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**INTERNATIONAL PATENT COOPERATION UNION
(PCT UNION)**

MEETING OF INTERNATIONAL AUTHORITIES UNDER THE PCT

Eighth Session
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DRAFT PCT INTERNATIONAL SEARCH AND
PRELIMINARY EXAMINATION GUIDELINES:

COMMENTS AND PROPOSALS BY
THE UNITED STATES PATENT AND TRADEMARK OFFICE,
THE EUROPEAN PATENT OFFICE, ROSPATENT AND IP AUSTRALIA

Document prepared by the International Bureau

1. Document PCT/MIA/8/2 contains a revised draft set of combined guidelines for International Search and Preliminary Examination under the PCT submitted by the United States Patent and Trademark Office. The Annexes to this document contain the following comments and proposals, related to possible additional or alternative material for these guidelines which has not yet been incorporated into the draft, as detailed below.

(a) Annex I contains examples by the United States Patent and Trademark Office for discussion in relation to Chapter 20 of the draft guidelines.

(b) Annex II contains proposals by the European Patent Office in relation to Example 4 under paragraph 20.11 of the draft guidelines.

(c) Annex III contains comments and proposals by the United States Patent and Trademark Office in relation to paragraph 21.02 of the draft guidelines, based on comments

which were made and discussed informally at the seventh session of the Meeting of International Authorities (see document PCT/MIA/7/5, paragraph 61).

(d) Annex IV contains proposals by the United States Patent and Trademark Office relating to paragraph 21.20 of the draft guidelines.

(e) Annex V contains proposals by Rospatent relating to paragraph 21.20 of the draft guidelines.

(f) Annex VI contains proposals by IP Australia relating to paragraph 21.21 of the draft guidelines, together with some suggestions in response by the United States Patent and Trademark Office.

4. The Meeting of International Authorities is invited to take note of the contents of the Annexes to this document in conjunction with the relevant parts of the draft guidelines in the Annex to document PCT/MIA/8/2.

[Annex I follows]

ANNEX I

EXAMPLES BY THE UNITED STATES PATENT AND TRADEMARK OFFICE FOR DISCUSSION IN RELATION TO CHAPTER 20 OF THE DRAFT GUIDELINES

Bioinformatics examples:

1. A computer readable media comprising the atomic coordinates of polypeptide Q.

2. A computer readable media comprising a computer program capable of displaying three dimensional coordinates of a polypeptide and the atomic coordinates of polypeptide Q.

More examples from Trilateral Study:

– *Case 1: 3-D structural data of a protein per se*

[Claim 1]
A computer model of protein P generated with the atomic coordinates listed in Fig. 1.

[Claim 2]
A data array comprising the atomic coordinates of protein P as set forth in Fig. 1 which, when acted upon by a protein modeling algorithm, yields a representation of the 3-D structure of protein P.

– *Case 2: Computer-readable storage medium encoded with structural data of a protein*

[Claim 1]
A computer-readable storage medium encoded with the atomic coordinates of protein P

– *Case 3: Protein defined by its tertiary structure*

[Claim]
An isolated and purified protein having the structure defined by the structural coordinates as shown in Fig. 1.

– *Case 6: In silico screening methods directed to a specific protein (1)*

[Claim 1]
A method of identifying compounds that can bind to protein P, comprising the steps of:
applying a 3-dimensional molecular modeling algorithm to the atomic coordinates of protein P shown in Fig. 1 to determine the spatial coordinates of the binding pocket of protein P; and
electronically screening the stored spatial coordinates of a set of candidate compounds against the spatial coordinates of the protein P binding pocket to identify compounds that can bind to protein P.

– *Case 7: In silico screening methods directed to a specific protein (2)*

[Claim 1]

A method of identifying compounds which can bind to protein P by comparing the 3-D structure of candidate compounds with the 3-D molecular model shown in Fig. 5 which comprises the following steps:

(1) ...
(2) ...
(..) ...
(n) ...

(The 3-D molecular model of Fig. 5 presents the positions of heteroatoms in the amino acids constituting the binding pocket of protein P (i.e., amino acids 223, 224, 227, 295, 343, 366, 370, 378 and 384) wherein said heteroatoms can form hydrogen bonds with hydrogen bonding functional groups in a candidate compound.

Steps (1) through (n) describe a data processing method in which

a) the coordinate data of the 3-D molecular model of Fig. 5 is input in a data structure such that the interatomic distances between the atoms of protein P are easily retrieved, and

b) the distances between hydrogen-bonding heteroatoms of different candidate compounds and the heteroatoms that form the binding pocket in the 3D molecular model are compared thereby allowing the identification of those candidate compounds which would theoretically form the most stable complexes with the 3-D molecular model binding pocket of protein P, based on optimal hydrogen bonding between the two structures.)

[Claim 2]

A compound identified by the method of claim 1.

[Claim 3]

A database encoded with data comprising names and structures of compounds identified by the method of claim 1.

[Annex II follows]

ANNEX II

PROPOSALS BY THE EUROPEAN PATENT OFFICE
RELATING TO EXAMPLE 4 UNDER
PARAGRAPH 20.11 OF THE DRAFT GUIDELINES

20.11 Examples

– *Examples Where Search or Preliminary Examination Possible, with an Indication in the Written Opinion (see paragraph 20.10[XR])*

[...]

Example 4

Some claims are directed towards more than one specific embodiment, for example Markush type claims. [* add an indication that Unity can be effective in tackling these claims? *]

(i) In certain extreme cases such claims may encompass a very large number of possible embodiments while the description discloses, and provides technical support for, only a relatively small proportion of those embodiments (see paragraph 13.44 [XR]).

In such extreme cases, the search should be carried out for those parts of the claim that are supported by the description, i.e. for which a technical enabling disclosure is provided. For example, in Markush-type claims, the search may be directed towards claimed embodiments that relate to specifically disclosed compounds, or prepared or tested compositions, and a structural generalisation of these. The written opinion should include observations on Articles 5 and 6 (sufficiency and support). The ISA should also include in the objection on non-prior grounds an indication as to what degree these objections have been taken into account for purposes of determining the extent of the search, and this extent should be indicated as precisely as possible, for example the specifically disclosed compounds, or prepared or tested compositions, and a structured generalisation of these.

(ii) In other cases, such claims contain so many options, variables, possible permutations and/or provisos, making the claim unclear and/or inconcise to the extent that the presentation of the claim obscures the subject matter for which protection is sought (see paragraph 13.42 [XR]).

In such cases, the search should be carried out for those parts of the claim that are clear and concise. For example, in Markush-type claims, the search may be directed towards claimed embodiments that relate to clearly disclosed compounds, or prepared or tested compositions, and a structural generalisation thereof. The written opinion should include observations on Article 6 (clarity and/or conciseness). The ISA should also include in the objection on non-prior grounds an indication as to what degree these objections have been taken into account for the purposes of determining the extent of the search, and this extent should be indicated as precisely as possible, for example the clearly disclosed compounds, or prepared and tested compositions, and a structural generalisation of these.

[...]

[Annex III follows]

ANNEX III

COMMENTS AND PROPOSALS BY THE UNITED STATES PATENT AND TRADEMARK OFFICE RELATING TO PARAGRAPH 21.02 OF THE DRAFT GUIDELINES

PCT Rule 13 specifies that the international application shall relate to one invention only or to a group of inventions so linked as to form a single general inventive concept ("requirement of unity of invention"). The rule further states that the requirement is fulfilled only when there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features; the latter phrase meaning those technical features that define a contribution which each of the claimed inventions, considered as a whole, makes over the prior art.

Currently, a "contribution" over the prior art is assessed only in terms of novelty and inventive step or obviousness. However, no "contribution" is made in the absence of a disclosure of the invention that is sufficiently clear and complete for a person skilled in the art to carry out the invention and determine the manner in which it can be made and used in industry. Therefore, a "contribution" over the prior art can be properly assessed only if the disclosure is considered in addition to novelty and inventive step or obviousness.

Consequently, paragraph 21.02 states that "whether or not any particular technical feature makes a 'contribution', and therefore constitutes a 'special technical feature,' over the prior art should be considered both with respect to the prior art itself, as well as with respect to reasons other than prior art, i.e. requirements under the Treaty, such as sufficient support by the description or industrial applicability." Because this proposal follows the plain language of PCT Rule 13 and simply represents a more expansive determination of exactly what constitutes a "contribution" over the art, amendment of PCT Rule 13 should not be required.

By way of example, an application may contain independent embodiments or species that would be considered to be distinct inventions, but for a claim to a genus that links these distinct inventions to purportedly form a single general inventive concept. By definition, if the common technical feature, namely the claim to the genus, does not define a "contribution" over the prior art, unity of invention is lacking among the inventions. Under current practice, absent prior art that demonstrates lack of novelty or inventive step, the unity of invention requirement is considered fulfilled and each of the otherwise distinct inventions must be searched/examined. Paragraph 21.02 clarifies the means to establish lack of unity and involves demonstrating that the genus does not constitute a "contribution" over the prior art for reasons other than novelty or inventive step; these other reasons involve a failure to meet other requirements of the Treaty, such as a sufficient description or industrial applicability. While this approach may be generally applied, it has particular applicability in certain sectors, such as biotechnology. The following example illustrates the proposed methodology.

Example:

Background

A double-stranded deoxyribonucleic acid (DNA) molecule has a structure that contains two chains. Each chain consists of nucleotides connected in a very precise sequence. The sequence of nucleotides in any given molecule relates to both the function of the DNA and its species of origin. Each nucleotide consists of a sugar, a phosphate, and one of four bases,

adenine (A), thymine (T), cytosine (C) and guanine (G). The bases on one chain pair with a specific complement on the other chain. In particular, A pairs with T and G pairs with C. This pairing binds the two chains together in a specific manner, as illustrated.

Chain 1 - Chain 2
A - T
T - A
G - C
G - C
A - T
C - G
T - A
C - G, etc.

A hybridization test takes advantage of this specific pairing between DNA chains and can be used to determine whether or not two distinct molecules of DNA have any blocks or segments of complementary nucleotide sequences. The two chains of a double-stranded DNA molecule are separated and then one single-stranded chain can be "hybridized" with a single-stranded chain of DNA of different origin. Thus, two DNA single-stranded chains that hybridize to each other have regions of identical or related sequences of nucleotides.

Bacterial species A (bsA) and *Bacterial species B* (bsB) belong to the same genus and are closely related. Both species are human pathogens and the prior art reveals an intense interest in the ability to distinguish one species from the other, and thereby differentially detect one species, and preferably all strains within that particular species, in the presence of the other species. Hybridization assays are routinely used to distinguish closely related pathogenic bacteria. However, the prior art discloses that the nucleotide sequence of the genomes of bsA and bsB are so closely related that identifying nucleic acid probes (fragments of DNA) that are capable of differentially hybridizing to, and thereby distinguishing the two species is a highly unpredictable endeavor. Any probe capable of detecting the presence of bsA DNA is likely to show a positive result when only bsB DNA is present. In the absence of guidance, determination of the characteristics a probe capable of differential detection should possess, such as length or the specific region of the roughly 3 million base pair bacterial genome to which the probe should be directed, requires undue experimentation.

The description states that to be useful to distinguish these two bacteria, and thereby aid in the diagnosis of bsA infections, the nucleic acid probes of the claimed invention must hybridize to bsA, but not to bsB. The description discloses 15 discrete nucleotide sequences that do not share any common structure, i.e. significant sequence identity, but are asserted to have this hybridization property. However, only one sequence, SEQ ID NO: 1, has been demonstrated by example to possess the requisite hybridization property. The description does not disclose any structural properties, such as length or consensus sequence, that must be present for the probe to be specific to bsA. The description also lacks any teachings that would direct a person skilled in the art to any other DNA sequences that possess the claimed property.

Claims

1. An isolated nucleic acid that hybridizes with *Bacteria species A* but does not hybridize to *Bacteria species B*.
2. The isolated nucleic acid of claim 1 where said nucleic acid consists of SEQ ID NO: 1.
3. The isolated nucleic acid of claim 1 where said nucleic acid consists of SEQ ID NO: 2.

4. The isolated nucleic acid of claim 1 where said nucleic acid consists of SEQ ID NO: 3.
5. The isolated nucleic acid of claim 1 where said nucleic acid consists of SEQ ID NO: 4.
6. The isolated nucleic acid of claim 1 where said nucleic acid consists of SEQ ID NO: 5.
7. The isolated nucleic acid of claim 1 where said nucleic acid consists of SEQ ID NO: 6.
8. The isolated nucleic acid of claim 1 where said nucleic acid is selected from the group consisting of SEQ ID NOs: 7 – 15.

Unity of Invention Analysis

Claims 2 through 8 (and each of the separate nucleic acids within claim 8) would be considered independent inventions but for claim 1 which recites a purported common technical feature, i.e. the ability of a nucleic acid to specifically hybridize with *Bacteria species A*, that links the claims to form a single general inventive concept. No nucleic acid possessing the recited hybridization property was known in the prior art. Therefore, under current unity of invention practice, all claimed 15 nucleotide sequences have unity of invention, and would require search and examination.

The invention of claim 1 is not described in a manner sufficiently clear and complete for the invention to be carried out by a person skilled in the art, as required by PCT Article 5, because the description does not provide sufficient guidance to lead a person skilled in the art to any DNA sequences that possess the property recited in claim 1, other than SEQ ID NO: 1, without undue experimentation. The sequences of the two bacterial genomes are very closely related, and while the description discloses 15 discrete nucleotide sequences that are asserted to have the claimed property, those sequences do not share any significant sequence identity, they are not the same length, nor are they derived from any particular location on the genome. The description does not indicate any particular features that the claimed DNA should possess to enable one skilled in the art to identify additional sequences, in the absence of undue experimentation. Furthermore, claim 1 is not fully supported by the description, as required by PCT Article 6. While the description asserts that the disclosed 15 structurally distinct nucleotide sequences have the claimed property, the description does not demonstrate that applicant recognized and described the invention as set forth in claim 1 as a whole at the time of filing because the description does not teach any structural or chemical properties shared by the members of the genus of claim 1, or any nucleic acid structural properties that correlate to the claimed function, i.e., the ability to differentially hybridize to bsA. Therefore, the common technical feature, i.e. the ability of a nucleic acid to specifically hybridize *Bacteria species A*, cannot be considered a “contribution” over the art as intended by PCT Rule 13. Consequently, the requirement for unity of invention is deemed not fulfilled, and a single species would be searched/examined, in the absence of the payment of additional fees.

[Annex IV follows]

ANNEX IV

PROPOSALS BY THE UNITED STATES PATENT AND TRADEMARK OFFICE RELATING TO PARAGRAPH 21.20 OF THE DRAFT GUIDELINES

Example 17 Revised

1. Isolated Protein X having SEQ ID NO: 1.
2. Isolated DNA molecule encoding protein X.
3. A vector comprising the DNA molecule of claim 2.
4. A host cell comprising the vector of claim 3.
5. A method of expressing protein X by culturing the host cell of claim 4.

Given an amino acid sequence, a person skilled in the art can deduce a DNA sequence that encodes that amino acid sequence. Many DNA sequences encoding a protein X can be identified due to the redundancy of the genetic code [1]. The protein and the DNA molecule (as well as a vector or host cell comprising said molecule) share corresponding special technical features because the products set forth in claims 2-4 can be considered as specially adapted or specifically designed to make Protein X. Claim 5 is directed to a method of making protein X. If both the protein and DNA are a contribution over the prior art, unity of invention is present between claims 1-5.

However, if any of the protein X, a DNA encoding protein X, or both fail to make a contribution over the prior art, the claims lack a corresponding special technical feature as required by PCT Rule 13.2, and unity of invention is lacking.

Example 17bis

1. Isolated protein selected from the group consisting of Protein X having SEQ ID NO: 1, variants[2] of Protein X, and functional equivalents of Protein X.
2. Isolated DNA molecule encoding protein X.

The DNA molecule of claim 2 encodes Protein X. However, the DNA molecule of claim 2 does not encode variants of Protein X (including those with *inter alia* amino acid substitutions) or functional equivalents of Protein X (where no structure is specified).

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[1] This reasoning relies upon the presence of only one open reading frame within the claimed DNA molecule that is acted upon to result in the production of the protein of claim 1. Note that a single DNA molecule possesses, at a minimum, 6 different open reading frames with many potential start, stop and splice sites. Regulatory sequences determine which of the many open reading frames are actually expressed in the host. Therefore one DNA molecule can potentially encode many different protein molecules. A more convincing reason to find unity between Protein X and DNA encoding Protein X relies upon knowledge of every amino acid acid and its corresponding coding sequences as explained in the revised example.

[2] Protein variants include those whose structure is described in part, for example, terms of percent identity or sequence substitutions.

Therefore the DNA of claim 2 is not specially adapted or specifically designed to make the protein of claim 1. The inventions of claims 1 and 2 therefore lack a corresponding special technical feature as required by PCT Rule 13.2. Unity of invention between the inventions of claims 1 and 2 is lacking.

Example 17ter

1. Isolated Protein X having SEQ ID NO: 1.
2. Isolated DNA molecule encoding protein X, or fragments or variants[3] of the DNA molecule.

While claim 2 includes within its scope isolated DNA molecules that encode Protein X, by virtue of the "fragments or variants" language, it also includes DNA molecules that may encode other proteins that do not share a common structure, common property and/or common activity with Protein X. The invention set forth in claim 2 is not specially adapted or specifically designed to make the protein of claim 1 because of the lack of a one-to-one correspondence between the proteins encoded by the various DNA molecules recited in claim 2 and Protein X. Therefore, the protein and the DNA lack a common technical feature. Claims 1 and 2 lack a corresponding special technical feature as required by PCT Rule 13.2. Unity between inventions of claims 1 and 2 is lacking.

Example 17quater

1. Isolated DNA molecule X having SEQ ID NO: 1.
2. An isolated protein encoded by the DNA of claim 1.

DNA molecule X is a fully characterized DNA molecule for which the one open reading frame, transcription initiation site, polyadenylation site, translation start and stop site are identified in the disclosure. As such, the isolated DNA of claim 1 is specially adapted or specifically designed to make the protein of claim 2. If both the DNA and protein are a contribution over the prior art, then unity of invention exists between the inventions of Claims 1 and 2.

Example 17quinquis

1. Isolated DNA molecule Y having SEQ ID NO: 2.
2. An isolated protein encoded by the DNA of claim 1.

The disclosure does not point to the one particular open reading frame within DNA molecule Y. Claim 2 is silent concerning the sequence of the protein encoded by DNA molecule Y. A single uncharacterized, genomic DNA molecule possesses, at a minimum, 6 possible open reading frames with many potential start, stop and splice sites. Thus, one uncharacterized or genomic DNA molecule can potentially encode many different protein molecules. DNA X, for example, may be a chromosome or a cosmid clone that comprises thousands of genes,

[3] DNA variants include DNA molecules described, for example, in terms of percent identity, hybridization conditions, or sequence substitutions.

each with their own open reading frames. Even within a single gene, many different proteins may be encoded depending upon the open reading frame, transcription initiation sites and polyadenylation site, translation start and stop sites and alternative splicing. No common structure, and no common property or activity is shared among the many different genes on one chromosome or cosmid or among the many different proteins encoded by one chromosome or cosmid. Therefore the isolated DNA of claim 1 is not specially adapted or specifically designed to make the protein of claim 2. Unity of invention is lacking because there is no technical feature shared between the DNA claimed and an individual protein that may be encoded by the DNA.

[Annex V follows]

ANNEX V

PROPOSALS BY ROSPATENT
RELATING TO PARAGRAPH 21.20 OF THE DRAFT GUIDELINES

Markush Practice: No Common Structure
(Comments To Example 23)

Under the present method in the situation of "Markush practice" the requirement of a technical interrelationship and the same or corresponding special technical features as defined in Rule 13.2 is considered met when the alternatives are of a similar nature. As it follows from the paragraphs relating to Markush practice and from example 23, when the Markush practice grouping is for alternatives of chemical compounds, they shall be regarded as being of similar nature where the following criteria are fulfilled (in cases of the absence of a common structure):

(A) all alternatives have a common property or activity, and
(B) all alternatives belong to a recognized class of chemical compounds in the art to which the invention pertains.

It seems reasonable to emphasize (and to illustrate by some examples) that the alternatives of chemical compounds without common structure can be regarded as being of a similar nature in cases where all alternatives belong to a plurality of classes if all alternatives exhibit a common property, which is substantial for using these compounds in claimed variants of the invention. In particular, a grouping of chemical compounds representing a plurality of classes can be acceptable when the compounds are unified by a specific property, for example:

(a) a group of compounds - phosphoric acid, phenol, ethyl alcohol, ascorbic acid - has the following common specific property: all of them are proton donors;
(b) a group of compounds - ozone, potassium permanganate, benzoyl peroxide, chloride acid - has the following common specific property: they are oxidizers.

If the exhibition of such common specific property by the alternative compounds is substantial in the invention, unity of invention shall be considered to be met. It is not necessary to include such common specific property into a claim, but it should be disclosed in the description.

Example

Claim 1. A process for preventing the formation of sediment in technical solution, characterized by adding an agent selected from the group consisting of phosphoric acid, phenol, ethyl alcohol and ascorbic acid.

If it is clear from the description that the addition of a substance - proton donor - is substantial for the achievement of a technical result, the alternative features (which can be considered as corresponding special technical features) are united by a common property, and the inventions of a group are so linked as to form a single general inventive concept, i.e. the requirement of unity of invention is satisfied.

If in the description there are no reasonable explanations of the grouping of said substances, it is concluded that the substances represent a plurality of classes and, consequently, the requirement of unity is not satisfied.

Such approach can be taken to the analysis of non-chemical alternatives. In this case the non-chemical alternatives shall be regarded as being of a similar nature where the following criteria are fulfilled:

(A) all alternatives are directed to the solution of a common specific problem
(B) the alternatives are known for a skilled person equivalents with relation to the solution of this specific problem.

The examples of such alternatives: group of substances relating to building materials, group of different materials having common physical property (or example, a melting point over the specified one or strength characteristics above the specified).

Example

Claim 1. A soil for growing plants indoors, comprising of ...(a composition common for all variants)... with the addition of 10% of the material selected from the group consisting of peat, river sand, sawdust, granulated polystyrene.

It is obvious from the description that said material have common property - they provide moisture permeability and soil drainage. The alternatives can be considered as being corresponding special technical features - unity of invention exists.

It should be added, that if in a claim there are not only alternative features which make a contribution over the prior art but others special technical features, common for all variants of the invention, the requirement of unity of invention is satisfied. Thus, if in Example 23 herbicide A is a new herbicide and defines a contribution over the prior art, unity of invention exists: the claimed variants of the inventions have common special technical feature - herbicide A- independently of whether alternative features relate to a recognized class.

[Annex VI follows]

ANNEX VI

PROPOSALS BY IP AUSTRALIA RELATING TO PARAGRAPH 21.21 OF THE DRAFT GUIDELINES, WITH ADDITIONAL SUGGESTIONS BY THE UNITED STATES PATENT AND TRADEMARK OFFICE

The proposal by IP Australia is set out first as a clean copy. This is followed by suggestions by the United States Patent and Trademark Office for amendments to the second additional example 24, the differences from the IP Australia proposal being shown using underline and ~~strikeout~~.

Proposal by IP Australia

[– *Additional Example 24 – no common property or activity*

Probe Fragments

> Claim 1 : An isolated nucleotide sequence of SEQUENCE ID NO 1 that codes for enzyme Y.
> Claim 2 : A fragment of SEQUENCE ID NO 1 selected from SEQUENCE ID NO 2, SEQUENCE ID NO 3 and SEQUENCE ID NO 4.

The description indicates that enzyme Y is known and that sequence ID 2, 3 and 4 are non-overlapping fragments of SEQUENCE ID NO 1 that codes for enzyme Y. SEQUENCE ID NO 2,3 and 4 are identified as useful as probes for SEQUENCE ID NO 1.

The only common property or activity shared by all the claimed nucleic acids is that they are all derived from SEQUENCE ID NO 1. However, SEQUENCE ID NO 1 is known and therefore cannot be considered a special technical feature. All of the fragments represent different portions of SEQUENCE ID NO 1 and thus different structural and functional regions within the nucleic acid sequence. Therefore, because the requirement under Rule 13.2 for the same or corresponding special technical feature is not met due to the fact that the alternatives of the Markush grouping are not of a similar nature, i.e. the alternatives are not known to have a common property or activity, unity is lacking.]

[– *Additional Example 24 –common property or activity*

Multiple nucleotide sequences

> Claim 1 : A nucleic acid selected from SEQUENCE ID NO 1, SEQUENCE ID NO 2 and SEQUENCE ID NO 3.

The description discloses that the three nucleic acids claimed are all dehydrogenases having the same tertiary structure and biochemical action but are isolated from different organisms. The structure and activity is defined in the specification as the feature of the invention that distinguishes it from the prior art.

The special technical feature present in each sequence is that the sequence encodes an enzyme having the same structure and biochemical action.

Therefore, there is unity between the separately claimed nucleic acids.]

USPTO suggestions for amendment to second additional example 24 above

[– *Additional Example 24 –common property or activity*

Multiple nucleotide sequences

> Claim 1 : A nucleic acid selected from SEQUENCE ID NO 1, SEQUENCE ID NO 2 and SEQUENCE ID NO 3.

The description discloses that the three nucleic acids claimed all encode ~~are all~~ dehydrogenases that have ~~having~~ the same overall tertiary structure and include conserved sequence motifs that define the catalytic site and dehydrogenase function of these proteins. The three nucleic acids were isolated from different organisms. The description concludes that these three nucleic acids are homologues based upon their overall sequence similiarity at both the nucleotide and amino acid sequence levels.~~and biochemical action but are isolated from different organisms.~~ The structure and activity is defined in the specification as the feature of the invention that distinguishes it from the prior art.

The special technical feature present in each sequence is that the sequence encodes an enzyme having the same structure and biochemical action.

Therefore, there is unity between the separately claimed nucleic acids.]

[End of Annex VI and of document]