mining a first nucleotide sequence of a first nucleic acid coding for the biosynthesis of at least a portion of the original peptide or protein; (b) ascertaining a second nucleotide sequence of a second nucleic acid which base-pairs with the first nucleotide sequence of the first nucleic acid, the first and second nucleic acids pairing in antiparallel directions; and (c) determining the amino acid sequence of the complementary polypeptide by the second nucleotide sequence when read in the same reading frame as the first nucleotide sequence. The complementary polypeptide whose amino acid sequence is thus determined may be obtained by diverse means such as, for example, chemical synthesis, derivation from a protein or larger polypeptide containing said amino acid sequence, or, when the second nucleic acid is DNA, inserting the second nucleotide sequence into a plasmid to form a recombinant DNA plasmid vector and transforming a unicellular organism therewith to produce a transformant unicellular organism biosynthesizing said complementary polypeptide. The ascertainment of particular nucleotide sequences may be circumvented, in one aspect, by utilizing the relationships of amino acids having complementary hydropathies for substitutions as generally dictated by base-pairing nucleotide complementarity.

5212074

GENETIC MATERIAL ENCODING NEW INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN IGFBP-6

Michael C Kiefer, Frank R Masiarz assigned to Chiron Corporation

A purified binding protein selected from the group consisting of insulin-like growth factor binding protein having an amino acid sequence which is at least 85% homologous to the amino acid sequence of FIG. 1 and fragments thereof comprising at least 10 consecutive amino acids of the sequence that are capable of binding to an antibody specific for the protein or to an insulin-like growth factor is described. Recombinant DNA molecules encoding the binding proteins and subsequences thereof are also described along with recombinant microorganisms and cell lines containing the DNA molecules and methods for preparing the binding proteins by growing the recombinant hosts containing the relevant DNA molecules. Antibodies to the protein, identified as IGFBP-6, which are useful in various diagnostic applications, are also described.

5212080

METHOD OF DNA SEQUENCING USING DNA TRANSPOSON TN5SEQL

Dilip K Nag, Henry V Huang, Douglas E Berg assigned to Washington University

A novel transposon useful for sequencing long DNAs is disclosed which comprises a partial sequence of transposon Tn5 with the oligonucleotide primers from phages SP6 and T7 inserted near the opposite ends, respectively, of said transposon Tn5.

5212082

GENETICALLY MODIFIED TYROSINE HYDROXYLASE AND USES THEREOF

Menek Goldstein, Jing Wu, David Filer, Arnold J Friedhoff assigned to New York University

Modification of the DNA encoding the enzyme tyrosine hydroxylase (TH) resulting in amino acid substitution in one of the first fifty five N-terminal residues, in particular replacing Ser-40 with Tyr or Leu, produced TH variants having substantially increased enzymatic activity upon transfection of suitable host cells. Cells transfected with the variant TH having enhanced enzymatic activity are useful for treating neurological or psychiatric disorders associated with deficient TH or dopamine, in particular Parkinson's disease, by grafting such cells into the brain.

5212083

SEQUENCE FOR STABILIZING PROTEINS IN BACTERIA

William G Haldenwang assigned to Board of Regents The University of Texas System

The invention relates to a protein stabilizing sequence particularly useful for stabilization of proteolytically sensitive proteins. The sequence includes a relatively small number of amino acids that may be expressed fused with a proteolytically sensitive protein. The most effective stabilization sequences assume alpha-helix structures with a hydrophobic face and a positively charged polar face which appear to require proper orientation with respect to each other.