Case A

[Claim 1] A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:1.

[Description of the invention]

A cDNA library was constructed from human liver using oligo (dT) primers. The nucleotide sequence of SEQ ID NO:1 is one of the sequences which were analyzed using an automated DNA sequencer. The sequences analyzed were only part (500bp) of the cDNAs of the library.

The polynucleotide consisting of the nucleotide sequence of SEQ ID NO:1 is part of a structural gene, and it can be used as a probe in one of the steps to obtain the full-length DNA.

However, there is no working example indicating that the full-length DNA was actually obtained, and there is no description of the function or biological activity of the DNA and its corresponding protein.

[Result of the prior-art search]

There is no known nucleotide sequence with high similarity to that of SEQ ID NO:1.

Case B

[Claim 1] A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:2.

[Description of the invention]

A cDNA library was constructed from human liver using oligo (dT) primers. The nucleotide sequence of SEQ ID NO:2 is one of the sequences which were analyzed using automated DNA sequencer. The sequences analyzed were only part (500bp) of the cDNAs of the library.

Each sequence obtained in this manner was automatically computer-searched in a DNA sequence database. The peptide sequence deduced from the cDNA sequence was also automatically computer-searched in an amino acid sequence database.

As a result of a similarity search, the polynucleotide consisting of the nucleotide sequence of SEQ ID NO:2 was assumed to be part of a structural gene encoding human protein X. The polynucleotide demonstrated 95% homology to part of a structural gene encoding rat protein X, which has a known specific function and a biological activity (e.g. insulin). The corresponding amino acid sequence also showed 95% homology to part of the amino acid sequence of rat protein X. The size of the full-length DNA encoding rat protein X is 2400bp.

This polynucleotide can be used as a probe in one of the steps to obtain the full-length DNA.

However, there is no working example indicating that the full-length DNA is actually obtained.

[Result of the prior-art search]

The DNA sequence encoding rat protein X was known.

Case C

[Claim 1] A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:3.

[Description of the invention]

A cDNA library was constructed from human liver using oligo (dT) primers. The nucleotide sequence of SEQ ID NO:3 is one of the sequences which were analyzed using an automated DNA sequencer. Those analyzed sequences were only part (500bp) of the cDNAs of the library.

As the amino acid sequence deduced from the nucleotide sequence of SEQ ID NO:3 has a potential site of glycosylation, the polynucleotide was assumed to be part of a structural gene encoding a glycoprotein. This polynucleotide can be used as a probe in one of the steps to obtain the full-length DNA. However, there is no working example indicating that the full-length DNA is actually obtained.

[Result of the prior-art search]

There is no known nucleotide sequence with high similarity to that of SEQ ID NO:3.

Case D

[Claim 1] A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:4.

[Description of the invention]

The polynucleotide is one of the 500bp long cDNAs which were found in a cDNA library derived from the hepatocyte of a patient with disease Y, but not found in those of normal persons.

It was confirmed by northern hybridization that the corresponding mRNAs were expressed only in the patients' hepatocyte. Therefore, the polynucleotide can be used as a probe to diagnose disease Y.

[Result of the prior-art search]

There is no known DNA that is unique in the patients with disease Y.

There is no known nucleotide sequence with high homology to that of SEQ ID NO:4.

Case E

[Claim 2] A polynucleotide comprising the nucleotide sequence of SEQ ID NO:4.

[Description of the invention]

The polynucleotide is one of the 500bp long cDNAs which were found in a cDNA library derived from the hepatocyte of a patient with disease Y, but not found in those of normal persons.

It was confirmed by northern hybridization that the corresponding mRNAs were expressed only in the patients' hepatocyte. Therefore, the polynucleotide can be used as a probe to diagnose disease Y.

[Result of the prior-art search]

There is no known DNA that is unique in the patients with disease Y.

There is no known nucleotide sequence with high homology to that of SEQ ID NO:4.

Case F

[Claim 3] A structural gene comprising the nucleotide sequence of SEQ ID NO:2.

[Description of the invention]

A cDNA library was constructed from human liver using oligo (dT) primers. The nucleotide sequence of SEQ ID NO:2 is one of the sequences which were analyzed using automated DNA sequencer. The sequences analyzed were only part (500bp) of the cDNAs of the library.

Each sequence obtained in this manner was automatically computer-searched in a DNA sequence database. The peptide sequence deduced from the cDNA sequence was also automatically computer-searched in an amino acid sequence database.

As a result of a similarity search, the polynucleotide consisting of the nucleotide sequence of SEQ ID NO:2 was assumed to be part of a structural gene encoding human protein X. The polynucleotide demonstrated 95% homology to part of a structural gene encoding rat protein X, which has a known specific function and a biological activity (e.g. insulin). The corresponding amino acid sequence also showed 95% homology to part of the amino acid sequence of rat protein X. The size of the full-length DNA encoding rat protein X is 2400bp.

This polynucleotide can be used as a probe in one of the steps to obtain the full-length DNA.

However, there is no working example indicating that the full-length DNA is actually obtained.

[Result of the prior-art search]

The DNA sequence encoding rat protein X was known.

Case G

[Claims]

1. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:1.

2. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:2.

3. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:3.

4. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:4.

5. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:5.

6. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:6.

7. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:7.

8. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:8.

9. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:9.

10. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:10.

11. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:11.

[Description of the invention]

A cDNA library was constructed from human liver using oligo (dT) primers. Each claimed polynucleotide is one of the sequences which were analyzed using an automated DNA sequencer. The sequences analyzed were only part (500bp) of the cDNAs of the library.

The polynucleotides consisting of the nucleotide sequence of SEQ ID NO:1- SEQ ID NO:11 are part of structural genes, and they can be used as probes in one of the steps to obtain the full-length DNAs.

However, there is no working example indicating that the full-length DNAs were actually obtained and there is no description of the function or biological activity of the DNAs and their corresponding proteins.

These polynucleotides are not highly homologous to each other.

Case H

[Claims]

1. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:1.

2. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:2.

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11. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:11.

[Description of the invention]

A cDNA library was constructed from human liver using an oligo (dT) primers. Each claimed polynucleotide is one of the sequences which were analyzed using an automated DNA sequencer. The sequences analyzed were only part (500bp) of the cDNAs of the library.

As the amino acid sequences deduced from the nucleotide sequences of SEQ ID NO:1- SEQ ID NO:11 had potential sites of glycosylation, the polynucleotides were assumed to be part of structural genes encoding glycoproteins. These polynucleotides can be used as probes in one of the steps to obtain the full-length DNAs. However, there is no working example indicating that the full-length DNAs are actually obtained.

These polynucleotides are not highly homologous to each other.

Case I

[Claims]

1. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:1.

2. A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:2.

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11.A polynucleotide consisting of the nucleotide sequence of SEQ ID NO:11.

[Description of the invention]

These polynucleotides are the 500bp long cDNAs which were found in cDNA library derived from hepatocyte of a patient with disease Y but not found in those of normal persons.

It was confirmed by northern hybridization that the corresponding mRNAs were expressed only in the patients' hepatocyte. Therefore, these polynucleotides can be used as probes to diagnose disease Y.

These polynucleotides are not highly homologous to each other

[Result of the prior-art search]

There is no known DNA that is unique in the patients with disease Y.