

Sequence of the rat serine dehydratase gene

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The entire nucleotide sequence of the rat serine dehydratase (EC 4.2.1.13) gene is presented. We have previously reported the isolation and nucleotide sequence of the cDNA for rat liver serine dehydratase mRNA and the structures of the 5' and 3' flanking regions of the gene (1). The 9578 base pairs-sequence of the two subclones (pGEM3 and pGEM6.6) of the gene has been determined on both strands by the method of Sanger *et al.* (2). 2'-Deoxy-7-deaza guanosine triphosphate (3) is used in place of dGTP, where required, to overcome the problem of the nucleotide compression. The serine dehydratase gene consists of 9 exons and 8 introns, whose boundary sequences are obeyed by the gt..ag rule (4). The average size of the exons was 167 bp, which is close to that reported for exons in other eukaryotic genes (5,6), and the introns ranged from 109 to 1562 bp in size, with the average size of 707 bp. No nucleotide discrepancy between the gene and cDNA sequences was found; this indicates the presence of a single gene. Although we found 19 sets of alternating GT sequence far upstream from the 5' flanking region of the gene, which might favor a change of chromatin conformation (1), 26 sets of alternating GT sequence are also present just after 39 sets of alternating purine/pyrimidine sequence within the second intron.

TTCCGGAGCTGCTGGGAC	AGCCGCCCTGGAATTGCGTG	TCACTGAGCAAGCTGTCTT	CACCTGAGGACATCCAAGG	AACATCTCCAGAGATTGCC	-2300
AGTGTCCCTGGGTCAAAA	ATCACACCACCTTGAGGACA	GCTGAGTTGAACAGAGGTGT	GGGAAGGAGGCGTGTGAGAA	TGATCGGCAAGCTGGTGGG	-2200
TGTGGGGCTGGGAATCCGG	CGCAGATGACTGAGGGCTTT	CCTGGCATTCTGAGGGACCT	GAGTCTGATCCTCAGTGCCA	TGTGAGGTGGGCACGGTTGG	-2000
CACGCGCCCTGAATGGCAGC	ATTCTGAAGGCGGAGGGCAGG	AGGATCGGGAGTTGAAGGGC	ATCTCTCAGCTACTCGGTGAG	TCCGAGGCGCAGCTGGGTTA	-1900
TGTGAGCCCTGACTCAATT	TAAATGATAGGTTGTGTCCA	AACTCAGTCCCTGTTGTCT	ATCTGTCCCCAGCCCAACC	AATCTCTCCACCTCAGCTCTG	-1800
CACCTCTTAAACACTATGAG	TCCCTGGGTTCAATCCAG	TGCTCTCAGCTACCCCTGTC	CCTGTGACTCTCAGCAAAAC	ACCATCTCTCCAGGCTGCC	-1700
TCACTTACAACAAGGACTAG	GGGAGCCCAACCCTGCTGT	GTCTTAAACACAGTGA AAC	CCCCACACAGGAGCAAAAT	ATGTGGAAACAGGGTCTCCC	-1600
ATTGCTTTGGCAATGAGATG	CTGGTCCAGAGAGTACAAGG	TAGCTGTGTCCACACATGGG	CTTTGTGTCTCTGGCTTG	CCTACTTCTCTTATCTCCCT	-1500
ACCCAAACCTGTGGTCACTC	CTAATGCGGATGGTCAGAAA	GAACAATGCACACCACAGGC	CAGAAAAAGCAGCAGAGCTG	GGGCTGGAGAGATGGCTCAG	-1400
TGGTTAAGGACACTGGCTCC	TCCCTCAGAGGTCCTGAGTT	CAAAATCCAGCAACCACATG	GTGGCTCACAACCATCTGTC	ATGGAATCTGATGCCCTCTT	-1300
CTGTGTGTCTGAAGTCAAG	GATGGTGTGCTCACATATAT	TAAATAACAATAAATCTT	TTTTAAAAAAGGCAATGTA	ACTCTGTGTGTGTGTGTGTG	-1200
TGTGTGTGTGTGTGTGTG	TGTTTATGCTGTGGACACAC	AGGTCTCTGCACACAGCCCTG	GAAACGGGTCAAGAGGATG	GTCCAGTGGTCAATAGTGGT	-1100
GGTGGTGTGATGTTACTG	GTGACTACTGATGGTGGATG	GCTGATAGTGTGACAGTGG	TGGCCAATAGTGAATAGTA	TGGTATGATAAAAGGTTACC	-1000
AAACATGGCTACTGTTCAA	TTTCAAGTCTCTCACTTAAC	GCAGTCCCACCTCTTCAAAG	CCTGGAACAGCGGTACCCAT	GTCTATCCCTGTTTACACAGC	-900
AACAGAGGCTCTCGAGGTTCA	AGGTTCTTGGCCAGAGGCTG	GTATCTAGTAAACAGCAGAGC	AGGACTTGAACCCAGATGG	CTTTGTCTAACCCATACGGC	-800
CTTTTATATGAAGAGGTTCA	CAGGGGATGGTGTAAAGCAA	GGGGTGTCAATCATAGCTTG	GGCCTCAACCCCAAGTCCC	GGCTTCTACATCTATACGA	-700
GCTGTGCTCAATTTCCACTC	GTACACAGACTGTTGGATGG	TTTTACATTGATTTGGGTTT	ATGAAGCTGAGGCCATACT	CCCGGCCCTTTTTTCTTCTA	-600
TTTTGAGACAGGCTCTCACT	CCTTAGTCCAGGCTGCTCCTT	CTGCTCAGCTCTTATTTGTT	CTGGCTGAAGGTGTGAGTT	GCCATATGGCTGGCCGTGTG	-500
GTTTCTTTGGCCATAAACAGA	CCAGCAACTGTCCGGCTTTT	CTGTTATTTCTGGGATTTGAC	CCCTGGGACTCTGGCAGGAG	CTCCTCAGTGTCCGCTGGC	-400
GCCTCCACGAGTCCCTATAGCC	CTTTGGAGATGAATGTCTTT	CATTTGCAACGGAAAAA	AAAAAATAAAGAGAGGAG	GGAGAGAAAGGTGAGGCGGAC	-300
CTTTGGAGGCGAACAAGTG	GTGCAGCTATGGCAACAGGGGG	CGGGGATTTCTGGGGCGTG	GCCTGCTTGGGCTCATTTG	GCTGCCGAGGCTCAGCC	-200
GGAGAATAAAGCCCTGGGGT	GTCTCTCCAACTTTCCACTC	TCCCAGGACAGACAAAAT	CTACCCCTCTGCTGCTCT	GTCACGCTCTCTGTGGCCG	-100
GGTATGTGGCCCTCAGCCTC	AGTCTCACCCCAAGATTTGAC	AGCCAGAGCAGGGTACC	AAGGGAGGAGGAGCTGGGAC	TCATCAGTCTTCAAGTCTCC	-1
ATGTACTGATCTGTAATAATG	GGACGATGATATAGGCCCTC	TAGATCAGGACGTGCCGGG	GTGGCTGTGACTTGGCCAAG	TGCTCGCATGAGTCAAAATGA	100
Exon 1					
CAAGGAAGAGACTTCTGCCG	TGGAACCCATGCCACC	CCACCTTTGCCAAGACCGCC	TGTGCCFTTTTCTCTCGCAG	GTCCATATCACCTATAGAGGC	200
Intron 1					
GGATGCGACTGGCTCTGGG	GTGGGAATCAGTATGGAGTA	CACCTGCCATTTTCCCAAAG	GTTTCCAAATGCTCAGCCTG	GGACAGGAACAGGCGAGGT	300
TGCGCAAGCCCTCTGGAAAG	GGGTCTGCCGTGGCGAAACT	ATCCACTAGCCAAAGGCTGC	ACTGGCTGGGCTTTTGGT	CCAGAGAAGCCCTGTATGT	400
CAGGATGGGCTGACTGAGGA	CAAAGCAAGAAATTTGGAG	TACTCTGTGTGCCATTGT	TTCGACTGCTTTCAAAGG	GCTCTTAGAAGAGGAGCT	500
TGTGGCTTGGCTATAAATCT	CAGCAATTCAGACACTGAGG	CAGGAGGATCACAAGCTGT	CTCTGTCTGTCTCTCTG	CTCTGAGGAGAGAATCACA	600
AGGAGTTAATCTCTCTACT	ACTCACACAGTCACTGCA	ATTCTGTAGATGCTGGGAA	GAGACACCACCTGCTTAGT	TGGTCCCACTGACTCTGT	700
ATCTCTTGGGGCTCTTCA	CAGGGCTCCAAGGTGAAAT	GGCTGAGCCGGTGTAAACCC	AAAGGCTTCTCACTGCTCT	GGCTCCAGAGGAGGCTCAG	800
GGTCCATTTAGCCAAACTTG	CGTGGAGCTCTATCTGCA	TCCAGGTTCCCTCTATTGT	GACGBCCTGTAGCAGGAGC	AAGCCAGAGGCTCTGTGTTG	900
CTCTTCCCCATGCCAAAGAA	AGCAATTCATAAATTTCTAT	TTTTTAAAGAAATGAGAGCC	TTTCAGAGCTGATGCTGGA	TTTCCAGGCTTTTGGGGGT	1000
TTTGTGTTGTTTGAAGAAA	ACTCTTAACTACAGCCAGGGT	GGCCCTCAACTCCCTACAT	AGCCAAGGTGACCTTGAAT	GGCTAGTCTCTTGGCCCTG	1100

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CCCCAAGCAATGGGATTAC	ASGCCCTCTGCACCAAGCCC	ATTTTTTCTTCAAATAAT	GTATTTGTGCAACACAGGTG	CGCGGGGCATACCTGTGAT	1200
CCCAGCAATTGGGAGACTGA	GACAGGAGGATCCAACCTC	AAAGTACATGGTAAGAACA	TACTGAGTTTGTTTAAAGC	ATGTGTGGGTTGGGATATG	1300
GCTCAGTCTAAGAGGGCT	CCTGGGAAAGCATGAGGGCC	TGTGTTCATATTCAGAAAT	GCACCTCAAAAATGCTGAGC	TCAACAATAAATGGCTATCA	1400
TCCCTGCACATGGGAGCAAG	AGACAGAAGGACTCAAGGG	ACATCCAGGGGCTCTGGAA	CCTCAGGGGACTCTGGGAA	CCTCTGGGGACTCAGAGCC	1500
TCCGGGTTCTCTGGCCAGC	CAGTTGGCTGAATCAGGGT	GCTCCTGGTTCAGTCAAGA	CCTCGCTCAAAAATAGTG	GCAGCTGAGGGGCTACTGA	1600
CTGATGTGACCTCTGGTTT	CTCCACACACACACACAC	ACACACACACACACACAC	GCACGCACGACGTCGCGC	GCACGCACACACACACAT	1700
GTTTAAGTAAATAATAAATG	GCCAAAATGCTGGCCGGTA	GGGGTCTGTGGCCGGAGG	GTCACCTTTCAGCTACCC	CATTGGCCCATTTTGTGTG	1800
TGTGTGTGTGTGTGTGTGT	TGTGTGTGTGTGTGTGTGT	TGTGTGTGTGTGTGTGTGT	GAGCTCATGGGAACAGGTCA	GGCCGGTGTGTGTGTGTGTG	1900
ACTTTGGCAAGACACACCTT	GGCTGACCTGGCTGTGCTT	TGTTCCCATCTTGTGGCCCT	ATTCTGACGAGTTTGAACA	AGCCCTCCCTCTGCAACTTT	2000
AGCCCAACGCTGCAGCTTAA	AGATGTTCTGAGCTTGTGA	CTTTTAACTTTGGGCCACT	GGGTAGTGGAGCTGAGCTT	TGATTTGGTGTCTTTCCTT	2100
ATCATTATGGGTATGAAGA	GTGGCTCAGAGCCAGGAG	GGCAGCCTCTTGTACCCTC	TGTATCTCTCTCTGCGCCC	AGCCATGCTGCTCCAGGAGT	2200
CCCTGCACGTGAAGACCCCA	CTACGTGACAGCATGGCATT	GTCCAAGTGGCCGGCATA	GTGTGTTCTTAAGATGGAC	AGCTCTCAGCCCTCTGGCTC	2300
erLeuHisValLysThrPro	LeuArgAspSerIleAlaLe	uSerLysValAlaGlyThrS	erValPheLeuLysMetAsp	SerSerGlnProSerGlySe	
CTTCAAGATCCGAGGCATTG	GGCATCTCTGCAAGATGGTA	CAAGGCAGGGTGGCATACTG	GCAGGAGAGGCAGTCCCTCC	TACCTGACAGCTGTAGAGGC	2400
rPheLysIleArgGlyIleG	lyHisLeuCysLysMetL	Intron 3			
AGGTTGCGAGATACACACCC	AGGATCCAAACCGAGGGCAG	GAAAGTGGAAAGTGAATGGT	ATCCAGAGTGCATAGCAAG	AACCTGTCTTAAGGAATAA	2500
TAATAAATTTAGGACATCCA	GTTGAGACGCTCGCCGGCT	GAGAGCACTGGCTGCTTTTG	CAGGGGACTTGCAGCTAGT	CCCCAGCCCCATGGTGGCT	2600
CACGATCAACTAATCTCCA	GCTCCAGGAGATCCAACACT	CTCTCTGATTTCCCGGAGC	AACGATCATCAGTCAATATA	ATTCAAATAAAGTAATAAT	2700
GGGCTGAGCGATAAATCCGA	TCTTTCAGAACACCCATGT	CTTTTCAGAACACCCATGT	CACCTCCAGCCATCCAAGTA	AGCCCTCCCTCTGCAACTTT	2800
CTGACGGGATCAAAATGGCT	TCTCTGCCCTCTACAGGCCA	ATACGTCACACACAGACAAA	GTGCACATAAAGAAAAACA	TCCTTTTTTTTTTTTTTTAA	2900
GAATTTTTTATTTTACT	TATGAGGACCACTGTTGCT	GTCTTCAGAAACACCAAGAG	AGGGCAGCAGATCCCATCG	AGATGGTGTGAGGACCATC	3000
GTGGTGTGCGGGATGTAAAC	TACGAGCCTCTGGAAGAGCA	GTCAAGTCTTAAACCCCTA	AGCCATCTCCAGCCCAAG	AAAGCCACTTAAATAAAT	3100
AAATAAATAATTTTAAAGC	AAATAAATAAATTTTAAATA	GGTTCACACATCAGGGCTC	TCCTGTGCTTAAAGGGTCC	ACCACACAGCTGACACCTG	3200
CCTCCTTACCACAGTAAATC	ACCTTGGGGAGATGAGCCT	GAGAGAGTGGTTCAGATACC	AAGTGGCCAGCTCAGATGT	TCCAGTGTGAGGACGTGTC	3300
CTAGGCAGGACTTGGGGGT	GGCCTGATCTTCTCTGTG	CCCCACAGAAGGCAAAACA	GGCTGTAAACATTTCTGCTG	CTCTCAGGTGAGTGCCACG	3400
TTGGTTTCTTCCCTCTCT	ACCTGTCTCTGTGTGCTCT	LysAlaLysGln	GlyCysLysHisPheValCys	TrpGlnProSerGlySe	
TTGGTTTCTTCCCTCTCT	ACCTGTCTCTGTGTGCTCT	TGGCCAGCACAGGCATTC	TCCTGGACTCTGGCTCTG	CAACAACATCCATCTGTA	3500
GTGTCACAGATTTGGGTTTC	CAGAATGAGGGGCAGAAGTC	ACTCTGGAGATGAGCAGCCC	CACGTGAGTCCCAGGCCCT	CTTCTGATACACCTCTC	3600
aValIleGlnIleTrpGlySe	rArgMetArgGlyArgSerH	isSerGlyAspGluGlnPro	HisValArgSerLeuIleAla	uLeuProAspThrProSerP	
CTCAGCAGCGGGCAGACGGC	GGCATGGGACTGCTCATGCT	TGCCAGGAGCTGGCCCTCC	CAGCCACTATGTTTGTGCA	AGCCACACACTGCCCCAC	3700
roLeuThrAlaGlyAsnAla	GlyPheAlaThrAlaTrpAl	aAlaArgArgLeuGlyLeuP	roAlaThrIleValValGly	SerThrProAlaLeuTh	
CATTGACGGCTGAAGAACC	AAAGGGCCACATGValVal	GTGGAGAGTGTGATGACAGA	CCTATTGTGGGAGCAGAGC	TGGCGGTTGAGGGTGGGG	3800
rIleGluArgLeuLysAsnG	uGlyAlaThrValIleGluV	AlaGlyGlu	Intron 5		
CTGATAACCTGGATAGAGCC	TGCTTCTCACTCACTCTCT	TCGCCCCACCCCTGCAGAT	Exon 6		
AAACACCCAGGTTGGGTGTA	CATCTCCCCCTCGATGACC	CTCTCATCTGGTAAGTTGGA	Me		
AsnAsnProGlyTrpValTy	rIleSerProPheAspAspP	roLeuIleTr	Intron 6		
TTCTCGCCGCGCACCCAGCC	ATGAGGGGTCACCAAGTGA	GAGATTCGAGAGATCGACT	isSerGlyAspGluGlnPro	HisValArgSerLeuIleAla	
TCGGTGGAGGTGGCTTTCAT	GTGCCAGCATCTGCCCTGAA	CACCTGAAGCTTGGCCCTGC	CCACAGCCATCTCCTCTCT	CAGGTTCACTATGGCCCTGC	3900
TGTCACGTGTGGCGAGAA	ATGGGGTTTATCTACACCA	GACAGCGGGAGGTTCAGAGT	Exon 7		
TCCTCTACCTGTGCCCTGA	CGACGAGGGAGGTTCAGAGT	CGTGTGAGTGGGAGG	Exon 8		
CCCTTGTGCTTCAAGGAAGC	CCTGACCTGAGCTGCCACCC	CTCTCTTGCACAGGGAAGCC	CACACTTCCCTTGTGAAGGA	GCTGAAGGAGACACTGAGCC	4500
CCAAGCCCGGGCCATTGTG	CTGTCTGTGGGCGGTGGAGG	CCTGCTGTGGCGAGTGGTCC	AGGGGCTGCGGGAGTGGCC	TGGGAGGATGTGCCAAT	4600
IaLysProGlyAlaIleValI	erSerValTGlYgLyGlyG	yLeuLeuCysGlyValValG	InGlyLeuArgGluValGly	TrpGluAspValProIleI	
CGCCATGGAGACTCTCGGGC	CCACAGCTTCCAGCTGTCC	GTCAGGAAAGGAAAGCTGGT	CACCTTCCCAAGATCAACA	GGTGAAGCCGGGGCACCCT	4700
eAlaMetGluThrPheGlyA	IaHisSerPheHisAlaAla	ValLysGluGlyLysLeuVa	lThrLeuProLysIleThrS	e	
CGACGACACAGCGGGTGGAG	CTGAGCCTTGGCTCTTGGC	CGAAAGCCACACTCTCGCC	CGCCGTCTGGGCTTGAAGCT	GAGTCCGCTTCTTATGTGAC	4800
AGTCTTAAGTGAGCTCTCT	CGCTCTTGGAGGCTCTCAGC	CCTCATTTCTTTTGTGCTG	TTTGTATCTGGCTCGAAAT	GTGCCAGACCTTGGCTGCT	4900
CTGAGCTCAGCTGGGAGAA	AAACAATCTCGGCTGCAAA	CTTTAGTCCTTGTCCCGCC	AGCTAGAGTCTTGAACCTAGG	CTTCAAAGTGGCTCTTTG	5000
AGACTATTAGGGGCAACTCT	TGCAACCGAGGGCTCAGTTC	AGCAAGGACAGAAGTGTTC	TAAACTTTAAAGACCAAGTA	AGCTCTTTTGGCACAGCGTA	5100
TGCCAGCCAGCCACACACA	CTCCCTCTGAAAAGAGGCTA	CTATGAATGAGTTGAACCT	GTCTGCTGGAGCCTTACCT	AAGCTTTTGGCACAGCGTA	5200
ATGGGGTACACCAACTCTT	TAACCATCTGTAAAGATTG	CTCTCCCTCAAGCTGCCACT	GGGCAACCCAAAGCGGATG	GTACTGCAAAACCAATAGCT	5300
CAGAACTGGTGTCTIcG	TGATAGGCTGATGGGAGGG	CCTCTTGGAGTTTTTTTTT	TTTTTGACACCAACAGTGTG	ACTCTCATAGACCAACCTC	5400
GAGAAAAGGCTGAGTCAA	CTCTCAAGGTTGGTTTTGTA	GGGCAGTGTGGTGCATAG	AGGATGGCTTCTGTATAG	AGCCAGGGACAGGTTCAAC	5500
AGAAATCAGAGCTGCTGTA	TAGAAGGATTTCTAGAGAG	AGGATGGCTTCTGTATAG	GGGATGGCTTCTGTATAG	AAAAAGCTTCCAATATTT	5600
TAGGCATCCAAGAAGACAG	TAGGAGGATTTCTAGAGAG	TCTCTCTTATCATGCACT	TAGGAGGATTTCTAGAGAG	CTCAGCAGCCATTTTGGTA	5700
TGGCACCATTGGTGAAGCT	ATGGCATCTGCTACCACTA	TGTTTCCCACTATACACT	CTGTCTGAGAGCCTCAACTA	CTCAGCAGCCATTTTGGTA	5800
CCCTAATTAATGACCCCT	GGGGCAGATATGGCTCATC	GTGTTCCCACTATACACT	GGCAGGCTGGGGGTGGGGT	ATGAGGTGATCTCTGGCC	5900
GGAAAGGACTAGTCTCCCTG	TTTGTAGAGTGTGGGAGGG	GGGATGGCTTCTGATAG	GGGTTGCCACTTCCACTGT	CCTCGGGAGTCTCCCTGAG	6000
AGAGGTAGCAAGTGAGCAAA	GCAGGCGGAGGTTCAAGCT	CAGGTTCTGGGGCTGGGCA	Exon 9		
TGATATCTAGACCAGCTGTA	Exon 8				
TGTCTCTCCCATGTCCACC	CCCCCTCAATCCCACTCC	CAGTGTGGCAAGGCCCTGG	rValAlaLysAlaLeuG	lThrLeuLysLeuPheTy	
CGAAACCCCAATTTTCTCTG	AGGTCACTCAGACCAGGAG	GCTGTGACTGCTATCGAGAA	AlaValThrAlaIleGluLy	sPheValA	
rGluHisProGlyIlePheSerG	uValIleSerAspGlnGlu	AAAGCCAGTCAAGGTAAGC	GCAAAGGCTGCTCGAAGAAA	CATGAACCTGGTTAAACATG	6500
TCTTCCCTCTCCAGCTAGA	CTCATCTCAAAAAGAAACT	GTTTATTAAGTGCAGATTT	GTGAGGAAAGGGGCAAG	ATGAGGTGATCTCTGGCC	6600
ATAGCAGGAGGACAACTA	GGTATTAAGTGCAGATTT	AGGAACGAGAGTAGTGACA	TTGCTACACCACCTAGAGAGC	AACCTTCTCAGGGGCCAAG	6700
TAAGCTGGGAGATGTGCAA	Exon 9				
AAACCCAGCAGAGACTGTA	GAAACCGAGACTGGGTTCA	AACAACACTGCTGGCCACA	GTGACTGACGAGAGCTGACG	AGCCCCCTCCCTCAGAGC	6800

ATGAGAAGATCCTGGTGGAG	CCCCGGTGTGGCGCTGCCCT	GGCTGCAGTGTACAGCGGTG	TGGTGTGCAGGCTGCAGGCT	GAGGGCCGACTGCAAACCCC	6900
spGluLys11eLeuValGlu	ProAlaCysGlyAlaAlaLe	uAlaAlaValTy-SerGlyV	alValCysArgLeuGlnAla	GluGlyArgLeuGlnThrPr	
ACTGGCCCTGGCTGGTTGTCA	TTGTGTGGTGGCAGCAAC	ATCAGCCTGGCACAGCTGCA	GGCACTCAAGGCACAGCTGG	GCCTGAATGAGCTACTCAAG	7000
oLeuAlaSerLeuValValI	1eValCysGlyGlySerAsn	11eSerLeuAl 3InLeuG1	nAlaLeuLysAlaGlnLeuG	1yLeuAsnGluLeuLeuLys	
TGATATCTGCTGCTGCCCTG	GCCACCCCTGAGGGGTACCA	GCACCCCTGAGTAGGCTGGG	TGGGCGTCCGCTGACAGTG	GCCACCCCTCCTTTATCCAT	7100
GTTTATAATATGCACCTTTT	CATTGTAATAAAAAATTAAT	ATATATATGTTTATAAAGCA	AAGATCTTTTGAGCTTTGTT	ATTGACATGGGGTCTATGTG	7200
CAGCCCGAGGCTGGCTCAAA	CTGGAGATCCAAGCTTGGGT	GAGGTGCAGCTTAGAGGATC	GATCCCGGGCGAGCT		7276

Fig. 1. Nucleotide sequence of the rat serine dehydratase gene and its deduced amino acid sequence. The transcription start site is numbered +1 (1). The alternating GT sequences and alternating purine/pyrimidine sequence are underlined.

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