

Supplementary figure 3. Alignment of the SREB receptors from human, *Asterias rubens*, and *Octopus vulgaris* that were cloned and tested in receptor assays in this study. Conserved residues are highlighted, with similar amino acids in gray and 100% conserved residues in black.

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SREBhsap85  -----MANYSHAADNILQNLS 17
SREBhsap173 -----MANTTGEPEEVSGALS 17
SREBhsap27  -----MANASEPGSGGG 13
SREBARub    MSHIITTRIRPPPARLSFAPTGMSELSTAMSTLLDLGFTNGSTGLNSSAGDSISVTARTVLHAGVRPGEEGGGDADLLAD 80
SREB0vu1    -----MHTEVYTHASYSYYSE 16

SREBhsap85  --LTAFLKLTSIGFTIGVSVGNLLISILVVKDKTLHRAPYYFLDLCCSDILRSAICFPFVNSVKNGSTWT---YGT 92
SREBhsap173 PSASAYVKLVLLGLIMCVSLAGNAILSLVLKERALHKAPYYFLDLCLADGIRSAVCFPFVLASVRHGSSWT---FSAL 94
SREBhsap27  EAAALGLKLATLSLLCVSLAGNVLFALLIVRERSLHRAPYYLLDLCLADGLRALACLPAVMLAARRAAAAAGAPPGAL 93
SREBARub    DHGPRVLWCASLIVVILSVVGNILALVFGNSRLRRPSYFFLNCALADFVRSLLCFPFVVSADVSRDWIY----SNS 156
SREB0vu1    PQYVLALKIISLALIFTGILGNSMVVYTIIRDKRLHRPPFYFLVSLAMSDLARSVFCLPFVLTTVIQGYVWVY---GEN 93

SREBhsap85  TCKVIAFLGVLSCFHTAFMLFCISVTRYLAIAHHRFYTKRLTFWTCLA-VICMVVTLVMAFPFVLDVGTYSFIREEDQ 171
SREBhsap173 SCKIVAFMAVLFCFHAAFMLFCISVTRYMAIAHHRFYAKMTLWCAA-VICMANTLSVMAFPFVFDVGTYKFIREEDQ 173
SREBhsap27  GCKLLAFLAALFCFHAAFLLLGVGTRYLAIAHHRFYAERLAGWPCAAMLVCAAWALALAAAFPPVLDGGGD---DEDAP 170
SREBARub    LCEILAFFNVYLYTYGVLYTLFLISTERYVVLRFHRRHQKLGPAQLL-LVLSMALAVSMAFPFVFNTRTYSFIEIENQ 235
SREB0vu1    ACILVGFTNTFFIYSSAVTFLLISGDYVGVVQTRFYRRKCGGLLSLA-FIVFGWGVAFVLSFPPIFGLGSYTFVPSEAQ 172

SREBhsap85  CTFAQHRSFRANDSLGFMLLLALILLATQLVYLKLIFFVHRRKMKPVQFVAAVSQNWTFHGPASGQAAANWLAGFGRGP 251
SREBhsap173 CIFEHYRFKANDTLGFMLMLAVLMAATHAVYGKLLLEFYRHRKMKPVQMVPAISQNWTFHGPATGQAAANWLAGFGRGP 253
SREBhsap    CALEQRPDGPAGLGFLLLLAVVVGATHLYLRLFFIHDRKMRPARLVPAVSHDWTFHGPATGQAAANWLAGFGRGP 250
SREBARub    CTFKHQEQYKNETLCFLLFFVAVIAFTHFAYFRVFLFMRHRKMRPMQFVPAVSNWTFYGPSTGQAAANWFLGYRQGP 315
SREB0vu1    CTYSHTHYRNDTLVFLLLVFTFIMSLSLLYYRI LMFRLNRHKMYPFFHQPARSNWTFHGPANGQALVNWLNGETGFR 252

SREBhsap85  TPPTLLGIRQNANTTGRRLVLVLEFKME-KRISRMFYIMTFLFLTLWGPLYLVACYWRVFARGPVVPGGFLTAAVWMSFA 330
SREBhsap173 MPPTLLGIRQNGHAASRR-LLGMDEVKGE-KQLGRMFYAITLLFLLWSPYIVACYWRVFVKACAVPHRYLATAVWMSFA 331
SREBhsap27  TPAALVGIRPAGPGRGARRLLVLEEFKTE-KRLCRMFYAVTLLFLLWGPYVWASYLRVLVRPGAVPQAYLTASVMTFA 329
SREBARub    TPPPLIGLAP--PANGNSTLSKSDFERE-EKFSKLSLTITISFSVLWLPYTVYCFWQVFQHNPLPYTYVSIATWLTFF 392
SREB0vu1    QNPWLNPIAAGFQMPPRQLGRTVNLKVVKGHELSLFFFTVLVFDILWPLYLVLSYWQVFEVSHQLSSTIGVAAMCSYL 332

SREBhsap85  QAGINPVFCIFSRELRCFSTTLLYCRK--SRLPREPYCVI---- 370
SREBhsap173 QAAVNPIVCFLLNKDLKKCLRTHAPCWGTGGAPAPREPYCVM---- 373
SREBhsap27  QAGINPVVCFLFNRELRCFRAQFPCCQSPRTTQATHPCDLKGIGL 375
SREBARub    QACINPILCFVVSKEFRQIALQHVFGASAFQEGHNVQL----- 431
SREB0vu1    AVAVNPLVYLCCSGTLRRRAFRPEIESYSKRGTLRE----- 367

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