Sequence of two rat insulin-like growth factor I mRNAs differing within the 5' untranslated region

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A cDNA library, constructed from rat liver polyadenylated RNA in lambda gt10, was screened by hybridization with probes derived from the rat insulin-like growth factor I (IGF-I) gene (1). Ten recombinant phage were characterized by restriction endonuclease mapping. Representative cDNAs of two types were sequenced (2). Both sequences encode identical IGF-I protein precursors of 159 amino acids. The large NH₂-terminal signal peptide matches the human prepeptide at 43/48 residues (3). The remainder of the protein, including 70 amino acid IGF-I (underlined), is also highly conserved among mammalian species (1,4). The COOH-terminal 25 amino acids appear to be derived via alternative RNA processing involving exons 4 and 5, as has been described for mouse IGF-IB (4). The two rat IGF-IB cDNAs differ within the 5' untranslated region by an insertion/deletion of 186 bp whose junctions conform to consensus splice signals (5). Multiple mechanisms, including alternative RNA processing and alternative polyadenylation (1), are involved in the generation of IGF-I mRNAs.

IGF-IB ₁	CGAATGTTCCCCGAGCTGTTTCTGTCTACAGTGTCTGTGTTTTGTAGATAAATGTGAGGATTTCTCTAAATCCCTCTTCTGCTTGCTA	90
IGF-IB ₂	GAATGTTCCCCGAGCTGTTTCTGTCTACAGTGTCTGTGTTTTGTAGATAAAT-----	(53)
IGF-IB ₁	AATCTCACTGTGCTGTCTAAATTACAGACAGATAGAGCCTGCGCAATCGAAATAAAGTCTCAAAATTGAAATGTGACTTTGCTCTAACA	180
IGF-IB ₂	-----	
IGF-IB ₁	TCTCCATCTCTCTGGATTCTTTTGCCTCATTATCTCTGCCACCAATTCAATTTCCAGACTTTGTACTTCAGAAGCGATGGGGAAAAATC	270
IGF-IB ₂	-----ACTTTGTACTTCAGAAGCGATGGGGAAAAATC	(84)
	MetGlyLysIle	
IGF-IB ₁	AGCAGTCTTCCAACCTCAATTATTTAAGATCTGCTCTGTGACTTCTTGAAGATAAAGATACACATCATGTGCTCTTCACATCTCTCTAC	360
IGF-IB ₂	AGCAGTCTTCCAACCTCAATTATTTAAGATCTGCTCTGTGACTTCTTGAAGATAAAGATACACATCATGTGCTCTTCACATCTCTCTAC	(174)
	SerSerLeuProThrGlnLeuPheLysIleCysLeuLysAspPheLeuLysIleLysIleHisIleMetSerSerSerHisLeuPheTyr	
IGF-IB ₁	CTGGCACTCTGCTGTCTGCTCACTTTTACCAGCTCGGCCACAGCCGGACAGAGACCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTTC	450
IGF-IB ₂	CTGGCACTCTGCTGTCTGCTCACTTTTACCAGCTCGGCCACAGCCGGACAGAGACCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTTC	(264)
	LeuAlaLeuLysLeuLeuThrPheThrSerSerAlaThrAlaGlyProGluThrLeuLysGlyAlaGluLeuValAspAlaLeuGlnPhe	
IGF-IB ₁	GTGTGTGGACCAAGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGCGAGGGGCACACAGACGGGCATTGTGGATGAG	540
IGF-IB ₂	GTGTGTGGACCAAGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGCGAGGGGCACACAGACGGGCATTGTGGATGAG	(354)
	ValCysGlyProArgGlyPheTyrPheAsnLysProThrGlyTyrGlySerSerIleArgArgAlaProGlnThrGlyIleValAspGlu	
IGF-IB ₁	TGTTGCTTCCGGAGCTGTGATCTGAGGAGCTGGAGATGTACTGTGCTCCGCTGAAGCTACAAAGTCAGCTCGTTCCATCCGGGCCCCAG	630
IGF-IB ₂	TGTTGCTTCCGGAGCTGTGATCTGAGGAGCTGGAGATGTACTGTGCTCCGCTGAAGCTACAAAGTCAGCTCGTTCCATCCGGGCCCCAG	(444)
	CysCysPheArgSerCysAspLeuArgArgLeuGluMetTyrCysAlaProLeuLysProThrLysSerAlaArgSerIleArgAlaGln	
IGF-IB ₁	CGCCCACTGACATGCCCAAGACTCAGAAGTCCCGCCCTATCGACACACAAAGAAAGGAGCTGCAAGGAGAAGGAAAGGAAGTACA	720
IGF-IB ₂	CGCCCACTGACATGCCCAAGACTCAGAAGTCCCGCCCTATCGACACACAAAGAAAGGAGCTGCAAGGAGAAGGAAAGGAAGTACA	(534)
	ArgHisThrAspMetProLysThrGlnLysSerGlnProLeuSerThrHisLysLysArgLysLeuGlnArgArgArgLysGlySerThr	
IGF-IB ₁	CTTGAAGAACAACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATGTAGGAGGAGCCTCCGAGGAAACAGAAAATGCCACGTCACCG	810
IGF-IB ₂	CTTGAAGAACAACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATGTAGGAGGAGCCTCCGAGGAAACAGAAAATGCCACGTCACCG	(624)
	LeuGluGluHisLys***	
IGF-IB ₁	CAAGATCCTTTGCTGCTGTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTCAGAGATGGGCA	900
IGF-IB ₂	CAAGATCCTTTGCTGCTGTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTCAGAGATGGGCA	(714)

IGF-IB ₁	TTTCCCTCAATGAAATACACAAGTAAACATTCCGACATTGCTTTAGGAGTGTTTGTGTAATAAAAAAAAAAAAAAAAAAAAAA	968
IGF-IB ₂	TTTCCCTCAATGAAATACACAAGTAAACATTCCGACATTGCTTTAGGAGTGTTTGTGTAATAAAAAAAAAAAAAAAAAAAAAA	(804)

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