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Nucleotide sequence of rat invariant γ chain cDNA clone pLRγ34.3

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The invariant γ chain represents the principal constituent of a group of invariant polypeptide chains that were identified in transient association with polymorphic MHC class II α,ß heterodimers during their intracellular transport to the cell surface (rev. in 1). Because studies involving rat class II antigens revealed an interesting relationship between γ and the polymorphic α,ß heterodimers at the posttranslational level (2,3) we decided to determine the primary structure of the rat invariant γ chain. A λgt11 cDNA library was constructed using poly(A) RNA enriched from LEW rat spleen cells. Clones hybridizing to a mouse γ chain cDNA probe (4) were identified and the phages purified. The complete nucleotide sequence of the longest insert representing clone pLRγ34.3 was determined, employing the dideoxy chain termination method (Fig. 1). Comparison of the γ chain nucleotide sequences of rat, mouse, and human revealed high levels of homology (89,8% identity between rat and mouse and 82,6% between rat and human).

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                                                  Met Asp Asp Gln Arg Asp Leu Ile Ser Asn His Glu Gln Leu Pro   15
GCAGCAGCAGCAGCACCAGCAGCACTTGGGGGAAAAGCTAGAGGCTAGAGTC ATG GAT GAC CAG CGC GAC CTC ATC TCT AAC CAT GAG CAG CTG CCC   97
 Asn Gln Gly Gln Arg Ala Arg Ala Pro Glu Ser Asn Cys Asn Arg Gly Val Leu Tyr Thr Ser Val Ser Val Leu Val Ala Leu   43
ATC CTG GGC CAG CGT GCT AGA GCC CCA GAA AGC AAT TGC AAC CGT GGA GTC CTG TAC ACC AGT GTC TCT GTC CTG GTG GCT CTG  181
Leu Leu Ala Gly Gln Ala Thr Thr Ala Tyr Phe Leu Tyr Gln Gln Gln Gly Arg Leu Asp Lys Leu Thr Val Thr Ser Gln Asn   71
CTC TTG GCT GGG CAG GCC ACC ACT GCT TAC TTC CTG TAC CAG CAG CAG GGC CGC CTG GAC AAG CTG ACC GTC ACC TCC CAG AAC  265
Leu Gln Leu Glu Asn Leu Arg Met Lys Leu Pro Lys Ser Ala Lys Pro Val Ser Pro Met Arg Met Ala Thr Pro Leu Leu Met   99
CTG CAA CTG GAG AAC CTT CGC ATG AAG CTT CCG AAA TCT GCC AAA CCT GTG AGC CCG ATG CGC ATG GCT ACT CCC TTG CTG ATG  349
Arg Pro Leu Ser Met Asp Asn Met Leu Gln Ala Pro Val Lys Asn Val Thr Lys Tyr Gly Asn Met Thr Gln Asp His Val Met  127
CGC CCA CTG TCC ATG GAT AAC ATG CTC CAA GCG CCC GTG AAG AAT GTT ACC AAG TAT GGC AAC ATG ACC CAG GAC CAC GTG ATG  433
His Leu Leu Thr Lys Ser Gly Pro Leu Asn Tyr Pro Gln Leu Lys Gly Ser Phe Pro Gly Asn Leu Lys His Leu Lys Asn Ser  155
CAC CTG CTT ACG AAG TCT GGA CCC GTG AAC TAC CCA CAG CTG AAG GGG AGC TTC CCG GAG AAT CTG AAG CAC CTT AAG AAC TCT  517
Met Asn Gly Leu Asp Trp Lys Val Phe Glu Ser Trp Met Lys Gln Trp Leu Leu Phe Glu Met Ser Lys Asn Ser Leu Glu Glu  183
ATG AAT GGT CTG GAC TGG AAG GTC TTT GAG AGC TGG ATG AAA CAG TGG CTG TTG TTT GAA ATG AGC AAG AAC TCC CTG GAG GAG  601
Lys Gln Pro Thr Gln Thr Pro Pro Lys Glu Pro Leu Asp Met Glu Asp Pro Ser Ser Gly Leu Gly Val Thr Lys Gln Asp Met  211
AAG CAG CCC ACC CAG ACT CCA CCT AAA GAG CCA CTG GAC ATG GAA GAC CCA TCT TCT GGC CTG GGA GTG ACC AAG CAG GAT ATG  685
Gly Gln Met Phe Leu                                                                                           216
GGC CAA ATG TTC TTG TGA AGACAGAAGCCAGCTCTGCACGGCGGCACGTCCCCTGCTCCTCAGCCCTTCTTACACTCCCTAACATCACACCCATTCCGTCTTCCT  790
GCACCTGGGCTTGAGACTGGTATCTGCTTCACCGTCCCTGACACAACAAATGAAACCGGAACAGAATGAGAACACTGGAGGGAGGGCCTTGCTGCCTACCCCCATCTAAGG  901
GACCCCCATTTCTGACCCATTAGCAGTCTTTAATGTGGGGCTCTGAGATCTAGGCCCACTGACAGGGATAGGGGATGCCCTACCCTTAATCTAGGCTGGATACATTTGCTG 1012
TCTTCTCAAGGAAGAGGCCAAGCCCTCCCAGCAACCCTTCCTCATGTCCTGCCGACGCCCCTGGGATCCCTGCTCAGCCAAGCTTGTCAGCAGCCTGTAGGACCATGGTTC 1123
ACGTGACAATAAAAGGTAGAAGGTAAA                                                                                   1150
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Fig. 1: Nucleotide sequence of cDNA clone pLRγ34.3 including the deduced amino acid sequence. The stretch of sequence belonging to the putative transmembrane region is underlined. The two asterisks denote potential N-glycosylation sites.

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