Nucleotide sequence of the plasmid stimulating portion of *Xrep*

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An X-linked sequence which improves the yields of bacterial and yeast plasmids has been described (1). This 2,356 bp DNA fragment, termed "Xrep", has notable similarities with papovaviral replication and control regions. I now present the sequence containing the 225 bp Xrepb fragment which has the largest effect on plasmid yield. Viral genome similarities were found specifically mapping to the same region of sequence that boosts plasmid yield (underlined). This region includes a 76% similarity with the short terminal repeat of herpes virus (bold type). The yield-boosting portion of the sequence is open in all three reading frames and hybridizes with RNA from fibroblasts. At the amino acid level, the sequence has a short region of similarity with a proline rich sequence (consensus: P(R/P)PPP(S/R)) which is unique to the gag polypeptide of several leukemia and sarcoma viruses (2-5).

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ACACACACACACACACACACACACACACACACAGCCAGAAGCGCACTCTGGCGTGCACAC      64
ACATGAGACTGACCTCACTTGGGTACATTATCTAGTCACACACATTCACACCCACACTCTGAC    128
CCACACCATCATCCATGCAAAACCCCTCACACACTTAAACACATCCCTCCCCAGAACCAAATTTG  192
ACCTAACATGGCTGATGGGGCGTGGGAGGGTCCAGTCAGGATGTCCCCTCTGGACCTGGCCCCAC  256
TCACCGACCTGTGAACTCCAGGCCCTTGTCTCAAGGTGGAGCCCCACCTGTCCCTGTCCCTAGT   320
GGTCACAGGTCTGTAACACCCCCACTCTCGGCCCCCGAAGCCTGGTCACCATCGCGTGCACAGA   384
ATCCTGGGAGCCTGGCTGGCCCTTAGGGTAGGGGGTATGGGAAAAGGGAAAGATGTGGGGCATAG  448
TGCCCTGCCCTGTCTAGCCGCTCCTCCCTCGGGATTTCCATCCCGGCTCGCGCGGGGCCGCT    512
AGAAGCCGGTGCCTTTGTCTCCCGCCCCGCTCCTGGCACGTTTCCGTGGAAGCTTCCCGCGCC   576

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      E A P P P R (P R P P P S) P R R
GGCCCGAAGCCCCCTTCGCGGCCGCGCCCCCGCCAGCCGCGCGCAGGCCCTGCCAGTGC    640
GGCGACCGCGCTTTGTCTCTCGAGGATGCCTGGGCCGAGCGCGAAAGCCCCATGCCTTGGAG    704
CGAGCCACCGCGCTCTGGAAGCAGGTCCCCGAGCCTCGGTTTGGGGTGCGCCCTGCATCGGA    768
CGGAGCAGCCCCCAAGATTGCGGGGCACAAGGTTGGGGGTAGCGTCTACCTGGAGCTCTTGAG    832
TGCTTGAGGGGGAGACCCGCCCTCCTCCGCTCTGTACATGCCCATCTGGGATTGGCCCCAGCTG  896
CGGTGCCAGAGGCTCGGTCCCCGGGGCGTGGTGGGCTAGGGCGGGTCTGTTACTTAGAGCCC    960
CAGGCTGGATCC                                                                973

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