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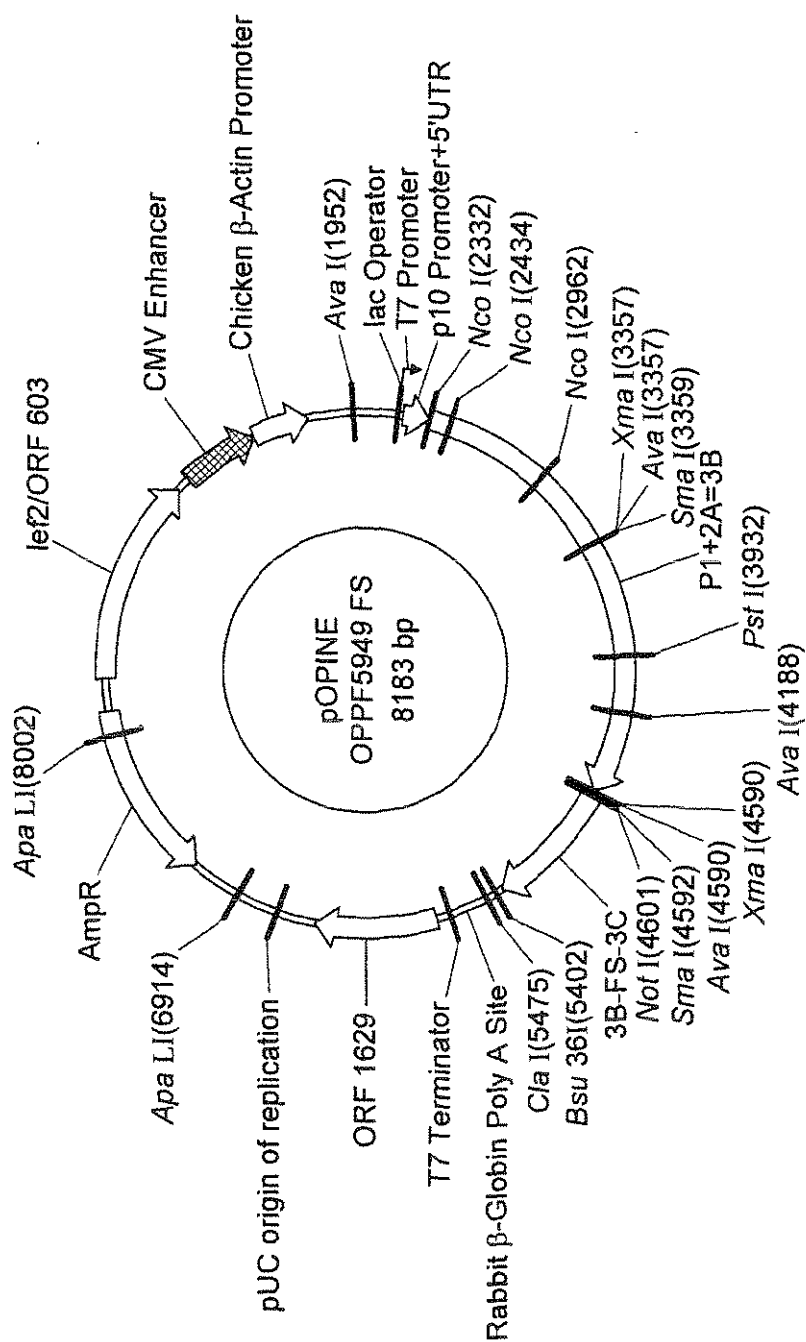


FIG. 1

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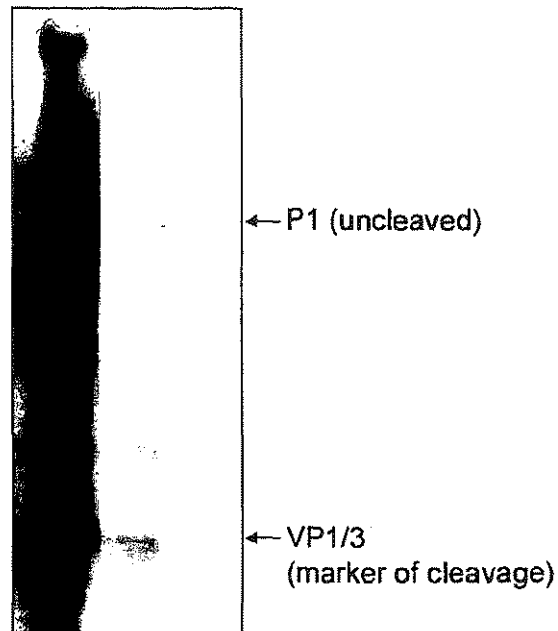


FIG. 2

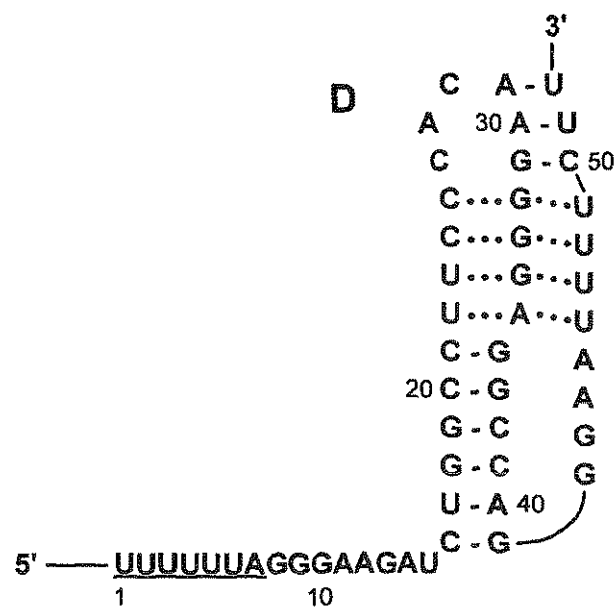


FIG. 3

4261	CTACACCCGC	CCACACCCGC	TGTTGGGCAAC	AGTGTACAAC	GGGACGAGCA	AGTACTCCGC	GATGTGGCGC	GGTGTGGCGC	ACAACCGTTG	TCACATGTTG	CCCTGCTCGT	TCATGAGGCG	
	*2 Ala Gly Gly Thr	Gly Arg Arg	Gly Asp Leu Gly	Pro Leu Ala	Ala Arg Val	Ala Ala Gln Leu							
4321	AGGTGGTACG	GGCAGACGGG	GCGACCTAGG	GCTCTCGCG	GCGAGGGTCG	CCGCTCAGCT	TCCACCATGC	CCGTCTGCCC	CGCTGGATCC	CGGAGAGCGC	CGCTCCAGC	GGCGAGTCGA	
	*2 Leu Pro Ala Ser	Phe Asn Phe	Gly Ala Ile	Gln Ala Thr Thr	Ile His Glu	Leu Leu Val Arg							
4381	TCCTGCTTCT	TTCAACTTTG	GTGCAATTCA	AGCCACGACC	ATCCACGAGC	TCCTCGTGCG	AGGACGAAGA	AAGTTGAAAC	CACGTTAAGT	TCGGTGCTGG	TAGGTGCTCG	AGGAGCACGC	
	*2 Arg Met Lys Arg	Ala Glu Leu	Tyr Cys Pro Arg	Pro Leu Leu	Ala Val Glu	Val Ser Ser Gln							
4441	CATGAAGCGT	GCCGAACCTCT	ACTGCCCCAG	ACCACTGTTG	GCACTGGAGG	TGTCGTCTCA	GTACTTCCGA	CGGCTTGAGA	TGACGGGGTC	TGGTGACAAC	CGTCACCTCC	ACAGCAGAGT	
	*2 Gln Asp Arg His	Lys Gln Lys	Ile Ile Ala Pro	Ala Lys Gln	Leu Leu Asn	Phe Asp Leu Leu							
4501	AGACAGACAC	AAACAGAAGA	TCATTGCACC	TGCAAAACAA	CTTTTGAAC	TCGATTTGCT	TCTGTCTGTG	TTTGTCTTCT	AGTAACGTGG	ACGTTTGTG	GAAAACTTGA	AGCTAAACGA	
				Small									
				Xmal									
				Aval									
					NotI								
	*2 Leu Lys Leu Ala	Gly Asp Val	Glu Ser Asn	Pro Gly Pro	Ser Gly Arg	Gly Pro	Phe Leu Gly						
	*1												Phe Arg
4561	CAAGTTGGCA	GGAGACGTTG	AGTCCAACCC	CGGGCCACGC	GGCCGCGGAC	CTTTTTTAGG	GTTCAACCGT	CCTCTGCAAC	TCAGGTTGGG	GCCCGGGTCG	CCGGCGCCTG	GAAAAAATCC	
	*2 Gly Lys Ile Trp	Pro Ser Tyr	Lys Gly Arg	Pro Gly Asn	Phe Leu Thr	Arg Asp Arg	...						
	*1	Glu Asp Leu	Ala Phe Leu	Gln Gly Lys	Ala Arg Glu	Phe Ser Tyr	Glu Gly	Pro Val Lys					
4621	GAAGATCTGG	CCTTCCTACA	AGGGAAGGCC	AGGGAATTTT	CTTACGAGGG	ACCGGTGAAG	CTTCTAGACC	GGAAGGATGT	TCCTTCCGG	TCCCTTAAAA	GAATGCTCCC	TGGCCACTTC	
	*1	Lys Pro Val	Ala Leu Lys	Val Lys Ala	Lys Asn Leu	Ile Val Thr	Glu Ser Gly	Ala Pro					
4681	AAGCCTGTCT	CTTTGAAAGT	GAAAGCTAAG	AACCTTGATTG	TCAGTGAAG	TGGAGCCCCA	TTCCGACAGC	GAAACTTTCA	CTTTCGATT	TTGAACTAAC	AGTGAAGTCT	ACCTCGGGGT	
	*1	Pro Thr Asp	Leu Gln Lys	Met Val Met	Gly Asn Thr	Lys Pro Val	Glu Leu	Ile Leu Asp					
4741	CCGACCGACT	TGCAAAAGAT	GGTCATGGGC	AACACCAAGC	CTGTTGAGCT	CATCCTCGAC	GGCTGGCTGA	ACGTTTTCTA	CCAGTACCCG	TTGTGGTTTCG	GACAACTCGA	GTAGGAGCTG	
	*1	Gly Lys Thr	Val Ala Ile	Cys Cys Ala	Thr Gly Val	Phe Gly Thr	Ala Tyr	Leu Val Pro					
4801	GGGAAGACGG	TGGCCATTTG	TTGTGCTACC	GGAGTGTGTTG	GCACTGCGTA	CCTCGTGCC	CCCTTCTGCC	ACCGGTAAAC	AACACGATGG	CCTCAAAAC	CGTGACGCAT	GGAGCACGGA	
	*1	Arg His Leu	Phe Ala Glu	Lys Tyr Asp	Lys Ile Met	Leu Asp	Gly Arg	Ala Met	Thr Asp				
4861	CGTCATCTTT	TTGCAGAAAA	ATATGACAAG	ATCATGCTGG	ACGGCAGAGC	CATGACAGAC							

FIG. 4

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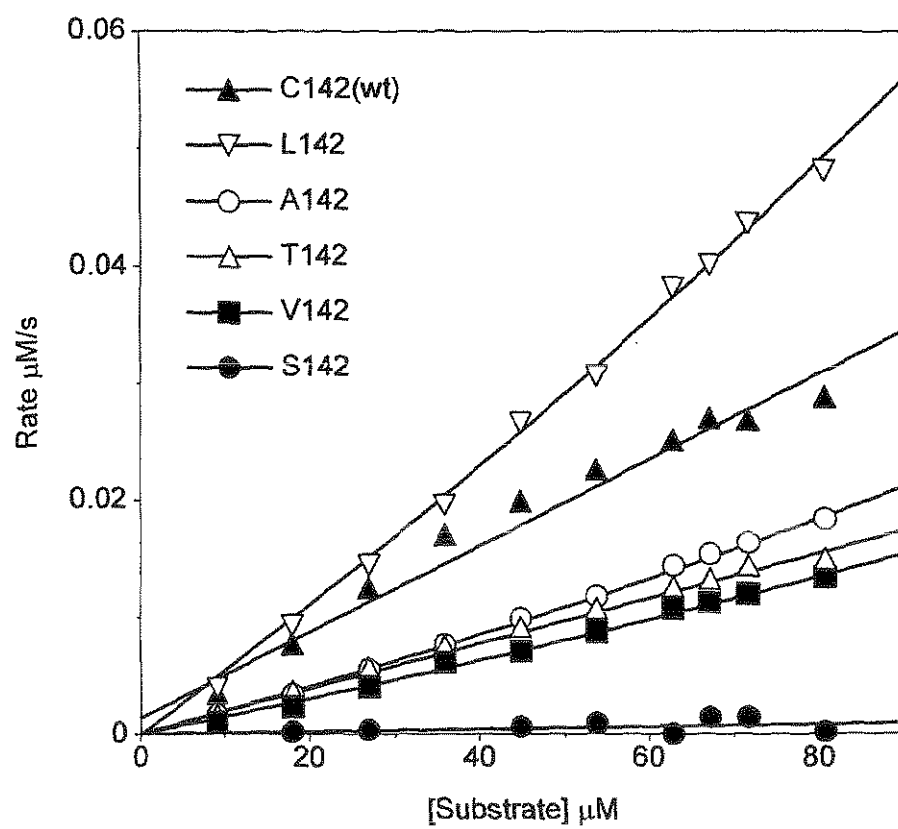


FIG. 5

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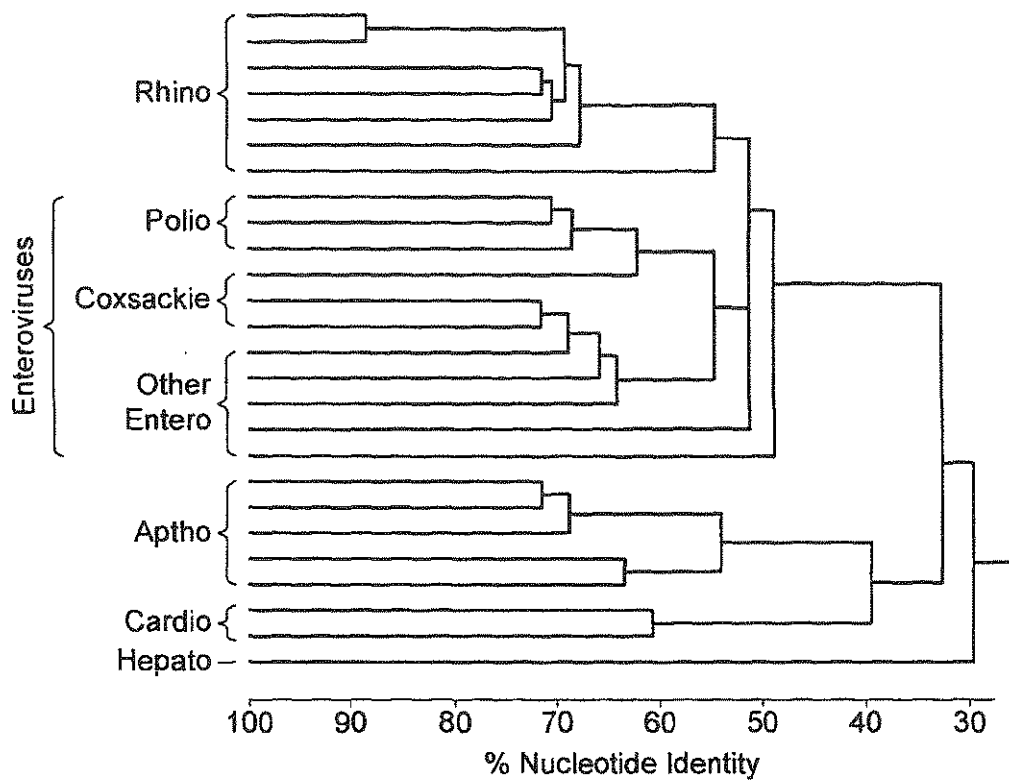


FIG. 6

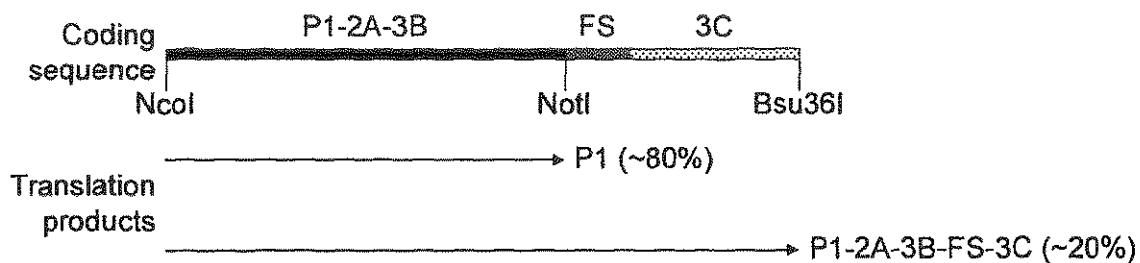


FIG. 7

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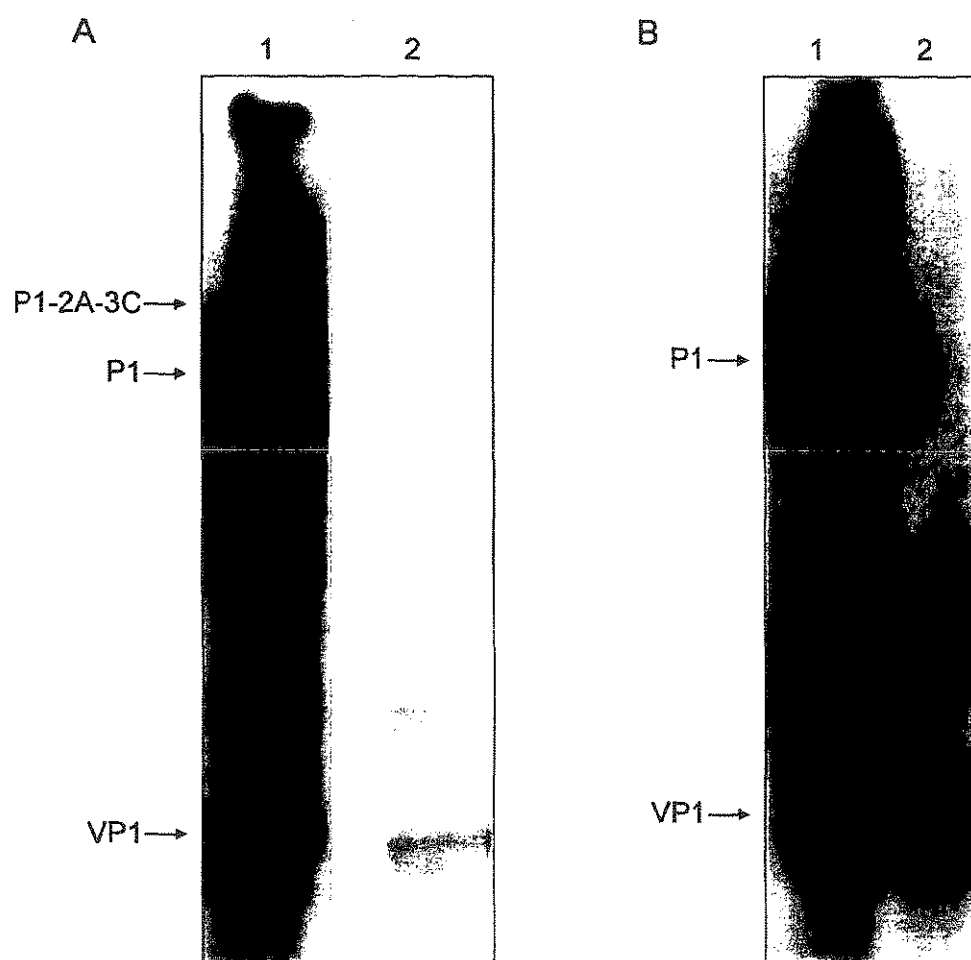


FIG. 8

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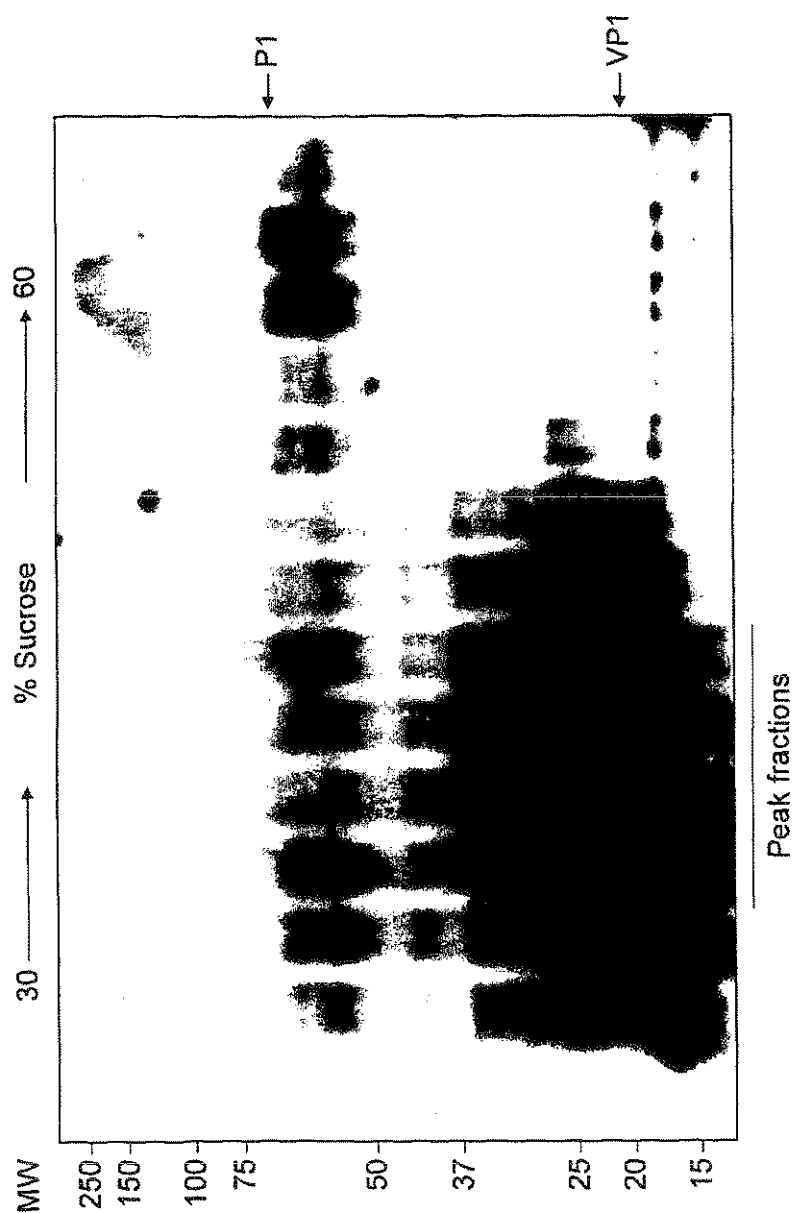


FIG. 9

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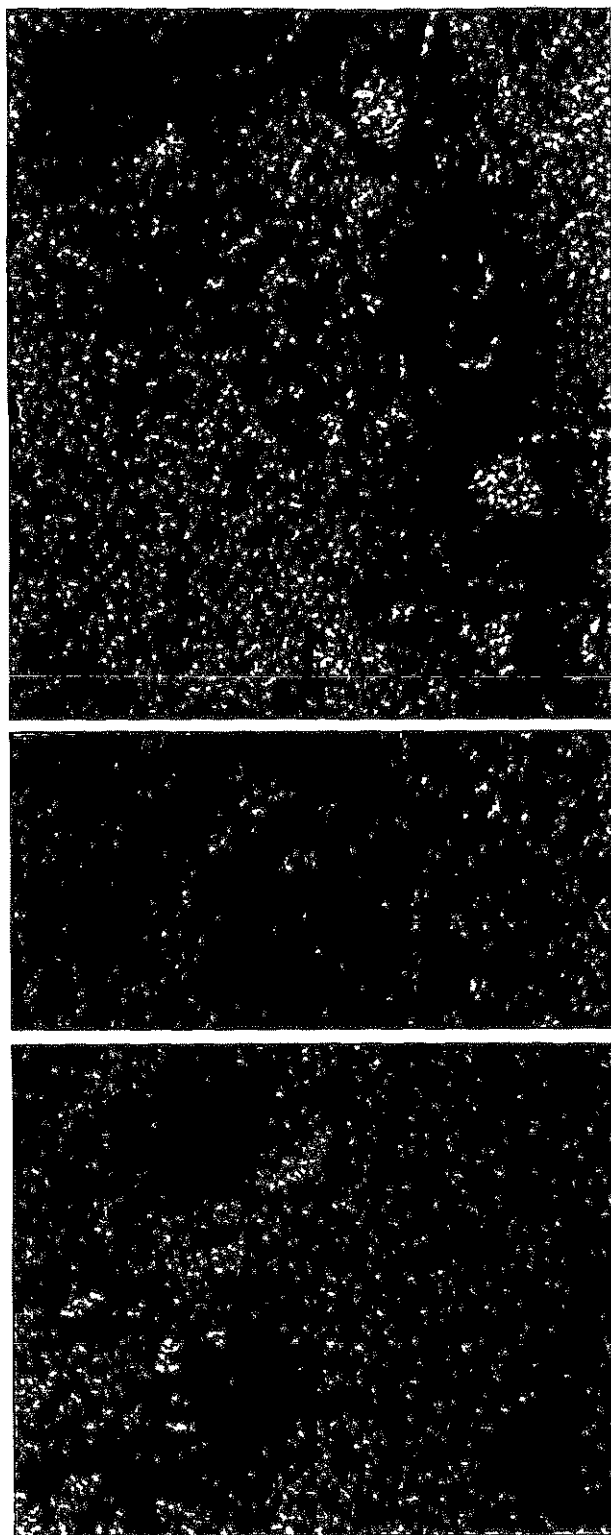


FIG. 10

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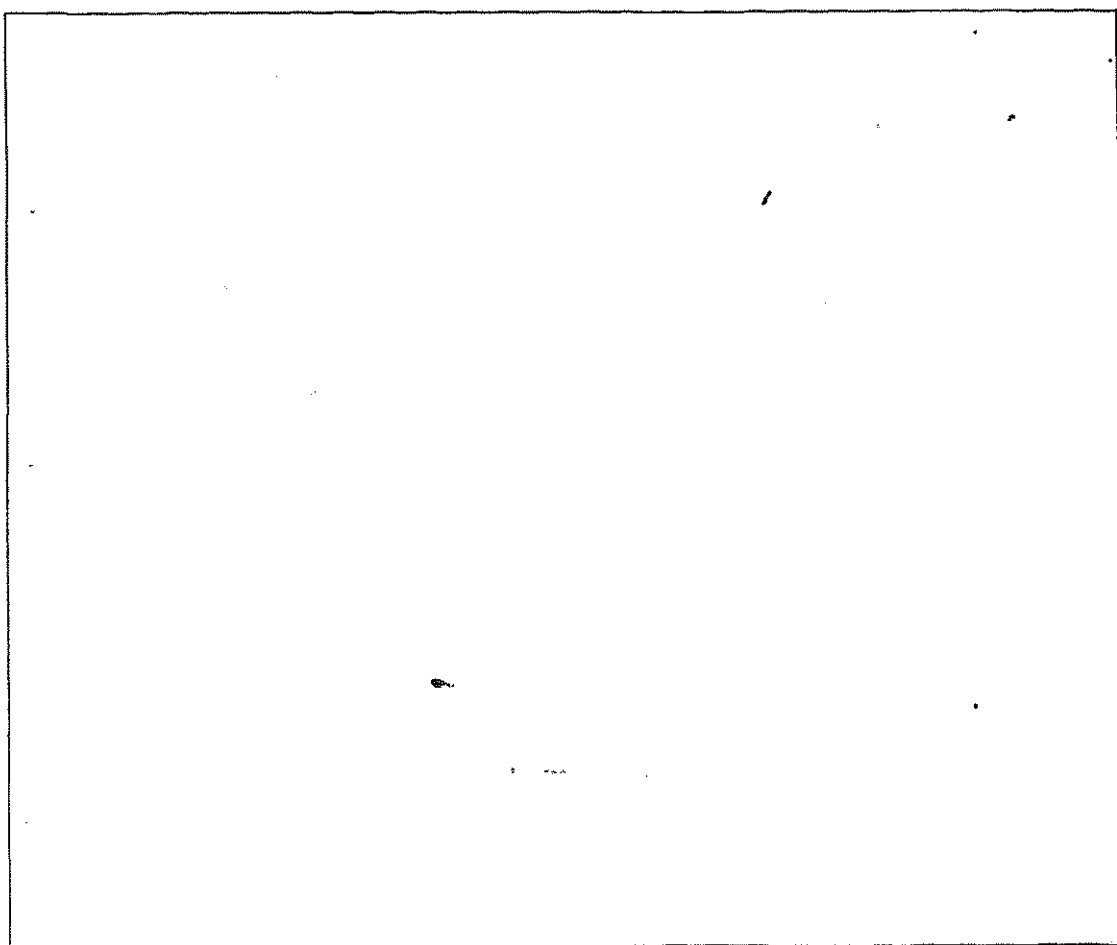


FIG. 11

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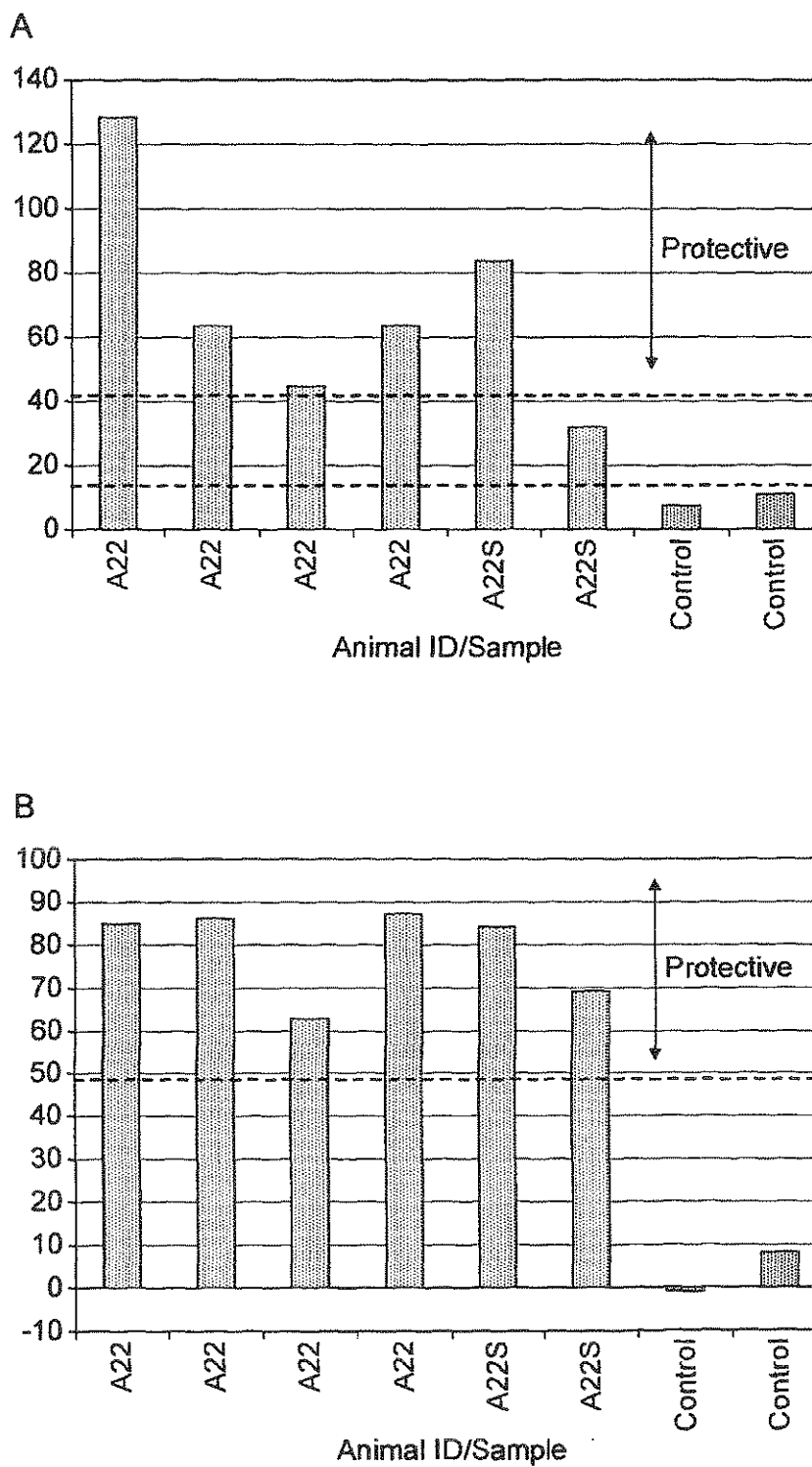


FIG. 12