Amino terminal sequence of heavy and light chains from ratfish immunoglobulin

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Abstract

The ratfish, *Callorhinchus callorhinchus*, a representative of the Holocephali, has a natural serum hemagglutinin (*M* r 960 000), composed of heavy (*M* r 71000), light (*M* r 22 500), and J (*M* r 16 000) chains. To approach the mechanisms that generate diversity at this level of evolution, the amino terminal sequence of the heavy and light chains was determined by automated microsequencing. The chains are unblocked and have modest internal sequence heterogeneity. The heavy chains show sequence similarity with the terminal region of the heavy chain from the horned shark, *Heterodontus francisci*, and other species. In contrast to the heavy chain, the ratfish light chains display low sequence similarity with their shark kappa counterparts. However, their similarity with the variable region of the chicken lambda light chains is about 75%.

Keywords Sequence Similarity, Light Chain, Variable Region, Heavy Chain, Terminal Region