELKDVKVYTYLLRKHRHQTKKSNLRSADIGKTVSSASRMFTN 196
NBCe1-D QLVEMIVDHIQIETGLLKPELKDVKVYTYLLRKHRHQTKKSNLRSADIGKTVSSAS----- 191
NBCe1-B QLVEMIVDHIQIETGLLKPELKDVKVYTYLLRKHRHQTKKSNLRSADIGKTVSSASRMFTN 240
NBCe1-E QLVEMIVDHIQIETGLLKPELKDVKVYTYLLRKHRHQTKKSNLRSADIGKTVSSAS----- 235
NBCe1-C QLVEMIVDHIQIETGLLKPELKDVKVYTYLLRKHRHQTKKSNLRSADIGKTVSSASRMFTN 240
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NBCe1-A	PDNGSPAMTHRNLTSSSLNDISDKPEKDQLKNKFMKKLPRDAEASNVLVGEVDFLDTPFI	256
NBCe1-D	----SPAMTHRNLTSSSLNDISDKPEKDQLKNKFMKKLPRDAEASNVLVGEVDFLDTPFI	247
NBCe1-B	PDNGSPAMTHRNLTSFSLNDISDKPEKDQLKNKFMKKLPRDAEASNVLVGEVDFLDTPFI	300
NBCe1-E	----SPAMTHRNLTSFSLNDISDKPEKDQLKNKFMKKLPRDAEASNVLVGEVDFLDTPFI	291
NBCe1-C	PDNGSPAMTHRNLTSSSLNDISDKPEKDQLKNKFMKKLPRDAEASNVLVGEVDFLDTPFI	300

NBCe1-A	AFVRLQQAVMLGALTEVPVTRFLFILLGPKGKAKSYHEIGRAIATLMSDEVFHDIA YKA	316
NBCe1-D	AFVRLQQAVMLGALTEVPVTRFLFILLGPKGKAKSYHEIGRAIATLMSDEVFHDIA YKA	307
NBCe1-B	AFVRLQQAVMLGALTEVPVTRFLFILLGPKGKAKSYHEIGRAIATLMSDEVFHDIA YKA	360
NBCe1-E	AFVRLQQAVMLGALTEVPVTRFLFILLGPKGKAKSYHEIGRAIATLMSDEVFHDIA YKA	351
NBCe1-C	AFVRLQQAVMLGALTEVPVTRFLFILLGPKGKAKSYHEIGRAIATLMSDEVFHDIA YKA	360

NBCe1-A	KDRHDLIAGIDEFLDEVIVLPPGEWDPAIRIEPPKSLPSSDKRKNMYSGGENVQMNGDTP	376
NBCe1-D	KDRHDLIAGIDEFLDEVIVLPPGEWDPAIRIEPPKSLPSSDKRKNMYSGGENVQMNGDTP	367
NBCe1-B	KDRHDLIAGIDEFLDEVIVLPPGEWDPAIRIEPPKSLPSSDKRKNMYSGGENVQMNGDTP	420
NBCe1-E	KDRHDLIAGIDEFLDEVIVLPPGEWDPAIRIEPPKSLPSSDKRKNMYSGGENVQMNGDTP	411
NBCe1-C	KDRHDLIAGIDEFLDEVIVLPPGEWDPAIRIEPPKSLPSSDKRKNMYSGGENVQMNGDTP	420

	Nt---//---TM1	
NBCe1-A	HDGGHGGGGHGDCEELQRTGRFCGGLIKDIKRKAPFFASDFYDALNIQALSAILFIYLAT	436
NBCe1-D	HDGGHGGGGHGDCEELQRTGRFCGGLIKDIKRKAPFFASDFYDALNIQALSAILFIYLAT	427
NBCe1-B	HDGGHGGGGHGDCEELQRTGRFCGGLIKDIKRKAPFFASDFYDALNIQALSAILFIYLAT	480
NBCe1-E	HDGGHGGGGHGDCEELQRTGRFCGGLIKDIKRKAPFFASDFYDALNIQALSAILFIYLAT	471
NBCe1-C	HDGGHGGGGHGDCEELQRTGRFCGGLIKDIKRKAPFFASDFYDALNIQALSAILFIYLAT	480

NBCe1-A	VTNAITFGGLLGDATDNMQVLESFSLGTAVSGAIFCLFAGQPLTILSSTGPVLFERLLF	496
NBCe1-D	VTNAITFGGLLGDATDNMQVLESFSLGTAVSGAIFCLFAGQPLTILSSTGPVLFERLLF	487
NBCe1-B	VTNAITFGGLLGDATDNMQVLESFSLGTAVSGAIFCLFAGQPLTILSSTGPVLFERLLF	540
NBCe1-E	VTNAITFGGLLGDATDNMQVLESFSLGTAVSGAIFCLFAGQPLTILSSTGPVLFERLLF	531
NBCe1-C	VTNAITFGGLLGDATDNMQVLESFSLGTAVSGAIFCLFAGQPLTILSSTGPVLFERLLF	540

NBCe1-A	NFSKDNDFDYLEFRLWIGLWSAFLCLILVATDASFLVQYFTRFTEEGFSSLISFIFIYDA	556
NBCe1-D	NFSKDNDFDYLEFRLWIGLWSAFLCLILVATDASFLVQYFTRFTEEGFSSLISFIFIYDA	547
NBCe1-B	NFSKDNDFDYLEFRLWIGLWSAFLCLILVATDASFLVQYFTRFTEEGFSSLISFIFIYDA	600
NBCe1-E	NFSKDNDFDYLEFRLWIGLWSAFLCLILVATDASFLVQYFTRFTEEGFSSLISFIFIYDA	591
NBCe1-C	NFSKDNDFDYLEFRLWIGLWSAFLCLILVATDASFLVQYFTRFTEEGFSSLISFIFIYDA	600

NBCe1-A	FKKMIKLADYYPINSNFKVGYNLTFSTCVPPDPANISISNDTTLAPEYLPMSSTD MYH	616
NBCe1-D	FKKMIKLADYYPINSNFKVGYNLTFSTCVPPDPANISISNDTTLAPEYLPMSSTD MYH	607
NBCe1-B	FKKMIKLADYYPINSNFKVGYNLTFSTCVPPDPANISISNDTTLAPEYLPMSSTD MYH	660
NBCe1-E	FKKMIKLADYYPINSNFKVGYNLTFSTCVPPDPANISISNDTTLAPEYLPMSSTD MYH	651
NBCe1-C	FKKMIKLADYYPINSNFKVGYNLTFSTCVPPDPANISISNDTTLAPEYLPMSSTD MYH	660

NBCe1-A	NTTFDWAFLSKKECSKYGGNLVGNNCNFVPDITLMSFILFLGTYTSSMALKKFKTSPYFP	676
NBCe1-D	NTTFDWAFLSKKECSKYGGNLVGNNCNFVPDITLMSFILFLGTYTSSMALKKFKTSPYFP	667
NBCe1-B	NTTFDWAFLSKKECSKYGGNLVGNNCNFVPDITLMSFILFLGTYTSSMALKKFKTSPYFP	720
NBCe1-E	NTTFDWAFLSKKECSKYGGNLVGNNCNFVPDITLMSFILFLGTYTSSMALKKFKTSPYFP	711
NBCe1-C	NTTFDWAFLSKKECSKYGGNLVGNNCNFVPDITLMSFILFLGTYTSSMALKKFKTSPYFP	720

NBCe1-A	TTARKLISDFAILLSILIFCVIDALVGVDTPKLI V PSEFKPTSPNRGWFVPPFGENPWWV	736
NBCe1-D	TTARKLISDFAILLSILIFCVIDALVGVDTPKLI V PSEFKPTSPNRGWFVPPFGENPWWV	727
NBCe1-B	TTARKLISDFAILLSILIFCVIDALVGVDTPKLI V PSEFKPTSPNRGWFVPPFGENPWWV	780
NBCe1-E	TTARKLISDFAILLSILIFCVIDALVGVDTPKLI V PSEFKPTSPNRGWFVPPFGENPWWV	771

NBCe1-C TTARKLISDFAILLSILIFCVIDALVGVDTPKLIIVPSEFKPTSPNRGWFVPPFGENPWWV 780

NBCe1-A CLAAAIPALLVTILIFMDQQITAVIVNRKEHKLKKGAGYHLDLFWVAILMVICSLMALPW 796
NBCe1-D CLAAAIPALLVTILIFMDQQITAVIVNRKEHKLKKGAGYHLDLFWVAILMVICSLMALPW 787
NBCe1-B CLAAAIPALLVTILIFMDQQITAVIVNRKEHKLKKGAGYHLDLFWVAILMVICSLMALPW 840
NBCe1-E CLAAAIPALLVTILIFMDQQITAVIVNRKEHKLKKGAGYHLDLFWVAILMVICSLMALPW 831
NBCe1-C CLAAAIPALLVTILIFMDQQITAVIVNRKEHKLKKGAGYHLDLFWVAILMVICSLMALPW 840

NBCe1-A YVAATVISIAHIDSLKMETETSAPGEQPKFLGVREQRVTGTLVFLTGLSVFMAPILKFI 856
NBCe1-D YVAATVISIAHIDSLKMETETSAPGEQPKFLGVREQRVTGTLVFLTGLSVFMAPILKFI 847
NBCe1-B YVAATVISIAHIDSLKMETETSAPGEQPKFLGVREQRVTGTLVFLTGLSVFMAPILKFI 900
NBCe1-E YVAATVISIAHIDSLKMETETSAPGEQPKFLGVREQRVTGTLVFLTGLSVFMAPILKFI 891
NBCe1-C YVAATVISIAHIDSLKMETETSAPGEQPKFLGVREQRVTGTLVFLTGLSVFMAPILKFI 900

NBCe1-A PMPVLYGVFLYMGVASLNGVQFMDRLKLLMPLKHQPDFIYLRHVPLRRVHLFTFLQVLC 916
NBCe1-D PMPVLYGVFLYMGVASLNGVQFMDRLKLLMPLKHQPDFIYLRHVPLRRVHLFTFLQVLC 907
NBCe1-B PMPVLYGVFLYMGVASLNGVQFMDRLKLLMPLKHQPDFIYLRHVPLRRVHLFTFLQVLC 960
NBCe1-E PMPVLYGVFLYMGVASLNGVQFMDRLKLLMPLKHQPDFIYLRHVPLRRVHLFTFLQVLC 951
NBCe1-C PMPVLYGVFLYMGVASLNGVQFMDRLKLLMPLKHQPDFIYLRHVPLRRVHLFTFLQVLC 960

TM14---//---Ct

NBCe1-A LALLWILKSTVAAIIFPVMILALVAVRKGMDYLFSDHLSFLDDVIPEKDKKKKEDEK 976
NBCe1-D LALLWILKSTVAAIIFPVMILALVAVRKGMDYLFSDHLSFLDDVIPEKDKKKKEDEK 967
NBCe1-B LALLWILKSTVAAIIFPVMILALVAVRKGMDYLFSDHLSFLDDVIPEKDKKKKEDEK 1020
NBCe1-E LALLWILKSTVAAIIFPVMILALVAVRKGMDYLFSDHLSFLDDVIPEKDKKKKEDEK 1011
NBCe1-C LALLWILKSTVAAIIFPVMILALVAVRKGMDYLFSDHLSFLDDVIPEKDKKKKEDEK 1020

NBCe1-A KKKKGSLSDNDDSDCPYSEKVPKIPMDIMEQQPFLSDSKPSDRERSPTFLERHTSC- 1035
NBCe1-D KKKKGSLSDNDDSDCPYSEKVPKIPMDIMEQQPFLSDSKPSDRERSPTFLERHTSC- 1026
NBCe1-B KKKKGSLSDNDDSDCPYSEKVPKIPMDIMEQQPFLSDSKPSDRERSPTFLERHTSC- 1079
NBCe1-E KKKKGSLSDNDDSDCPYSEKVPKIPMDIMEQQPFLSDSKPSDRERSPTFLERHTSC- 1070
NBCe1-C KKKKGSLSDNDD**EKD**HQ**HS**L**NATH**H**AD**K**I**P**FL**Q**SL**G**M**P**SP**R**TP**V**K**V**VP**Q**I**R**I**E**L**E**P**E**D** 1080
***** . . . : : : * . : . . : : * : . .

NBCe1-A -----
NBCe1-D -----
NBCe1-B -----
NBCe1-E -----
NBCe1-C **NDYFWRSKGTETTL** 1094

Alignment 2: NBCe2 variants. An alignment of human NBCe2-a and NBCe2-c as depicted in Figure 27 of the review. Shown is the 16-aa insert.

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NBCe2-a      MKVKEEKAGVGKLDHTNHRRRFPDQKECPPIHIGLPVPTYPQRKTDQKGHLSGLQKVHWG 60
NBCe2-c      MKVKEEKAGVGKLDHTNHRRRFPDQKECPPIHIGLPVPTYPQRKTDQKGHLSGLQKVHWG 60
*****

NBCe2-a      LRPDQPQQELTGP GSGASSQDSSMDLISRTRSPA AEQLQDILGEEDEAPNPTLFTEM DTL 120
NBCe2-c      LRPDQPQQELTGP GSGASSQDSSMDLISRTRSPA AEQLQDILGEEDEAPNPTLFTEM DTL 120
*****

NBCe2-a      QHDGDQMEWKESARWIKFEEKVEEGGERWSKPHVSTLSLHSLFELRTCLQTGTVLLDLD S 180
NBCe2-c      QHDGDQMEWKESARWIKFEEKVEEGGERWSKPHVSTLSLHSLFELRTCLQTGTVLLDLD S 180
*****

NBCe2-a      GSLPQIIDDVIEKQIEDGLLRPELRERSYVLLRRHRHQTKKPIHRSLADIGKSVSTTNR 240
NBCe2-c      GSLPQIIDDVIEKQIEDGLLRPELRERSYVLLRRHRHQTKKPIHRSLADIGKSVSTTNR 240
*****

NBCe2-a      SPARSPGAGPSLHHSTEDLRMRQSANYGRLCHAQSRSMNDISLTPNTDQRKNKFMKKIPK 300
NBCe2-c      SPARSPGAGPSLHHSTEDLRMRQSANYGRLCHAQSRSMNDISLTPNTDQRKNKFMKKIPK 300
*****

NBCe2-a      DSEASNVLVGEVDFLDQPFIAFVRLIQSAMLGGVTEVPVPTRFLLFILLGPSGRAKSYNEI 360
NBCe2-c      DSEASNVLVGEVDFLDQPFIAFVRLIQSAMLGGVTEVPVPTRFLLFILLGPSGRAKSYNEI 360
*****

NBCe2-a      GRAIATLMVDDLFSVDVAYKARNREDLIAGIDEFLDEVIVLPPGEWDPNIRIEPPKKVPSA 420
NBCe2-c      GRAIATLMVDDLFSVDVAYKARNREDLIAGIDEFLDEVIVLPPGEWDPNIRIEPPKKVPSA 420
*****

NBCe2-a      DKRKS VFSLAELGQMNGSVGGGGGAPGGGNGGGGGGSGGGAGSGGAGGTSSGDDGEMPA 480
NBCe2-c      DKRKS VFSLAELGQMNGSVGGGGGAPGGGNGGGGGGSGGGAGSGGAGGTSSGDDGEMPA 480
*****

NBCe2-a      MHEIGEELIWTGRFFGGLCLDIKRKLPWFPSDFYDGFHIQ SISAILFIYLCITNAITFG 540
NBCe2-c      MHEIGEELIWTGRFFGGLCLDIKRKLPWFPSDFYDGFHIQ SISAILFIYLCITNAITFG 540
*****

NBCe2-a      GLLGDATDNYQGVMESFLGTAMAGSLFCLFSGQPLIILSSTGPILIFEKLLDFDFSKGNGL 600
NBCe2-c      GLLGDATDNYQGVMESFLGTAMAGSLFCLFSGQPLIILSSTGPILIFEKLLDFDFSKGNGL 600
*****

NBCe2-a      DYMEFRLWIGLHSAVQCLILVATDASFIIKYITRFTEEGFSTLISFIFIYDAIKKMIGAF 660
NBCe2-c      DYMEFRLWIGLHSAVQCLILVATDASFIIKYITRFTEEGFSTLISFIFIYDAIKKMIGAF 660
*****

NBCe2-a      KYYPINMDFKPNFITTYKCECVAPDVTNTVFNASAPLAPDTNASLYNLLNLTALDWSLL 720
NBCe2-c      KYYPINMDFKPNFITTYKCECVAPDVTNTVFNASAPLAPDTNASLYNLLNLTALDWSLL 720
*****

NBCe2-a      SKKECLSYGGRLGN SCKFIPDLALMSFILFFGTYSMTLTLKFKFSRYFPTKVRALVAD 780
NBCe2-c      SKKECLSYGGRLGN SCKFIPDLALMSFILFFGTYSMTLTLKFKFSRYFPTKVRALVAD 780
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NBCe2-a      FSIVFSILMFCGIDACFGLLETPKLVHPSVIKPTRPDRGWFVAPFGKNPWWVYPASILPAL 840
NBCe2-c      FSIVFSILMFCGIDACFGLLETPKLVHPSVIKPTRPDRGWFVAPFGKNPWWVYPASILPAL 840
*****

NBCe2-a      LVTILIFMDQQITAVIVNRKENKLLKKAAGYHLDLFWVGILMALCSFMGLPWYVAATVISI 900
NBCe2-c      LVTILIFMDQQITAVIVNRKENKLLKKAAGYHLDLFWVGILMALCSFMGLPWYVAATVISI 900
*****

                                     TM11
NBCe2-a      AHIDSLKMETETSAPGEQPQFLGVREQRVTGIIVFILTGISVFLAPILKCIPLPVLYGVF 960
NBCe2-c      AHIDSLKMETETSAPGEQPQFLGVREQRVTGIIVFILTGISVFLAPILKCIPLPVLYGVF 960
*****

LYMGVASLNGIQMGTGGSEFKIQKLLTPFWERCKLFLMPAKHQPDHAFLRHVPLRRIHLE 1020
NBCe2-a      LYMVASLNGIQ-----FWERCKLFLMPAKHQPDHAFLRHVPLRRIHLE 1004
NBCe2-c      *****

                                     TM13          TM14---//---Ct
NBCe2-a      TLVQILCLAVLWILKSTVAAIIFPVMILGLIIVRRLDFIFSQHDLAWIDNILPEKEKKE 1080
NBCe2-c      TLVQILCLAVLWILKSTVAAIIFPVMILGLIIVRRLDFIFSQHDLAWIDNILPEKEKKE 1064
*****

TDKRRKRKKGAEHDCDEEPQFPSPSVIKIPMESVQSDPQNGIHCIARKRSSWSYSL 1137
NBCe2-a      TDKRRKRKKGAEHDCDEEPQFPSPSVIKIPMESVQSDPQNGIHCIARKRSSWSYSL 1121
NBCe2-c      *****

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Alignment 3: NBCn1 variants. An alignment of human NBCn1-A, NBCn1-B, NBCn1-C, NBCn1-D, and NBCn1-E as depicted in Figure 32 of the review. Shown are the alternate Nt sequences (11-aa 'MERF' vs 16-aa 'MEAD'), the 13-aa cassette I, the 124-aa cassette II, and the 36-aa cassette III. Note that the D' sequence (not depicted in Figure 32) includes an additional 4-aa sequence 'VTSR' not present in NBCn1-D.

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NBCn1-B      MEADGAGEQMRPLLTR----GPDEEAVVDLGTKSSTVNTKFEKEEESHRAVYIGVHVPF 56
NBCn1-E      MEADGAGEQMRPLLTR----GPDEEAVVDLGTKSSTVNTKFEKEEESHRAVYIGVHVPF 56
NBCn1-A      -----MERFRLKPKLP-----GPDEEAVVDLGTKSSTVNTKFEKEEESHRAVYIGVHVPF 51
NBCn1-C      MEADGAGEQMRPLLTR----GPDEEAVVDLGTKSSTVNTKFEKEEESHRAVYIGVHVPF 56
NBCn1-D      MEADGAGEQMRPLLTR----GPDEEAVVDLGTKSSTVNTKFEKEEESHRAVYIGVHVPF 56
NBCn1-D'     MEADGAGEQMRPLLTRVTSRGPDEEAVVDLGTKSSTVNTKFEKEEESHRAVYIGVHVPF 60
                *****

NBCn1-B      SKESRRRHRHRGHKHHHRRRKDKESDKEDGRESPSYDTPSQRVQFILGTEDDDEEHI PHD 116
NBCn1-E      SKESRRRHRHRGHKHHHRRRKDKESDKEDGRESPSYDTPSQRVQFILGTEDDDEEHI PHD 116
NBCn1-A      SKESRRRHRHRGHKHHHRRRKDKESDKEDGRESPSYDTPSQRVQFILGTEDDDEEHI PHD 111
NBCn1-C      SKESRRRHRHRGHKHHHRRRKDKESDKEDGRESPSYDTPSQRVQFILGTEDDDEEHI PHD 116
NBCn1-D      SKESRRRHRHRGHKHHHRRRKDKESDKEDGRESPSYDTPSQRVQFILGTEDDDEEHI PHD 116
NBCn1-D'     SKESRRRHRHRGHKHHHRRRKDKESDKEDGRESPSYDTPSQRVQFILGTEDDDEEHI PHD 120
                *****

NBCn1-B      LFTEMDEL CYRDGEEYEWKETARWLKFEEDVEDGGDRWSKPYVATLSLHSLFELRSCILN 176
NBCn1-E      LFTEMDEL CYRDGEEYEWKETARWLKFEEDVEDGGDRWSKPYVATLSLHSLFELRSCILN 176
NBCn1-A      LFTEMDEL CYRDGEEYEWKETARWLKFEEDVEDGGDRWSKPYVATLSLHSLFELRSCILN 171
NBCn1-C      LFTEMDEL CYRDGEEYEWKETARWLKFEEDVEDGGDRWSKPYVATLSLHSLFELRSCILN 176
NBCn1-D      LFTEMDEL CYRDGEEYEWKETARWLKFEEDVEDGGDRWSKPYVATLSLHSLFELRSCILN 176
NBCn1-D'     LFTEMDEL CYRDGEEYEWKETARWLKFEEDVEDGGDRWSKPYVATLSLHSLFELRSCILN 180
                *****

NBCn1-B      GTVMLDMRASTLDEIADMVLDNMIASGQLDESIRENVREALLKRHHHQNEKRFTSRIPLV 236
NBCn1-E      GTVMLDMRASTLDEIADMVLDNMIASGQLDESIRENVREALLKRHHHQNEKRFTSRIPLV 236
NBCn1-A      GTVMLDMRASTLDEIADMVLDNMIASGQLDESIRENVREALLKRHHHQNEKRFTSRIPLV 231
NBCn1-C      GTVMLDMRASTLDEIADMVLDNMIASGQLDESIRENVREALLKRHHHQNEKRFTSRIPLV 236
NBCn1-D      GTVMLDMRASTLDEIADMVLDNMIASGQLDESIRENVREALLKRHHHQNEKRFTSRIPLV 236
NBCn1-D'     GTVMLDMRASTLDEIADMVLDNMIASGQLDESIRENVREALLKRHHHQNEKRFTSRIPLV 240
                *****

                Casette I                Casette II
NBCn1-B      RSFADIGKKHSDPHLLERNGEGLSASRHSRLRTGLSASNLSLRGESPLSLLLGHLLPSSRA 296
NBCn1-E      RSFADIGKKHSDPHLLERN----- 256
NBCn1-A      RSFADIGKKHSDPHLLERNGEGLSASRHSRLRTGLSASNLSLRGESPLSLLLGHLLPSSRA 291
NBCn1-C      RSFADI-----GEGLSASRHSRLRTGLSASNLSLRGESPLSLLLGHLLPSSRA 283
NBCn1-D      RSFADIGKKHSDPHLLERNGEGLSASRHSRLRTGLSASNLSLRGESPLSLLLGHLLPSSRA 296
NBCn1-D'     RSFADIGKKHSDPHLLERNGEGLSASRHSRLRTGLSASNLSLRGESPLSLLLGHLLPSSRA 300
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NBCnl-B GTPAGSRCTTPVPTPQNSPPSSPSISRLLTSRSSQESQRQAPPELLVSPASDDIPTVVIHPP 356
NBCnl-E -----GILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF
NBCnl-A GTPAGSRCTTPVPTPQNSPPSSPSISRLLTSRSSQESQRQAPPELLVSPASDDIPTVVIHPP 351
NBCnl-C GTPAGSRCTTPVPTPQNSPPSSPSISRLLTSRSSQESQRQAPPELLVSPASDDIPTVVIHPP 343
NBCnl-D GTPAGSRCTTPVPTPQNSPPSSPSISRLLTSRSSQESQRQAPPELLVSPASDDIPTVVIHPP 356
NBCnl-D' GTPAGSRCTTPVPTPQNSPPSSPSISRLLTSRSSQESQRQAPPELLVSPASDDIPTVVIHPP 360

NBCnl-B EEDLEAALKGEEQKNEENVDLTPGILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF 416
NBCnl-E -----GILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF 292
NBCnl-A EEDLEAALKGEEQKNEENVDLTPGILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF 411
NBCnl-C EEDLEAALKGEEQKNEENVDLTPGILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF 403
NBCnl-D EEDLEAALKGEEQKNEENVDLTPGILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF 416
NBCnl-D' EEDLEAALKGEEQKNEENVDLTPGILAS PQSAPGNLDNSKSGEIKGNSSGGSRENSTVDF 420

NBCnl-B SKVDMNFMRK IPTGAEASNVLVGEVDFLERP I IAFVRLAPAVLLTGLTEVPVPTFRFLFLL 476
NBCnl-E SKVDMNFMRK IPTGAEASNVLVGEVDFLERP I IAFVRLAPAVLLTGLTEVPVPTFRFLFLL 352
NBCnl-A SKVDMNFMRK IPTGAEASNVLVGEVDFLERP I IAFVRLAPAVLLTGLTEVPVPTFRFLFLL 471
NBCnl-C SKVDMNFMRK IPTGAEASNVLVGEVDFLERP I IAFVRLAPAVLLTGLTEVPVPTFRFLFLL 463
NBCnl-D SKVDMNFMRK IPTGAEASNVLVGEVDFLERP I IAFVRLAPAVLLTGLTEVPVPTFRFLFLL 476
NBCnl-D' SKVDMNFMRK IPTGAEASNVLVGEVDFLERP I IAFVRLAPAVLLTGLTEVPVPTFRFLFLL 480

NBCnl-B LGPAGKAPQYHEIGRSIATLMTDEIFHDVAYKAKDRNDLLSGIDEFLDQVTVLPPGEWDP 536
NBCnl-E LGPAGKAPQYHEIGRSIATLMTDEIFHDVAYKAKDRNDLLSGIDEFLDQVTVLPPGEWDP 412
NBCnl-A LGPAGKAPQYHEIGRSIATLMTDEIFHDVAYKAKDRNDLLSGIDEFLDQVTVLPPGEWDP 531
NBCnl-C LGPAGKAPQYHEIGRSIATLMTDEIFHDVAYKAKDRNDLLSGIDEFLDQVTVLPPGEWDP 523
NBCnl-D LGPAGKAPQYHEIGRSIATLMTDEIFHDVAYKAKDRNDLLSGIDEFLDQVTVLPPGEWDP 536
NBCnl-D' LGPAGKAPQYHEIGRSIATLMTDEIFHDVAYKAKDRNDLLSGIDEFLDQVTVLPPGEWDP 540

NBCnl-B SIRIEPPKSVPSQEKRKIPVFHNGSTPTLGETPKEAAHHAGPELQRTGRLFGGLILDIKR 596
NBCnl-E SIRIEPPKSVPSQEKRKIPVFHNGSTPTLGETPKEAAHHAGPELQRTGRLFGGLILDIKR 472
NBCnl-A SIRIEPPKSVPSQEKRKIPVFHNGSTPTLGETPKEAAHHAGPELQRTGRLFGGLILDIKR 591
NBCnl-C SIRIEPPKSVPSQEKRKIPVFHNGSTPTLGETPKEAAHHAGPELQRTGRLFGGLILDIKR 583
NBCnl-D SIRIEPPKSVPSQEKRKIPVFHNGSTPTLGETPKEAAHHAGPELQRTGRLFGGLILDIKR 596
NBCnl-D' SIRIEPPKSVPSQEKRKIPVFHNGSTPTLGETPKEAAHHAGPELQRTGRLFGGLILDIKR 600

Nt---/---TM1

NBCnl-B KAPFFLSDFKDALS LQCLASILFLYCACMSPVITFGGLLGEATEGRISAIESLFGASLTG 656
NBCnl-E KAPFFLSDFKDALS LQCLASILFLYCACMSPVITFGGLLGEATEGRISAIESLFGASLTG 532
NBCnl-A KAPFFLSDFKDALS LQCLASILFLYCACMSPVITFGGLLGEATEGRISAIESLFGASLTG 651
NBCnl-C KAPFFLSDFKDALS LQCLASILFLYCACMSPVITFGGLLGEATEGRISAIESLFGASLTG 643
NBCnl-D KAPFFLSDFKDALS LQCLASILFLYCACMSPVITFGGLLGEATEGRISAIESLFGASLTG 656
NBCnl-D' KAPFFLSDFKDALS LQCLASILFLYCACMSPVITFGGLLGEATEGRISAIESLFGASLTG 660

NBCnl-B IAYSLFAGQPLTILGSTGPVLVFEKILYKFCRDYQLSYLSLRTSIGLWTSFLCIVLVATD 716
NBCnl-E IAYSLFAGQPLTILGSTGPVLVFEKILYKFCRDYQLSYLSLRTSIGLWTSFLCIVLVATD 592
NBCnl-A IAYSLFAGQPLTILGSTGPVLVFEKILYKFCRDYQLSYLSLRTSIGLWTSFLCIVLVATD 711
NBCnl-C IAYSLFAGQPLTILGSTGPVLVFEKILYKFCRDYQLSYLSLRTSIGLWTSFLCIVLVATD 703
NBCnl-D IAYSLFAGQPLTILGSTGPVLVFEKILYKFCRDYQLSYLSLRTSIGLWTSFLCIVLVATD 716
NBCnl-D' IAYSLFAGQPLTILGSTGPVLVFEKILYKFCRDYQLSYLSLRTSIGLWTSFLCIVLVATD 720

NBCn1-B	ASSLVCIYITRFTEEAFAALICIIIFIYEALEKLFDLGETYAFNMHNNLDKLTYSYSCVCTEP	776
NBCn1-E	ASSLVCIYITRFTEEAFAALICIIIFIYEALEKLFDLGETYAFNMHNNLDKLTYSYSCVCTEP	652
NBCn1-A	ASSLVCIYITRFTEEAFAALICIIIFIYEALEKLFDLGETYAFNMHNNLDKLTYSYSCVCTEP	771
NBCn1-C	ASSLVCIYITRFTEEAFAALICIIIFIYEALEKLFDLGETYAFNMHNNLDKLTYSYSCVCTEP	763
NBCn1-D	ASSLVCIYITRFTEEAFAALICIIIFIYEALEKLFDLGETYAFNMHNNLDKLTYSYSCVCTEP	776
NBCn1-D'	ASSLVCIYITRFTEEAFAALICIIIFIYEALEKLFDLGETYAFNMHNNLDKLTYSYSCVCTEP	780

NBCn1-B	PNPSNETLAQWKKNITAHNISWRNLTVSECKKLRGVFLGSACGHHGPYIPDVLFWCVIL	836
NBCn1-E	PNPSNETLAQWKKNITAHNISWRNLTVSECKKLRGVFLGSACGHHGPYIPDVLFWCVIL	712
NBCn1-A	PNPSNETLAQWKKNITAHNISWRNLTVSECKKLRGVFLGSACGHHGPYIPDVLFWCVIL	831
NBCn1-C	PNPSNETLAQWKKNITAHNISWRNLTVSECKKLRGVFLGSACGHHGPYIPDVLFWCVIL	823
NBCn1-D	PNPSNETLAQWKKNITAHNISWRNLTVSECKKLRGVFLGSACGHHGPYIPDVLFWCVIL	836
NBCn1-D'	PNPSNETLAQWKKNITAHNISWRNLTVSECKKLRGVFLGSACGHHGPYIPDVLFWCVIL	840

NBCn1-B	FFTTFFLSSFLKQFKTKRYFPTKVRSTISDFAVFLTIVIMVTIDYLVGVSPKLVHVEKFL	896
NBCn1-E	FFTTFFLSSFLKQFKTKRYFPTKVRSTISDFAVFLTIVIMVTIDYLVGVSPKLVHVEKFL	772
NBCn1-A	FFTTFFLSSFLKQFKTKRYFPTKVRSTISDFAVFLTIVIMVTIDYLVGVSPKLVHVEKFL	891
NBCn1-C	FFTTFFLSSFLKQFKTKRYFPTKVRSTISDFAVFLTIVIMVTIDYLVGVSPKLVHVEKFL	883
NBCn1-D	FFTTFFLSSFLKQFKTKRYFPTKVRSTISDFAVFLTIVIMVTIDYLVGVSPKLVHVEKFL	896
NBCn1-D'	FFTTFFLSSFLKQFKTKRYFPTKVRSTISDFAVFLTIVIMVTIDYLVGVSPKLVHVEKFL	900

NBCn1-B	EPTHPERGWIISPLGDNPWWTLLIAAIPALLCTILIFMDQQITAVIINRKEHKLKKGAGY	956
NBCn1-E	EPTHPERGWIISPLGDNPWWTLLIAAIPALLCTILIFMDQQITAVIINRKEHKLKKGAGY	832
NBCn1-A	EPTHPERGWIISPLGDNPWWTLLIAAIPALLCTILIFMDQQITAVIINRKEHKLKKGAGY	951
NBCn1-C	EPTHPERGWIISPLGDNPWWTLLIAAIPALLCTILIFMDQQITAVIINRKEHKLKKGAGY	943
NBCn1-D	EPTHPERGWIISPLGDNPWWTLLIAAIPALLCTILIFMDQQITAVIINRKEHKLKKGAGY	956
NBCn1-D'	EPTHPERGWIISPLGDNPWWTLLIAAIPALLCTILIFMDQQITAVIINRKEHKLKKGAGY	960

NBCn1-B	HLDLLMVGVMGLGVCSVMGLPWFAATVLSISHVNSLKVSECSAPGEQPKFLGIREQRVT	1016
NBCn1-E	HLDLLMVGVMGLGVCSVMGLPWFAATVLSISHVNSLKVSECSAPGEQPKFLGIREQRVT	892
NBCn1-A	HLDLLMVGVMGLGVCSVMGLPWFAATVLSISHVNSLKVSECSAPGEQPKFLGIREQRVT	1011
NBCn1-C	HLDLLMVGVMGLGVCSVMGLPWFAATVLSISHVNSLKVSECSAPGEQPKFLGIREQRVT	1003
NBCn1-D	HLDLLMVGVMGLGVCSVMGLPWFAATVLSISHVNSLKVSECSAPGEQPKFLGIREQRVT	1016
NBCn1-D'	HLDLLMVGVMGLGVCSVMGLPWFAATVLSISHVNSLKVSECSAPGEQPKFLGIREQRVT	1020

NBCn1-B	GLMIFILMGLSVFMTSVLKFIPMPVLYGVFLYMGVSSLKGIQLFDRIKLFGMPAKHQPD	1076
NBCn1-E	GLMIFILMGLSVFMTSVLKFIPMPVLYGVFLYMGVSSLKGIQLFDRIKLFGMPAKHQPD	952
NBCn1-A	GLMIFILMGLSVFMTSVLKFIPMPVLYGVFLYMGVSSLKGIQLFDRIKLFGMPAKHQPD	1071
NBCn1-C	GLMIFILMGLSVFMTSVLKFIPMPVLYGVFLYMGVSSLKGIQLFDRIKLFGMPAKHQPD	1063
NBCn1-D	GLMIFILMGLSVFMTSVLKFIPMPVLYGVFLYMGVSSLKGIQLFDRIKLFGMPAKHQPD	1076
NBCn1-D'	GLMIFILMGLSVFMTSVLKFIPMPVLYGVFLYMGVSSLKGIQLFDRIKLFGMPAKHQPD	1080

	TM14---//---Ct	
NBCn1-B	IYLRVPLWKVHIIFTVIQLTCLVLLWVIVKVSAAAVVFPMMVLALVFVRKLMDLCTFKREL	1136
NBCn1-E	IYLRVPLWKVHIIFTVIQLTCLVLLWVIVKVSAAAVVFPMMVLALVFVRKLMDLCTFKREL	1012
NBCn1-A	IYLRVPLWKVHIIFTVIQLTCLVLLWVIVKVSAAAVVFPMMVLALVFVRKLMDLCTFKREL	1131
NBCn1-C	IYLRVPLWKVHIIFTVIQLTCLVLLWVIVKVSAAAVVFPMMVLALVFVRKLMDLCTFKREL	1123
NBCn1-D	IYLRVPLWKVHIIFTVIQLTCLVLLWVIVKVSAAAVVFPMMVLALVFVRKLMDLCTFKREL	1136
NBCn1-D'	IYLRVPLWKVHIIFTVIQLTCLVLLWVIVKVSAAAVVFPMMVLALVFVRKLMDLCTFKREL	1140

NBCnl-B	SWLDDLMPESKKKKEDDKKKKEKEEAERMLQDDDDTVHLPFEGGSLLQIPVKALKYS---	1192
NBCnl-E	SWLDDLMPESKKKKEDDKKKKEKEEAERMLQDDDDTVHLPFEGGSLLQIPVKALKYS---	1068
NBCnl-A	SWLDDLMPESKKKKEDDKKKKEKEEAERMLQDDDDTVHLPFEGGSLLQIPVKALKYS---	1187
NBCnl-C	SWLDDLMPESKKKKEDDKKKKEKEEAERMLQDDDDTVHLPFEGGSLLQIPVKALKYS	VDP 1183
NBCnl-D	SWLDDLMPESKKKKEDDKKKKEKEEAERMLQDDDDTVHLPFEGGSLLQIPVKALKYS	VDP 1196
NBCnl-D'	SWLDDLMPESKKKKEDDKKKKEKEEAERMLQDDDDTVHLPFEGGSLLQIPVKALKYS	VDP 1200

Cassette III

NBCnl-B	-----PDKPVSVKISFEDEPRKKYVDAETSL	1219
NBCnl-E	-----PDKPVSVKISFEDEPRKKYVDAETSL	1095
NBCnl-A	-----PDKPVSVKISFEDEPRKKYVDAETSL	1214
NBCnl-C	SIVNISDEMAKTAQWKALSMNTENAKVTRSNMSPDKPVSVKISFEDEPRKKYVDAETSL	1242
NBCnl-D	SIVNISDEMAKTAQWKALSMNTENAKVTRSNMSPDKPVSVKISFEDEPRKKYVDAETSL	1255
NBCnl-D'	SIVNISDEMAKTAQWKALSMNTENAKVTRSNMSPDKPVSVKISFEDEPRKKYVDAETSL	1259

Alignment 4: NDCBE variants. An alignment of human NDCBE-A, NDCBE-B, NDCBE-C, and NDCBE-D as depicted in Figure 37 of the review. Shown are the alternate Nt appendages (red vs purple) and the alternative long and short Ct that includes an auto inhibitory domain. Only the Nt appendage of NDCBE-E is included in this alignment, the remainder of the protein is identical to NDCBE-B.

NDCBE-E	MFNKNNSNKL RSTPRYRRGDPGYLNFTELGLPKPEQKDQWSQH	43
NDCBE-B	MPAAGSNEPDGVL SYQRPDEEAVVDQGGTSTILNIHYEKEELEGHRTL YVGV RMP LGRQS	60
NDCBE-D	-----MPLGRQS	7
NDCBE-A	MPAAGSNEPDGVL SYQRPDEEAVVDQGGTSTILNIHYEKEELEGHRTL YVGV RMP LGRQS	60
NDCBE-C	-----MPLGRQS	7

NDCBE-B	HRHHRTHGQKHRRRGRGKGASQGEEGLEALAHDTPSQRVQFILGTEEDEEHVPHELFTTEL	120
NDCBE-D	HRHHRTHGQKHRRRGRGKGASQGEEGLEALAHDTPSQRVQFILGTEEDEEHVPHELFTTEL	67
NDCBE-A	HRHHRTHGQKHRRRGRGKGASQGEEGLEALAHDTPSQRVQFILGTEEDEEHVPHELFTTEL	120
NDCBE-C	HRHHRTHGQKHRRRGRGKGASQGEEGLEALAHDTPSQRVQFILGTEEDEEHVPHELFTTEL	67

NDCBE-B	DEICMKEGEDAEWKETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCLINGTVLL	180
NDCBE-D	DEICMKEGEDAEWKETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCLINGTVLL	127
NDCBE-A	DEICMKEGEDAEWKETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCLINGTVLL	180
NDCBE-C	DEICMKEGEDAEWKETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCLINGTVLL	127

NDCBE-B	DMHANSIEEISDLILDQQELSSDLNDSMRVKVREALLKKHHHQNEKKRNLIPIVRSFAE	240
NDCBE-D	DMHANSIEEISDLILDQQELSSDLNDSMRVKVREALLKKHHHQNEKKRNLIPIVRSFAE	187
NDCBE-A	DMHANSIEEISDLILDQQELSSDLNDSMRVKVREALLKKHHHQNEKKRNLIPIVRSFAE	240
NDCBE-C	DMHANSIEEISDLILDQQELSSDLNDSMRVKVREALLKKHHHQNEKKRNLIPIVRSFAE	187

NDCBE-B	VGKKQSDPHLMDKHGQTVSPQSVPTTNLEVKNGVNCESHPVDLSKVDLHFMKKIPTGAEA	300
NDCBE-D	VGKKQSDPHLMDKHGQTVSPQSVPTTNLEVKNGVNCESHPVDLSKVDLHFMKKIPTGAEA	247
NDCBE-A	VGKKQSDPHLMDKHGQTVSPQSVPTTNLEVKNGVNCESHPVDLSKVDLHFMKKIPTGAEA	300
NDCBE-C	VGKKQSDPHLMDKHGQTVSPQSVPTTNLEVKNGVNCESHPVDLSKVDLHFMKKIPTGAEA	247

NDCBE-B	SNVLVGEVDILDRPIVAFVRLSPAVLLSGLTEVPIPTRFLFILLGPVKGQQYHEIGRSM	360
NDCBE-D	SNVLVGEVDILDRPIVAFVRLSPAVLLSGLTEVPIPTRFLFILLGPVKGQQYHEIGRSM	307
NDCBE-A	SNVLVGEVDILDRPIVAFVRLSPAVLLSGLTEVPIPTRFLFILLGPVKGQQYHEIGRSM	360
NDCBE-C	SNVLVGEVDILDRPIVAFVRLSPAVLLSGLTEVPIPTRFLFILLGPVKGQQYHEIGRSM	307

NDCBE-B	ATIMTDEIFHDVAYKAKERDDLLAGIDFLDQVTVLPPGEWDPSIRIEPPKNVPSQEKRK	420
NDCBE-D	ATIMTDEIFHDVAYKAKERDDLLAGIDFLDQVTVLPPGEWDPSIRIEPPKNVPSQEKRK	367
NDCBE-A	ATIMTDEIFHDVAYKAKERDDLLAGIDFLDQVTVLPPGEWDPSIRIEPPKNVPSQEKRK	420
NDCBE-C	ATIMTDEIFHDVAYKAKERDDLLAGIDFLDQVTVLPPGEWDPSIRIEPPKNVPSQEKRK	367

	Nt---//---TM1	
NDCBE-B	MPGVPNGNVCHIEQEPHGGHSGPELQRTGRLFGGLVLDIKRKAPWYSDYRDALSQCLA	480
NDCBE-D	MPGVPNGNVCHIEQEPHGGHSGPELQRTGRLFGGLVLDIKRKAPWYSDYRDALSQCLA	427
NDCBE-A	MPGVPNGNVCHIEQEPHGGHSGPELQRTGRLFGGLVLDIKRKAPWYSDYRDALSQCLA	480
NDCBE-C	MPGVPNGNVCHIEQEPHGGHSGPELQRTGRLFGGLVLDIKRKAPWYSDYRDALSQCLA	427

NDCBE-B	SFLFLYCACMSPVITFGGLLGEATEGRISAIESLFGASMTGAIYSLFAGQALTILGSTGP	540
NDCBE-D	SFLFLYCACMSPVITFGGLLGEATEGRISAIESLFGASMTGAIYSLFAGQALTILGSTGP	487
NDCBE-A	SFLFLYCACMSPVITFGGLLGEATEGRISAIESLFGASMTGAIYSLFAGQALTILGSTGP	540
NDCBE-C	SFLFLYCACMSPVITFGGLLGEATEGRISAIESLFGASMTGAIYSLFAGQALTILGSTGP	487

NDCBE-B VLVFEKILFKFCKDYALSYSLRACIGLWTAFLCIVLVATDASSLVCYITRFTEEFASL 600
NDCBE-D VLVFEKILFKFCKDYALSYSLRACIGLWTAFLCIVLVATDASSLVCYITRFTEEFASL 547
NDCBE-A VLVFEKILFKFCKDYALSYSLRACIGLWTAFLCIVLVATDASSLVCYITRFTEEFASL 600
NDCBE-C VLVFEKILFKFCKDYALSYSLRACIGLWTAFLCIVLVATDASSLVCYITRFTEEFASL 547

NDCBE-B ICIFIYEAEIekliHLAETYP IHMSQLDHLsLYYCRCTLPENPNNHTLQYWKDHNIVTA 660
NDCBE-D ICIFIYEAEIekliHLAETYP IHMSQLDHLsLYYCRCTLPENPNNHTLQYWKDHNIVTA 607
NDCBE-A ICIFIYEAEIekliHLAETYP IHMSQLDHLsLYYCRCTLPENPNNHTLQYWKDHNIVTA 660
NDCBE-C ICIFIYEAEIekliHLAETYP IHMSQLDHLsLYYCRCTLPENPNNHTLQYWKDHNIVTA 607

NDCBE-B EVHWANLTVSECQEMHGFEFMSACGHHGYPYTPDVLFWSCILFFTTFILSSTLTKTFKTSRY 720
NDCBE-D EVHWANLTVSECQEMHGFEFMSACGHHGYPYTPDVLFWSCILFFTTFILSSTLTKTFKTSRY 667
NDCBE-A EVHWANLTVSECQEMHGFEFMSACGHHGYPYTPDVLFWSCILFFTTFILSSTLTKTFKTSRY 720
NDCBE-C EVHWANLTVSECQEMHGFEFMSACGHHGYPYTPDVLFWSCILFFTTFILSSTLTKTFKTSRY 667

NDCBE-B FPTRVRSMVSDFAVFLTIFTMVIIDFLIGVSPKLVQPSVFKPTRDDRGWIINPIGPNPW 780
NDCBE-D FPTRVRSMVSDFAVFLTIFTMVIIDFLIGVSPKLVQPSVFKPTRDDRGWIINPIGPNPW 727
NDCBE-A FPTRVRSMVSDFAVFLTIFTMVIIDFLIGVSPKLVQPSVFKPTRDDRGWIINPIGPNPW 780
NDCBE-C FPTRVRSMVSDFAVFLTIFTMVIIDFLIGVSPKLVQPSVFKPTRDDRGWIINPIGPNPW 727

NDCBE-B WTVIAAIIIPALLCTILIFMDQQITAVIINRKEHKLKCGCYHLDLLMVAIMLGVCSIMGL 840
NDCBE-D WTVIAAIIIPALLCTILIFMDQQITAVIINRKEHKLKCGCYHLDLLMVAIMLGVCSIMGL 787
NDCBE-A WTVIAAIIIPALLCTILIFMDQQITAVIINRKEHKLKCGCYHLDLLMVAIMLGVCSIMGL 840
NDCBE-C WTVIAAIIIPALLCTILIFMDQQITAVIINRKEHKLKCGCYHLDLLMVAIMLGVCSIMGL 787

NDCBE-B PWFVAATVLSITHVNSLKLSECSAPGEQPKFLGIREQRVTGLMIFVLMGCSVFMTAILK 900
NDCBE-D PWFVAATVLSITHVNSLKLSECSAPGEQPKFLGIREQRVTGLMIFVLMGCSVFMTAILK 847
NDCBE-A PWFVAATVLSITHVNSLKLSECSAPGEQPKFLGIREQRVTGLMIFVLMGCSVFMTAILK 900
NDCBE-C PWFVAATVLSITHVNSLKLSECSAPGEQPKFLGIREQRVTGLMIFVLMGCSVFMTAILK 847

NDCBE-B FIPMPVLYGVFLYMGVSSLQGIQFFDRLKLFGMPAKHQPDFIYLRHVPLRKHVHLFTLIQL 960
NDCBE-D FIPMPVLYGVFLYMGVSSLQGIQFFDRLKLFGMPAKHQPDFIYLRHVPLRKHVHLFTLIQL 907
NDCBE-A FIPMPVLYGVFLYMGVSSLQGIQFFDRLKLFGMPAKHQPDFIYLRHVPLRKHVHLFTLIQL 960
NDCBE-C FIPMPVLYGVFLYMGVSSLQGIQFFDRLKLFGMPAKHQPDFIYLRHVPLRKHVHLFTLIQL 907

TM14---//---Ct

NDCBE-B TCLVLLWVIKASPAAIVFPMMLALVFVRKVMDLCSKRELSWLDDLMPESKKKKLDDAK 1020
NDCBE-D TCLVLLWVIKASPAAIVFPMMLALVFVRKVMDLCSKRELSWLDDLMPESKKKKLDDAK 967
NDCBE-A TCLVLLWVIKASPAAIVFPMMLALVFVRKVMDLCSKRELSWLDDLMPESKKKKLDDAK 1020
NDCBE-C TCLVLLWVIKASPAAIVFPMMLALVFVRKVMDLCSKRELSWLDDLMPESKKKKLDDAK 967

NDCBE-B KKAKEEEVIVLAPTVYLGASNYRT----- 1044
NDCBE-D KKAKEEEVIVLAPTVYLGASNYRT----- 991
NDCBE-A KKAKEEEEAEKMLEIGGDKFPLESRKLLSSPGKNISCRCDPSEINISDEMPKTTVWKALS 1080
NDCBE-C KKAKEEEEAEKMLEIGGDKFPLESRKLLSSPGKNISCRCDPSEINISDEMPKTTVWKALS 1027
***** : . . :

NDCBE-B -----
NDCBE-D -----
NDCBE-A MNSGNAKEKSLFN 1093
NDCBE-C MNSGNAKEKSLFN 1040

Alignment 4: NBCn2 variants. An alignment of human NBCn2-A, NBCn2-B, NBCn2-C, and NBCn2-D as depicted in Figure 40 of the review. Shown are the 30-aa cassette A and the alternative short and long Ct that includes a PDZ-protein binding motif. Note that the C-termini of human NBCn2-C and -D sequences are derived from an EST sequence ([CD102396](#)) as the full-length variants have not been cloned from human cDNA. Only the C-terminal sequence of rb3NCBE (emboldened) is included in this alignment.

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NBCn2-B      MEIKDQGAQMEPLLPTRNDEEAVVDRGGTRSILKTHFEKEDLEGHRTLFIGVHVPLGGRK 60
NBCn2-D      MEIKDQGAQMEPLLPTRNDEEAVVDRGGTRSILKTHFEKEDLEGHRTLFIGVHVPLGGRK 60
NBCn2-A      MEIKDQGAQMEPLLPTRNDEEAVVDRGGTRSILKTHFEKEDLEGHRTLFIGVHVPLGGRK 60
NBCn2-C      MEIKDQGAQMEPLLPTRNDEEAVVDRGGTRSILKTHFEKEDLEGHRTLFIGVHVPLGGRK 60
*****

NBCn2-B      SHRRHRHRGHKHKRKRDRERDSGLEDGRESFSFDTPSQRVQFILGTEDDDEEHIPHDLFTE 120
NBCn2-D      SHRRHRHRGHKHKRKRDRERDSGLEDGRESFSFDTPSQRVQFILGTEDDDEEHIPHDLFTE 120
NBCn2-A      SHRRHRHRGHKHKRKRDRERDSGLEDGRESFSFDTPSQRVQFILGTEDDDEEHIPHDLFTE 120
NBCn2-C      SHRRHRHRGHKHKRKRDRERDSGLEDGRESFSFDTPSQRVQFILGTEDDDEEHIPHDLFTE 120
*****

NBCn2-B      LDEICWREGEDAWEWRETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCILNGTVL 180
NBCn2-D      LDEICWREGEDAWEWRETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCILNGTVL 180
NBCn2-A      LDEICWREGEDAWEWRETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCILNGTVL 180
NBCn2-C      LDEICWREGEDAWEWRETARWLKFEEDVEDGGERWSKPYVATLSLHSLFELRSCILNGTVL 180
*****

NBCn2-B      LDMHANTLEEIADMVLDQQVSSGQLNEDVRHRVHEALMKQHHHQKQKLTNRIPIVRSFA 240
NBCn2-D      LDMHANTLEEIADMVLDQQVSSGQLNEDVRHRVHEALMKQHHHQKQKLTNRIPIVRSFA 240
NBCn2-A      LDMHANTLEEIADMVLDQQVSSGQLNEDVRHRVHEALMKQHHHQKQKLTNRIPIVRSFA 240
NBCn2-C      LDMHANTLEEIADMVLDQQVSSGQLNEDVRHRVHEALMKQHHHQKQKLTNRIPIVRSFA 240
*****

NBCn2-B      DIGKKQSEPNMSMDKNAGQVVSPPQSAPACVENKNDVSRENSTVDFSKGLGGQQKGHTSPCG 300
NBCn2-D      DIGKKQSEPNMSMDKNAGQVVSPPQSAPACVENKNDVSRENSTVDFSKGLGGQQKGHTSPCG 300
NBCn2-A      DIGKKQSEPNMSMDKNAGQVVSPPQSAPACVENKNDVSRENSTVDFSK----- 286
NBCn2-C      DIGKKQSEPNMSMDKNAGQVVSPPQSAPACVENKNDVSRENSTVDFSK----- 286
*****

NBCn2-B      MKQRHEKGPPHQQEREVDLHFMKKIPPGAEASNILVGELEFLDRTVVAFVRLSPAVLLQG 360
NBCn2-D      MKQRHEKGPPHQQEREVDLHFMKKIPPGAEASNILVGELEFLDRTVVAFVRLSPAVLLQG 360
NBCn2-A      -----VDLHFMKKIPPGAEASNILVGELEFLDRTVVAFVRLSPAVLLQG 330
NBCn2-C      -----VDLHFMKKIPPGAEASNILVGELEFLDRTVVAFVRLSPAVLLQG 330
*****

NBCn2-B      LAEVPIPTRFLFILLGPLGKGQQYHEIGRSIATLMTDEVFHDVAYKAKDRNDLVSGIDEF 420
NBCn2-D      LAEVPIPTRFLFILLGPLGKGQQYHEIGRSIATLMTDEVFHDVAYKAKDRNDLVSGIDEF 420
NBCn2-A      LAEVPIPTRFLFILLGPLGKGQQYHEIGRSIATLMTDEVFHDVAYKAKDRNDLVSGIDEF 390
NBCn2-C      LAEVPIPTRFLFILLGPLGKGQQYHEIGRSIATLMTDEVFHDVAYKAKDRNDLVSGIDEF 390
*****

NBCn2-B      LDQVTVLPPGEWDPSIRIEPPKNVPSQEKRKIPAVPNGTAAHGAEAPHGGHSGPELQRTG 480
NBCn2-D      LDQVTVLPPGEWDPSIRIEPPKNVPSQEKRKIPAVPNGTAAHGAEAPHGGHSGPELQRTG 480
NBCn2-A      LDQVTVLPPGEWDPSIRIEPPKNVPSQEKRKIPAVPNGTAAHGAEAPHGGHSGPELQRTG 450
NBCn2-C      LDQVTVLPPGEWDPSIRIEPPKNVPSQEKRKIPAVPNGTAAHGAEAPHGGHSGPELQRTG 450
*****

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Nt---//---TM1

NBCn2-B RIFGGLILDIKRKAPYFWSDFRDAFSLQCLASFLFLYCACMSPVITFGGLLGEATEGRIS 540
NBCn2-D RIFGGLILDIKRKAPYFWSDFRDAFSLQCLASFLFLYCACMSPVITFGGLLGEATEGRIS 540
NBCn2-A RIFGGLILDIKRKAPYFWSDFRDAFSLQCLASFLFLYCACMSPVITFGGLLGEATEGRIS 510
NBCn2-C RIFGGLILDIKRKAPYFWSDFRDAFSLQCLASFLFLYCACMSPVITFGGLLGEATEGRIS 510

NBCn2-B AIESLFGASMTGIAYSLFGGQPLTILGSTGPVLFVEKILFKFCKEYGLSYLSLRASIGLW 600
NBCn2-D AIESLFGASMTGIAYSLFGGQPLTILGSTGPVLFVEKILFKFCKEYGLSYLSLRASIGLW 600
NBCn2-A AIESLFGASMTGIAYSLFGGQPLTILGSTGPVLFVEKILFKFCKEYGLSYLSLRASIGLW 570
NBCn2-C AIESLFGASMTGIAYSLFGGQPLTILGSTGPVLFVEKILFKFCKEYGLSYLSLRASIGLW 570

NBCn2-B TATLCIILVATDASSLVCYITRFTEEFASLICIIFIYEALEKLFELSEAYPINMHNDLE 660
NBCn2-D TATLCIILVATDASSLVCYITRFTEEFASLICIIFIYEALEKLFELSEAYPINMHNDLE 660
NBCn2-A TATLCIILVATDASSLVCYITRFTEEFASLICIIFIYEALEKLFELSEAYPINMHNDLE 630
NBCn2-C TATLCIILVATDASSLVCYITRFTEEFASLICIIFIYEALEKLFELSEAYPINMHNDLE 630

NBCn2-B LLTQYSCNCVEPHNPSNGTLKEWRESNISASDIIWENLTVSECKSLHGEYVGRACGHDP 720
NBCn2-D LLTQYSCNCVEPHNPSNGTLKEWRESNISASDIIWENLTVSECKSLHGEYVGRACGHDP 720
NBCn2-A LLTQYSCNCVEPHNPSNGTLKEWRESNISASDIIWENLTVSECKSLHGEYVGRACGHDP 690
NBCn2-C LLTQYSCNCVEPHNPSNGTLKEWRESNISASDIIWENLTVSECKSLHGEYVGRACGHDP 690

NBCn2-B YVPDVLFWSVILFFSTVTLSATLKQFKTSRYFPTKVRISVSDFAVFLTILCMVLIDYAIG 780
NBCn2-D YVPDVLFWSVILFFSTVTLSATLKQFKTSRYFPTKVRISVSDFAVFLTILCMVLIDYAIG 780
NBCn2-A YVPDVLFWSVILFFSTVTLSATLKQFKTSRYFPTKVRISVSDFAVFLTILCMVLIDYAIG 750
NBCn2-C YVPDVLFWSVILFFSTVTLSATLKQFKTSRYFPTKVRISVSDFAVFLTILCMVLIDYAIG 750

NBCn2-B IPSPKLQVPSVFKPTRDRRGWFVTPGLPNPWWTVIAAIPALLCTILIFMDQQITAVIIN 840
NBCn2-D IPSPKLQVPSVFKPTRDRRGWFVTPGLPNPWWTVIAAIPALLCTILIFMDQQITAVIIN 840
NBCn2-A IPSPKLQVPSVFKPTRDRRGWFVTPGLPNPWWTVIAAIPALLCTILIFMDQQITAVIIN 810
NBCn2-C IPSPKLQVPSVFKPTRDRRGWFVTPGLPNPWWTVIAAIPALLCTILIFMDQQITAVIIN 810

NBCn2-B RKEHKLKKGCGYHLDLLMVAVMLGVCSIMGLPWFVAATVLSITHVNSLKESECSAPGEQ 900
NBCn2-D RKEHKLKKGCGYHLDLLMVAVMLGVCSIMGLPWFVAATVLSITHVNSLKESECSAPGEQ 900
NBCn2-A RKEHKLKKGCGYHLDLLMVAVMLGVCSIMGLPWFVAATVLSITHVNSLKESECSAPGEQ 870
NBCn2-C RKEHKLKKGCGYHLDLLMVAVMLGVCSIMGLPWFVAATVLSITHVNSLKESECSAPGEQ 870

NBCn2-B PKFLGIREQVRTGLMIFILMGSSVFMTSILKFIIPMPVLYGVFLYMGASSLKGIQFFDRIK 960
NBCn2-D PKFLGIREQVRTGLMIFILMGSSVFMTSILKFIIPMPVLYGVFLYMGASSLKGIQFFDRIK 960
NBCn2-A PKFLGIREQVRTGLMIFILMGSSVFMTSILKFIIPMPVLYGVFLYMGASSLKGIQFFDRIK 930
NBCn2-C PKFLGIREQVRTGLMIFILMGSSVFMTSILKFIIPMPVLYGVFLYMGASSLKGIQFFDRIK 930

NBCn2-B LFWMPAKHQPDFIYLRHVPLRKVHLFTIIQMSCLGLLWIKVSRAAIVFPMMLVLAIVFVR 1020
NBCn2-D LFWMPAKHQPDFIYLRHVPLRKVHLFTIIQMSCLGLLWIKVSRAAIVFPMMLVLAIVFVR 1020
NBCn2-A LFWMPAKHQPDFIYLRHVPLRKVHLFTIIQMSCLGLLWIKVSRAAIVFPMMLVLAIVFVR 990
NBCn2-C LFWMPAKHQPDFIYLRHVPLRKVHLFTIIQMSCLGLLWIKVSRAAIVFPMMLVLAIVFVR 990

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NBCn2-B KLMDLLFTKRELSWLDDLMPESKSKKKLEDAEKEEEQSMLAMEDEGTVQLPLEGHYRDDPS 1080
NBCn2-D KLMDLLFTKRELSWLDDLMPESKSKKKLEDAEKEEEQSMLAMEDEGTVQLPLEGHYRDDPS 1080
NBCn2-A KLMDLLFTKRELSWLDDLMPESKSKKKLEDAEKEEEQSMLAMEDEGTVQLPLEGHYRDDPS 1050
NBCn2-C KLMDLLFTKRELSWLDDLMPESKSKKKLEDAEKEEEQSMLAMEDEGTVQLPLEGHYRDDPS 1050
rb3NCBE KLMDFLFTKRELSWLDDLMPESKSKKKLEDAEKEH 1054
*****:*****

NBCn2-B VINISDEMSKTALWRNLLITADNSKDKESSFPSKSPS----- 1118
NBCn2-D VINISDEMSKTALWRNLLITADNSKDKESSFPSKIESRKEKKADSGKGVRETCL 1136
NBCn2-A VINISDEMSKTALWRNLLITADNSKDKESSFPSKSPS----- 1088
NBCn2-C VINISDEMSKTALWRNLLITADNSKDKESSFPSKIESRKEKKADSGKGVRETCL 1106
***** *

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