

Nucleotide sequence of a human oncogene active in tumors of secretory epithelium

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A novel human oncogene isolated from the human breast cancer cell line MCF7 and designated *sec*, was identified based upon its ability to transform NIH3T3 cells in culture. Sucrose gradient fractionated DNA from a tertiary transformant, enriched for transforming activity, was utilized to generate a restricted recombinant library in the PBR322 plasmid (1). The library was screened by sib selection and transfection to identify a plasmid containing a cellular insert of 4.0 kb whose transforming activity was 3.0×10^4 foci per microgram. The *sec* gene is altered in human breast, colon and prostate carcinomas by amplification, rearrangement or deletion.

The transforming region was localized to a 2.2 kb segment of the 4.0 kb cellular insert. This region was sequenced in both

directions and a single open reading frame was identified encoding a putative protein of 109 amino acids. Two polyadenylation signals were present beginning at 78 and 132 bases after the termination codon. *Sec* is an intronless gene having a message size of approximately 1.0 kb which has been detected in secretory epithelial tissue but not in lymphoid, myeloid or fibroblastic tissues. Screening of the 60.0 version of GenBank indicated that *sec* is not homologous to previously described genes.

REFERENCE

1. Lane, M.A., Sainten, A. and Cooper, G.M. (1981) *Proc. Natl. Acad. Sci. USA* 78, 5189–5195.

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      10      20      30      40      50      60
CCTTTTGGTCACAGCAGGAGATGCGGGCTCAGGACCGGCAGCTGGCAGGGCAGCCTGTCA
      M R A Q D R Q L A G Q P V

      70      80      90     100     110     120
GGCTGCGGGCCCGGCTGCACAGACTGAAAGTGGACCAAGTCTGTACCTGCACCCAGGAGC
R L R A R L H R L K V D Q V C H L H Q E

      130     140     150     160     170     180
TTCTGGATGAGGCTGAGCTGGAGATGGAGTTAGAGTCTGGGACTGGCTTGCCTCTGGCCC
L L D E A E L E M E L E S G T G L P L A

      190     200     210     220     230     240
CACCGCTGCGGCATCTGGGACTCACGCGCATGAACATCAGTCCAGACGCTTCACCTCTG
P P L R H L G L T R M N I S A R R F T S

      250     260     270     280     290     300
CTGACAGCAGACTTGGGTGTCTTTCAGTATCTGGGAGAAAAGGAAGGAAGGAGGTCC
A D S R L G C L L Q Y L G E R R K E E V

      310     320     330     340     350     360
CCGACCCCGGAGGCTCTGGCTACCTGCTGGGGAAGGTGGCAACACTTAGGTTTCCAAAA
P D P G G S G Y L L G K V G N T U

      370     380     390     400     410     420
GCTGAATTTAGAGAGCACAGGATGGAGGGGAGGAGGAGGAAACTCGGTGGGCCCCCAA

      430     440     450     460     470     480
TGTCTTAATAAAAAATGCATTGAATCCCATCAAGBTTTCTGTAGACTGTACAGAGCCTA

      490     500     510     520     530     540
AATAAATGTTGTTGTATATTCATCCTGTGTCACTGGGACTTTAGGGATTCCACAACAGGA

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