PKG phosphorylation site sequence alignment

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  1 ---------MARPREPSRSAAAGAGGA---STAGWSRPARARRRPRGPTQYGNIPVVRKMLEESRTLNVNCVDYMGQNAL  68
  1 MEGSPSLRRMTVMREKGRRQAV-RGPAFMFNDRGTSLTAEEERF-LDAAEYGNIPVVRKMLEESKTLNVNCVDYMGQNAL  78

 69 QLAVGNEHLEVTELLLKKENLARIGDALLLAISKGYVRIVEAILGHPGFAASRRLTLSPCEQELRDDDFYAYDEDGTRFS 148
 79 QLAVGNEHLEVTELLLKKENLARIGDALLLAISKGYVRIVEAILNHPGFAASKRLTLSPCEQELQDDDFYAYDEDGTRFS 158

149 PDITPIILAAHCHKYEVVHLLLLKGARIERPHDYFCRCADCAEKQRLDAFSHSRSRINAYKGLASPAYLSLSSEDPVLTA 228
159 PDITPIILAAHCQKYEVVHMLLMKGARIERPHDYFCKCGDCMEKQRHDSFSHSRSRINAYKGLASPAYLSLSSEDPVLTA 238

229 LELSNELAKLANIEKEFKNDYRKLSMQCKDFVVGVLDLCRDSEEVEAILNGDLESVEPLERHGHKASLSRVKLAIKYEVK 308
239 LELSNELAKLANIEKEFKNDYRKLSMQCKDFVVGVLDLCRDSEEVEAILNGDLESAEPLEVHRHKASLSRVKLAIKYEVK 318

309 KFVAHPNCQQQLLTIWYENLSGLREQTIAIKCLVVLVVALGLPFLAIGYWIAPCSRLGKILRSPFMKFVAHAASFIIFLG 388
319 KFVAHPNCQQQLLTIWYENLSGLREQTIAIKCLVVLVVALGLPFLAIGYWIAPCSRLGKILRSPFMKFVAHAASFIIFLG 398
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PKC phosphorylation site sequence alignment

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629 DHKFIENIGYVLYGIYNVTMVVVLLNMLIAMINSSYQEIEDDSDVEWKFARSKLWLSYFDDGKTLPPPFSLVPSPKSFVY 708
639 DHKFIENIGYVLYGIYNVTMVVVLLNMLIAMINSSYQEIEDDSDVEWKFARSKLWLSYFDDGKTLPPPFSLVPSPKSFVY 718

709 FIMRITNFSKCRRRRLQKDLELGMGNSKSRLNLFTQSNSRVFESHSFNSILNQPTRYQQIMKRLIKRYVLKAQVDKENDE 788
719 FIMRIVNFPKCRRRRLQKDIEMGMGNSKSRLNLFTQSNSRVFESHSFNSILNQPTRYQQIMKRLIKRYVLKAQVDKENDE 798

789 VNEGELKEIKQDISSLRYELLEDKSQATEELAILIHKLSEKLNPSALRCE 838
799 VNEGELKEIKQDISSLRYELLEDKSQATEELAILIHKLSEKLNPSMLRCE 848
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Supplementary Fig. 2: Sequence alignment of rat and human TRPC3 amino acid sequence.
Comparison of rat (top) with human (bottom) TRPC3 amino acid sequence. Yellow indicates identical amino acids. Red denotes Protein Kinase G (PKG) phosphorylation sites, green Protein Kinase C (PKC) phosphorylation sites. Note that the rat sequence is 10 amino acids shorter than the human sequence and that the main difference is found at the beginning of the two sequences, including lack of one PKG phosphorylation site in the rat clone.