

Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) gene

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Melanoma growth stimulatory activity (MGSA) is a polypeptide secreted by human melanoma cells and a number of other cell types (1). Recent studies have shown that MGSA has both mitogenic and neutrophil chemotactic activities (2) and there is growing evidence that transcription of the MGSA gene is regulated by a number of growth factors and mediators of the inflammatory response (including MGSA) (3, 4). In addition, the MGSA protein appears to be involved in growth regulation, tumor progression and the inflammatory response (4, 5, 6, 7). To enable further study of the regulation of MGSA we isolated a clone carrying the MGSA gene from a λ fix human blood genomic library. Comparison of the sequence of the genomic DNA with the sequence of a nearly full length cDNA previously characterized (3) showed exact correspondence within the exon sequences. A coupling of the sequence data with a determination of the initiation site of the gene (designated base +1) by primer-extension analysis of MGSA mRNA revealed the structure of the MGSA gene. The 1845 bp MGSA gene and 50 bp of its 5' flanking DNA are shown below. The gene is composed of four exons (underlined upper case letters) of 179, 124, 84, and 716 bp in size interrupted by three introns (lower case letters) of 98, 113, and 531 bp in size, respectively. The 5' flanking DNA contains a TATA box (CATAAAA) at position -30 to -24. The exons of the MGSA gene are similar in both size and

sequence to those of other members of the β -thromboglobulin superfamily (8).

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-50
 5' - GCTTCCAGCCCAACCATGCATAAAAGGGTTCGCGGATCTCGGAGGC
 +1 CACAGAGCCCGGGCCGAGGCACCTCCTCGCGAGCTCTTCGCTCCTCTCACAGCGCCAGACCCGCTGCTGAGCCCATGGCCGCGCTGCTCTCTCC 100
GCCGCCCCAGCAATCCCGGCTCCTGCGAGTGGCACTGCTGCTCCTGCTCCTGTAGCGCTGGCCGGCGCAGCAGtgggtaccggcgcctgggg 200
tccccgggcccggcgcgctgggtagggcaccagcgcgacagcctcctcagtcagtgagtcctctctccctagGAGCGTCCGTGGCCACTGA 300
CGCTGCCAGTCTGCAGACCTGCAGGGAATCACCCCAAGAACATCAAAGTGTGAACGTGAAGTCCCCGGACCCCACTGCGCCAAACCGAAGTCA 400
Igtaagtcctcccccgcctgctcctgcccaccgccccgggtcccagaccctcctgctgccccaccctgtccccagcccgcctcctgcctcacgagatc 500
ccttcctctgagAGCCCACTCAAGAATGGGGGAAAGCTTGCCTCAATCCTGCATCCCCATAGTTAAGAAAATCATCGAAAAGATGCTGAACAGt 600
gagttatgggttccatgtacacagggcactggagccgttggcagaactgagcagtgcccccaaaaaataaacaggaaaaccagggttagttg 700
aaggactagaaatgggattatgttttcacaattaaggttccctttacgataattactgctcgtggtgccagaggatattccaatgcctggcgtccccca 800
ccctgggtctctcctcgttccaatgaatgtaggtaaaactgccttcatttgaggcccagtaggacaaacagcaacaggttctggctgttttaaccaat 900
agtacagtgagaccaccgccccccccccattcctaaaagagcatcccaagcttagaggtccccgccacagcacagctgtcataggcagtagc 1000
cacttggttgccaggctgggaaactgattcggagaacttagaggtggaggagcaggcaggagaagagtggttgcaatcagcttccccgagcacc 1100
tactcagggcaccattttctcattgagTGACAAATCCAAGTACCAGAGGGAGGAGGAAGCTCACTGGTGGCTGTCTCGAAGGAGGCCCTGCCCTT 1200
ATAGGAACAGAAAGAGAGAGACACAGCTGCAGAGGCCACCTGGATTGTGCCTAATGTGTTGAGCATCGCTTAGGAGAAGTCTTCTATTATTAT 1300
TTATTCAATAGTTTTGAAGATCTATGTTAATATTTAGGTGTAATAATTAAGGGTATGATTAACCTACCTGCACACTGCTCTATTATATTCATCT 1400
TTTTGAAATGTCAACCCCAAGTGTAGTTCAATCTGGATTCATATTTAATTTGAAGGTAGAATGTTTTCAATGTTCTCCAGTCATTATGTTAATATTTCTG 1500
AGGAGCCTGCAACATGCCAGCCACTGTGATAGAGGCTGGCGGATCCAAGCAAAATGGCCAAATGAGATCATTGTGAAGGCAGGGAATGTATGTGCACATCT 1600
GTTTTGTAAGTGTATAGTGAATGTCAGTGTATTTATTTGAAATGATTTACAGTGTGTGGTCAACATTTCTCATGTTGAAACTTTAAGAACTAAAATG 1700
TTCTAATATCCCTTGGACATTTTATGTCTTCTGTGAAGGCATACTGCCTGTTTAAATGGTAGTTTTACAGTGTCTGGCTTAGAACAAAGGGGCTTA 1800
ATTATTGATGTTTTTCATAGAGAATATAAAAATAAAGCACTTATAG-3' 1845