Exhibit 6

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is indefinite and unduly broad. It is not clear what is meant by the recitation "but for the degeneracy of the genetic code." Also the language "would hybridize ..." is permissive and thus not an absolute limitation. Further the Markush member (c), and the sequence of claim 77 and 96 appear to embrace substantially all known DNA sequences since the isolated DNA sequence is not designated as encoding for erythropoietin. One that encodes for a protein having "a" therapeutic activity of erythropoietin is not the same thing. In order to embrace the subject matter of that Markush member (c) a separate claim drawn to an isolated DNA sequence encoding an erythropoietin selected from the group consisting of human and monkey erythropoeitin would be acceptable. The embodiments of claims 77 and 96 could properly be expressed as for example an isolated DNA sequence consisting of a DNA sequence encoding a polypeptide having the structure sufficiently duplicative of that of a naturally-occurring erythropoietin to allow possession of the biological properties of being able to cause bone marrow cells to increase hemoglobin synthesis and iron uptake and stimulate reticulocyte response. Claim 74 appears to read on naturally occurring erythropoeitin producing cells. Claims 84, 86, 87, 89, 90 and 99 are redundant of claim 77 or claim 96 since the DNA sequence has no memory of its creation.

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the messenger RNA for erythropoietin from kidney cells known to be rich therein and converting that mRNA to a cDNA library in the manner taught by Ullrich et al or Martial. If desired, substituting the lambda gt 11 phage library vector of Young et al for its advantages would be an obvious choice. It would further be obvious to use the Young et al or Broome et al gene isolating technique together with erythropoietin antibody of the primary references as a probe for isolating a clone producing erythropoietin. At best only routine genetic engineering techniques would be involved.

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