

Complete nucleotide sequence of the membrane form of the human IgM heavy chain

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We have cloned and sequenced a full length human immunoglobulin M chain cDNA of the membrane bound form. The variable region, nucleotides 119 to 529, is a member of the VH₁ family. Nucleotides 530 through 1831 encode the heavy chain constant region, which shows 73% identity to mouse and 79% identity with rabbit heavy chain sequences (1). Differences from previously published DNA and protein sequences, of the human constant gene, are underlined (2, 3). Exon boundaries are indicated by arrows.

REFERENCES

1. Kabat, E.A., Wu, T.T., Reid Miller, M., Perry, H.M. and Gottesman, K.S. (eds) (1987) *Sequences of Proteins of Immunological Interest*. Fourth edition. U.S. Department of Health and Human Services, Public Health Service, National Institutes of Health, Bethesda, pp. 293-331, 530-552.
2. Rabbitts, T.H., Forster, A and Milstein, C.P. (1981) *Nucl. Acids Res.* **9**, 4509-4524.
3. Haimanti, D. and Gillies, S.D. (1989) *Nucl. Acids Res.* **17**, 6412.

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1  GCTCTAGAAGTCTAGTGGATCCCCCGGGCTGCAGGAATCTCTAAAGAAGCCCCCTGGGAGCACAGCTCATCACCTGGACTGGACCTGGAGTTCTCTTTGTGGTGGCAGCAGCTACAGGTGCCAGTCCCAGGTGCAGCTGGTGCAGTCT
      M D W T W R F L F V V A A A T G V Q S Q V Q L V Q S
151 GGGCTGAGGTGAAGAAGCCCTGGGTCTCGTGAAGTCTCCTGCAAGGCTTCTGGAGGCACCTTCAGCAGCTATGCTATCAGCTGGTGGCAGCAGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCATCCCTATCTTTGGTACA
    G A E V K K P G S S V K V S C K A S G G T F S S Y A I S W V R Q A P G Q G L E W M G G I I P I F G T
301 GCAAACACTGCACAGAAAGTTCACGGCAGAGTACGATTACCGGACGAAATCCACGAGCAGCAGCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGTGCGAAACCCGGATCTGGGGCCGTATGACAGT
    A N Y A Q K F Q G R V T I T A D E S T S T A Y M E L S S L R S E D T A V Y Y C A K T G I L G P Y S S
451 GGCTGGTCCCGAAGTCCGACTACTACTACGGTATGGACCTGTGGGGCCAAAGGACCACGGTCACCGTCTCTCAGGGAGTGATCCGCCCAACCCCTTTCCCCCTCGTCTCCTGTGAGAATCCCGCTGGATACGAGCAGCGTG
    G W Y P N S D Y Y Y Y G M D V W G Q G T T V T V S S G S A S A P T L F P L V S C E N S P S D T S S V
601 GCCGTGGCTCCCGCAGGACTCTCTCCCGACTCCATCACTTCTCTCGAAATACAAGAACTCTGACATCAGCAGCACCCGGGGCTTCCCATCAGTCTGAGAGGGGGCAAGTACGCCACCTCACAGGTGCTGCTGCTCCT
    A V G C L A Q D F L P D S I T F S W K Y K N N S D I S S T R G F P S V L R G G K Y A A T S Q V L L P
751 TCCAAGGACGTATGACAGGCGACAGCAACACGTGGTGTGCAAGTCCAGCACCCCAACGGCAACAAGAAAGAAAGACGTGCTCTTCCAGTGATTGCTGAGCTGCCTCCCAAGTGAAGCTCTTCCGCCACCCCGGACGGCTTCTTC
    S K D V M Q G T D E H V V C K V Q R P N G N K E K N V P L P V I A E L P P K V S V F V P P R D G F F
901 GGCAACCCCGCAGCAAGTCCAAAGTCACTGCACAGGCCACGGGTTTCAGTCCCGGAGATTCAGGTGCTCCTGGCTGCGCGAGGGGAAGCAGTGGGGTCTGGCGTACCACGGACACAGTGCAGGCTGAGGCCAAAGAGTCTGGGGCC
    G N P R S K S K L I C Q A T G F S P R Q I Q V S L W L R E G K Q V G S G V T T D Q V Q A E A K E S G P
1051 ACGACCTACAAGGTGACCGACACTGACCATCAAAGAGAGGACTGGCTCAGCCAGAGCATGTTACCTGCCGGTGSATCAGAGGGGCTGACCTTCCAGCAGAATGCGTCTCCATGTGTGCCCGATCAAGACACAGCCATCCGG
    T T Y K V T S T L T I K E S D W L S Q S M F T C R V D H R G L T F P Q N A S S M C V P D Q D T A I R
1201 GTCTTCGCCATCCCCCATCTTTGGCAGCATCTTCCTCACCAAGTCCCAAGTTGACCTGCCTGGTTCACAGACTGACACCTATGACAGCGTGACCATCTCCTGGACCCCGCAGAATGGCGAAGCTGTGAAAACCCACACCAATC
    V F A I P P S F A S I F L T K S T K L T C L V T D L T T Y D S V T I S W T R Q N G E A V K T H T N I
1351 TCCGAGAGCCACCCCAATGCCACTTTCAGCCCGTGGGTGAGGCCAGCATCTGCGAGGATGACTGGAATCCGGGAGAGGTTACAGTGCACCGTGACCCACAGACCTTCCCTCGCCACTGAAGCAGACCATCTCCCGCCCAAGGGG
    S E S H P N A T F S A V G E A S I C E D D W N S G E R F T C T V T H T D L P S P L K Q T I S R P K G
1501 GTGGCCCTGCACAGCCCGATGCTACTTGTGCCACAGCCCGGAGCAGCTGAACCTCGGGAGTCGGCCACCATCAGCTGCCTGGTGAAGGGCTTCTCCCGCGGACGCTCTTCGTGAGTGGATGACAGGGGGCAGCCCTTGTCC
    V A L H R P D V Y L L P P A R E Q L N L R E S A T I T C L V T G F S P A D V F V Q W M Q R G Q P L S
1651 CCGGAGAAGTATGTACAGCGCCCAATGCCTGAGCCCGAGGCCAGCCCGGTACTTCGCCACAGCATCTGACCGTGTCCGAAGAGGAATGSAACACGGGGGAGACCTACACCTGCGTGGTGGCCCATGAGGCCCTGCCAACAGG
    P E K Y V T S A P M P E P Q A P G R Y F A H S I L T V S E E E W N T G E T Y T C V V A H E A L P N R
1801 GTCACCGAGAGGACCGTGGACAAAGTCCACCGAGGGGAGGTGAGCCCGAGGAGGGTTTGAACCTGTGGGCCACCGCCTCCACCTTCATCGTCTCTCTCTCTGAGCCTCTTCTACAGTACCACCGTCACTTGTCAAGGTG
    V T E R T V D K S T E G E V S A D E E G F E N L W A T A S T F I V L F L L S L F Y S T T V T L F K V
1951 AAATGATCCCAACAGAAGAACATCGGAGACCAGAGAGGAACCTAAAGGGGGCTGCCTCCGGTCTGGGGTCTGGCTCGTGGCTGTGGCAGTGTCTCTCCCGCCCGGCTCCAGTGTGTGCTCTCACAGGGCTTCT
    K *
2101 TCTCGACGGGCGGGGCTGGCTGGCTTGCAGGCCACGAGGTGGGCTCTACCCACACTGCTTTGCTGTATACGTTGTTGCCTGAAATAAATATGCACATTTTATCCATGAAAAAAAAA
    
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