

**Supplementary Figure 1. Alignment of the deduced amino acid sequences of mammalian NBCe1-A orthologs.** Protein sequence alignments were generated using Clustal W (<http://www.ebi.ac.uk/Tools/msa/clustalw2/>). The GenBank protein accession numbers for the sequences used in this alignment are AAC51645 (human), ADM25849 (mouse), AAC40034 (rat), and AFS49951 (rabbit). Amino acid residues that are conserved among human, mouse, rat, and rabbit sequences are marked with asterisks. Amino acid residues that are predicted to comprise NBCe1-A domains are marked with an N (cytosolic amino-terminus), T (putative transmembrane spans), L (predicted cytosolic or extracellular loops that join putative transmembrane spans), or C (cytosolic carboxy terminus). Residues that are colored in red are poorly conserved among orthologs. Residues that are highlighted in yellow are not conserved between human and rabbit NBCe1-A. DIDS-binding motifs at the extracellular end of transmembrane span 5 are highlighted in gray. The three putative glycosylation sites in the third extracellular loop are highlighted in green. The four conserved cysteines in the third extracellular loop are highlighted in cyan.





mouse VIPEKDKKKKKEDEKDKKKKKKGLSDSDNDDSDCPYSEKVPSIKIPMDIMEQQPF<sup>L</sup>SDNK<sup>PL</sup> 1020  
rat VIPEKDKKKKKEDEKDKKKKKKGLSDSDNDDSDCPYSEKVPSIKIPMDITEQQPF<sup>L</sup>SDNK<sup>PL</sup> 1020  
human VIPEKDKKKKKEDEKDKKKKKKGLSDSDNDDSDCPYSEKVPSIKIPMDIMEQQPF<sup>L</sup>SD<sup>K</sup>SK<sup>PS</sup> 1020  
rabbit VIPEKDKKKKKEDEKDKKKKKKGLSDSDNDDSDCPYSEKVPSIKIPMDIMEQQPF<sup>L</sup>ES<sup>K</sup>SK<sup>PS</sup> 1020  
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CC

mouse DRE<sup>R</sup>S<sup>S</sup>TFLERHTSC 1035  
rat DRE<sup>R</sup>S<sup>S</sup>TFLERHTSC 1035  
human DRE<sup>R</sup>S<sup>P</sup>TFLERHTSC 1035  
rabbit DRE<sup>K</sup>S<sup>S</sup>TFLERHTSC 1035  
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