GERMANY

Patent Regulations

Patent Ordinance of 1 September 2003 (Federal Law Gazette I p. 1702), last amended by Article 2 of the Ordinance of 17 December 2004 (Federal Law Gazette I p. 3532)

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Part I General Provisions

Section 1 Scope of application

In addition to the provisions of the Patent Law and the Ordinance Concerning the German Patent and Trade Mark Office, the provisions of this ordinance shall apply to procedures before the German Patent and Trade Mark Office, prescribed in the Patent Law.

Section 2 German industrial standards, measuring units, symbols and signs

(1) German industrial standards, referred to in this ordinance, have been published by Beuth-Verlag GmbH, Berlin and Cologne, and securely stored in an archive at the German Patent and Trade Mark Office in Munich.

(2) Measuring units shall be indicated in accordance with the Law on Measuring Units and the corresponding implementing regulations in the respective applicable versions. For chemical formulae the signs and symbols recognised in national or international practice in the field in question shall be used.

Part II Patent Applications; Patent Procedures

Section 3 Filing of the application

(1) The application (Sec. 34 Patent Law) and the abstract (Sec. 36 Patent Law) shall be filed in writing with the German Patent and Trade Mark Office. Section 12 of the Ordinance Concerning the German Patent and Trade Mark Office shall apply for electronic filing.

(2) In the cases of Sections 8, 14 to 21 the electronic form shall be excluded.

Section 4 Request for the grant of a patent

(1) The request for the grant of a patent (Sec. 34(3) No. 2 Patent Law) or for the grant of a patent of addition (Sec. 16 Patent Law) shall be filed on the form issued by the German Patent and Trade Mark Office or as an electronic file in accordance with the format requirements published by the German Patent and Trade Mark Office.

(2) The request shall contain:
1. the following information on the applicant:
a) if the applicant is a natural person, given name and the family name or, if registration is sought under the trade name, the trade name as recorded in the Commercial Register;
b) if the applicant is a legal entity or a partnership, the name of this entity or partnership; the usual abbreviation of the legal form can be used. If the legal entity or partnership is registered in a register, the name shall be indicated in a form corresponding to that of the register entry. In case of a partnership under the Civil Code, the name and address of at least one partner entitled to act as representative shall also be indicated;
it shall be made clear whether the patent is sought on behalf of one or more than one individual or partnership, or for the applicant under the trade name or under the civil name;
c) the residence or principal place of business and the address (street and house number, postal code, town);
2. a short and precise title of the invention;
3. a statement that the grant of a patent or patent of addition is requested for the invention;
4. if a representative has been appointed, his name and his address;
5. the signatures of all applicants or their representative;
6. if a patent of addition is sought, the file number of the parent patent

application or the number of the parent patent shall also be given.

(3) If the residence or principle place of business of the applicant is not in Germany, the applicant shall also indicate the country in addition to the town when indicating the address under subsection (2) No. 1 item c). Furthermore, the applicant may also indicate the district, county or state where he has his residence or principle place of business or to whose legal order he is subject to.

(4) If the German Patent and Trade Mark Office has assigned an applicant's number to the applicant, this number should be indicated in the application.

(5) If the German Patent and Trade Mark Office has assigned a representative's number or the number of a general power of attorney to the representative, this number should be indicated.

(6) In the event of employees signing the request on behalf of their employer who files an application, the authority to sign shall be proved to the satisfaction of the office; reference shall be made to any employee's authority to sign, deposited with the German Patent and Trade Mark Office, indicating the identification number communicated for this purpose.

Section 5 Application documents

(1) The documents making up the application and the abstract shall not contain any pictorial representation in the text matter. It may contain chemical and mathematical formulae as well as tables. Fancy names, trade marks or other designations which are not suited to clearly indicate the nature of an object, shall not be used. If, in exceptional cases, an indication can only be clearly denoted by using a trade mark, the said designation shall make it clear that it is a trade mark.

(2) Technical terms and designations as well as reference signs shall be used uniformly throughout the application unless the use of different terms is adequate. With respect to technical terms and designations, the same applies to applications of addition in relation to the parent application.

Section 6 Formal requirements for a written application

(1) The documents making up the application shall be so presented as to

admit of electronic data input. Extensive application documents consisting of more than 300 pages shall also be furnished on two data carriers each containing the application documents in machine-readable form. The standards prescribed in annex 1 (resp. Sec. 11(1), second sentence) No. 41 shall apply mutatis mutandis to the data carriers. A declaration shall be attached to the data carriers, stating that the information stored on the data carriers corresponds to the application documents.

(2) The patent claims, the description, the drawings as well as the text and the drawings of the abstract shall be filed on separate sheets in three copies. The size of the sheets shall be A4 according to DIN 476 (German industrial standard) and be used in upright position. For the drawings, the sheets may, if appropriate, be used sideways; in this case, the top of the figures shall be presented at the left side of the sheet in an upright position. This shall apply mutatis mutandis to the representation of chemical and mathematical formulae and tables. All sheets shall be free from creases, tears and folds. The paper of the sheets shall be non-transparent, pliable, strong, smooth, matt and durable.

(3) Only one side of the sheets shall be typed or printed or contain drawings. The sheets shall be connected in such a way that they can be easily separated and joined together again. Each of the documents making up the application (request form, patent claims, description, drawings) and the abstract (text matter, drawings) shall commence on a new sheet. The sheets of the description shall be numbered in consecutive Arabic numerals. These numbers shall be placed below the top margin of the sheet, in the middle. The lines and paragraphs should not be numbered nor any other numbering be applied.

(4) The margins of the sheets containing the request, the patent claims, the description and the abstract must be blank. The minimum margins shall be as follows:
top 2.0 cm
left side 2.5 cm
right side 2.0 cm
bottom 2.0 cm
The minimum margins may contain the name, the trade name or other designation of the applicant as well as the file number of the application.

(5) The request, the patent claims, the description and the abstract shall

be typed or printed, using single-column formatting. The right margin should not be justified. The letters of the type used shall be clearly separated and must not touch. Graphic symbols and characters and chemical or mathematical formulae may, if necessary, be written by hand or drawn. The typing shall be 1 1/2 spaced. The text matter shall be in characters, the capital letters of which are not less than 0.21 cm high (the minimum font size shall be 10 point) and shall be in dark, indelible colour. The typeface shall have sharp outlines and be high-contrast. Each sheet shall be reasonably free from erasures, alterations, overwriting and interlineations. If appropriate, non-compliance with this rule may be authorised. The text shall not be underlined, italicised, bolted; character spacing shall not be expanded.

(6) The documents making up an application shall clearly show to which application they pertain.

Section 7 Naming the inventor

(1) The applicant shall indicate the inventor on the form issued by the German Patent and Trade Mark Office or on an electronic file pursuant to the formatting requirements published by the German Patent and Trade Mark Office.

(2) This indication must contain:

1. the given name and family name, residence and the address (street and house number, postal code, town, postal district, if any) of the inventor;
2. the affirmation of the applicant that to his knowledge no other person has contributed to the invention (Sec. 37(1) Patent Law);
3. if the applicant is not the inventor or not the sole inventor, a statement by the applicant on how he acquired the right to the patent (Sec. 37(1), second sentence, Patent Law);
4. the title of the invention and the official file number, if already known;
5. the signature of the applicant or his representative; if the patent grant has been requested by several persons, each person or their representative shall sign the declaration.

Section 8 Omission of the mention of the inventor; change of the mention of the inventor

(1) The request by the inventor not to be mentioned as inventor, the withdrawal of this request (Sec. 63(1), third and fourth sentences, Patent Law) and the requests for correction or subsequent mention of the inventor

(Sec. 63(2) Patent Law) shall be filed in writing. The documents shall be signed by the inventor and shall contain the title of the invention and the official file number.

(2) The consent to the correction or subsequent mention of the inventor (Sec. 63(2) Patent Law) by the applicant or patentee and the person wrongly mentioned shall be given in writing.

Section 9 Patent claims

(1) Patent claims shall contain what is to be protected by the patent (Sec. 34(3) No. 3 of the Patent Law) and shall be drafted in one piece or shall be divided into generic part and characterising portion (two-piece). In both cases the version may be arranged according to features.

(2) If the two-piece claim formulation is chosen, the known features of the invention comprised in the state of the art shall be included in the generic part; the characterising portion shall include the features of the invention for which protection is sought in connection with the features of the generic part. The characterising portion shall be preceded by such words as “characterised in that” or “characterised by” or any other expressions to this effect.

(3) If patent claims are arranged according to features or groups of features, the said arrangement shall be set off by starting a new line for each feature or group of features. The features or groups of features shall be preceded by subdivision signs clearly set off against the text matter.

(4) The essential features of the invention shall be indicated in the first patent claim (principal claim).

(5) An application may contain several independent patent claims provided the principle of unity of the invention is respected (Sec. 34(5) of the Patent Law). Subsection (4) shall apply mutatis mutandis. Independent claims may contain a reference to at least one of the preceding patent claims.

(6) Any principal or independent patent claim, respectively, may be followed by one or more dependent claims concerning particular embodiments of the invention. Dependent claims shall contain a reference

to at least one of the preceding patent claims. They shall be grouped together to the extent and in the most appropriate way possible.

(7) If there are several patent claims, they shall be numbered consecutively in Arabic numerals.

(8) Claims shall not, except where absolutely necessary, rely, in respect of the technical features of the invention, on references to the description or drawings. In particular, they shall not rely on such references as: “as described in part ... of the description”, or “as illustrated in figure ... of the drawings”.

(9) If the patent application contains drawings, the features mentioned in the claims shall preferably be followed by reference signs, if the intelligibility of the claim can thereby be increased.

(10) For electronic filing, an electronic file pursuant to the formatting requirements published by the German Patent and Trade Mark Office shall be used.

Section 10 Description

(1) The description according to Section 34(3) No. 4 of the Patent Law shall first state the title of the invention as appearing in the request.

(2) Additionally, it shall:

1. specify the technical field to which the invention relates unless it follows from the claims or the indications concerning the state of the art;
2. indicate the state of the art known to the applicant which may be taken into account for the understanding of the invention and its protectability by indicating the sources known to the applicant;
3. describe the problem underlying the invention unless it follows from the indicated solution or the indications made with regard to No. 6, in particular, if it is indispensable for the understanding of the invention or for specifying its contents more closely;
4. indicate the invention for which protection is sought in the patent claims;
5. when it is not obvious from the description or the nature of the invention, indicate at least one way in which the invention is capable of exploitation in industry;
6. state any advantageous effects of the invention with reference to the

background art;
7. describe in detail at least one way of carrying out the invention claimed, using, where appropriate, examples or drawings, indicating the respective reference signs.

(3) The description shall not include any indications obviously not necessary in order to explain the invention. Repetitions of claims or parts of claims may be replaced by corresponding references.

(4) For electronic filing, an electronic file pursuant to the formatting requirements published by the German Patent and Trade Mark Office shall be used.

Section 11 Presentation of nucleotide and amino acid sequences

(1) If structural formulae in form of nucleotide or amino acid sequences are indicated and hence disclosed in concrete terms in the patent application, a corresponding sequence listing shall be filed as annex to the application, separately from the description and the claims. The sequence listing shall comply with the standards for the filing of sequence listings prescribed in annex 1.

(2) If the patent application is filed in writing, two data carriers each containing the sequence listing in machine readable form shall be submitted in addition to the written application documents. The data carriers shall be clearly marked as data carriers for a sequence listing and comply with the standards mentioned in subsection (1). The data carriers shall be accompanied by a statement that the information recorded on the data carriers is identical to the written sequence listing.

(3) If the sequence listing on the data carrier filed in the application is corrected subsequently, the applicant shall submit a statement that the corrected sequence listing does not include matter which goes beyond the content of the application as filed. Subsections (1) and (2) shall apply mutatis mutandis to the correction.

(4) In case of an application derived from an international patent application under the Patent Cooperation Treaty in respect of which the German Patent and Trade Mark Office is a designated or an elected office (Art. III Sec. 4(1), Sec. 6(1) of the Law on International Patent Treaties of 21 June 1976, Federal Law Gazette 1976 II p. 649), the rules of the Regulations under the Patent Cooperation Treaty shall apply directly,

insofar as they concern the standard for filing sequence listings.

(5) Electronic filing of the application by e-mail is possible only if the application with the sequence listing does not exceed the file size admissible for the transmission process.

Section 12 Drawings

Drawings furnished shall comply with the standards contained in annex 2.

Section 13 Abstract

(1) The abstract according to Section 36 of the Patent Law shall preferably not consist of more than 1,500 characters.

(2) The abstract may also indicate the chemical formula which best characterises the invention.

(3) Section 9(8) shall apply mutatis mutandis.

(4) For electronic filing, an electronic file pursuant to the formatting requirements published by the German Patent and Trade Mark Office shall be used.

Section 14 German translations

(1) German translations of documents forming part of the documentation relating to the application shall be certified by an attorney-at-law or patent attorney or be done by an officially authorised translator. The translator's signature shall be officially certified (Article 129 of the Civil Code) and it shall also be certified that he is officially authorised for such purposes.

(2) German translations of

1. priority documents submitted under the revised Paris Convention for the Protection of Industrial Property (Federal Law Gazette 1970 II p. 391), or
2. copies of earlier applications (Sec. 41(1), first sentence, Patent Law)

shall only be furnished upon invitation by the German Patent and Trade Mark Office.

(3) German translations of documents

1. not forming part of the documentation relating to the application and
2. filed in English, French, Italian or Spanish,
shall be subsequently furnished only upon invitation by the German Patent and Trade Mark Office.

(4) If foreign-language documents not forming part of the documentation relating to the application are filed in languages not mentioned in subsection (3) No. 2, German translations shall be filed subsequently within one month after receipt of the documents.

(5) The translation under subsection (3) or (4) shall be certified by an attorney-at-law or patent attorney or done by an officially authorised translator. If the translation is not filed in due time, the foreign-language document is deemed to have been received on the date of receipt of the translation.

Part III Other Formal Requirements

Section 15 Subsequently filed application documents; changes in application documents

(1) Any document filed after communication of the official file number shall indicate the complete file number. If the application documents are altered in the course of the procedure, the applicant shall submit clean copies incorporating any changes. Two clean copies shall be filed. Sec. 6(1) and Sec. 11(2) shall apply mutatis mutandis.

(2) If the applicant subsequently furnishes further copies of the application documents, the documents shall be accompanied by a declaration stating that the subsequently furnished documents correspond to the documents as originally filed.

(3) Insofar as the changes have not been proposed by the German Patent and Trade Mark Office, the applicant shall state in detail where the features of the invention described in the new documents are disclosed in the originally filed documents. In addition, the changes effected shall be marked either in a copy of the changed documents, by separate explanations, or in the clean copies. If the changes are marked in the clean copies, they shall be in bold lettering.

(4) Insofar as the changes have been proposed by the German Patent and Trade Mark Office and have been accepted by the applicant without further changes, the applicant shall attach a declaration to the clean copies mentioned in subsection (1), second and third sentences; this declaration shall state that the clean copies do not contain any other changes than the changes proposed by the German Patent and Trade Mark Office.

Section 16 Models and samples

(1) Models and samples shall only be supplied if the German Patent and Trade Mark Office invites the applicant to do so. They shall bear durable labels indicating the contents and the application to which they relate. If necessary, clear reference shall be made to the patent claim and the description.

(2) Fragile models and samples shall be submitted in sturdy containers clearly so marked. Small articles hall be fastened on stiff paper.

(3) Samples of chemical materials shall be submitted in durable and firmly

closed containers. If they are poisonous, corrosive or inflammable or have other dangerous characteristics, they shall bear an indication to this effect.

(4) Dyeing and tanning samples as well as other flat samples shall be firmly fixed on stiff paper (size A4 according to DIN 476). They shall be accompanied by a precise description of the process of manufacture or use.

Section 17 Official certification of signatures

Upon invitation by the German Patent and Trade Mark Office the signatures mentioned in Section 7(2) No. 5 and in Section 8 shall be officially certified (Section 129 of the Civil Code).

Section 18 (deleted)

Part IV Supplementary Protection Certificates

Section 19 Filing of the application

(1) The request for the grant of a supplementary protection certificate (Sec. 49a Patent Law) shall be furnished on the form issued by the German Patent and Trade Mark Office. Section 4(2) Nos. 1, 4 and 5, and Section 14(1), (3) to (5) shall apply mutatis mutandis.

(2) The request shall be accompanied by information setting forth the protection afforded by the parent patent.

Section 20 Supplementary protection certificates for medicinal products

The request for the grant of a supplementary protection certificate for medicinal products shall contain the information and documents specified in Article 8 of the Council Regulation (EEC) No. 1768/92 of 18 June 1992 concerning the creation of a supplementary protection certificate for medicinal products (OJ EC No. L 182 p. 1).

Section 21 Supplementary protection certificates for plant protection products

The request for the grant of a supplementary protection certificate for plant protection products shall contain the information and documents specified in Article 8 of the Council Regulation (EC) No. 1610/96 of 23 July 1996 concerning the creation of a supplementary protection certificate for plant protection products (OJ EC No. L 198 p. 30).

Part V Final Provisions and Transitory Provisions

Section 22 Transitory provisions

For patent applications, the naming of the inventor and requests for the grant of a supplementary protection certificate filed before the entry into force of the amendments to this ordinance, the provisions heretofore in force shall remain applicable in the version applicable until that date.

Section 23 Entry into force; abrogation

This ordinance shall enter into force on 15 October 2003. At the same date,

1. the Order Concerning Patent Applications of 29 May 1981 (Federal Law Gazette I p. 521), last amended by the ordinance of 1 January 2002 (Federal Law Gazette I p. 32), and
2. the order concerning the naming of the inventor of 29 May 1981 (Federal Law Gazette I p. 525)

shall be abrogated.

Annex 1 (resp. Sec. 11(1), second sentence) Standards for the Filing of Sequence Listings

Definitions

1. For the purposes of this Standard the following definitions shall be applicable:

(i) the expression “sequence listing” means a part of the description of the application as filed or a document filed subsequently to the application, which gives a detailed disclosure of the nucleotide and/or amino acid sequences and other available information;

(ii) sequences which are included are any unbranched sequences of four or more amino acids or unbranched sequences of ten or more nucleotides. Branched sequences, sequences with fewer than four specifically defined nucleotides or amino acids as well as sequences comprising nucleotides or amino acids other than those listed in paragraph 48, tables 1, 2, 3 and 4, are specifically excluded from this definition;

(iii) “nucleotides” embrace only those nucleotides that can be represented using the symbols set forth in paragraph 48, table 1. Modifications, for example, methylated bases, may be described as set forth in paragraph 48, table 2, but shall not be shown explicitly in the nucleotide sequence;

(iv) “amino acids” are those L-amino acids commonly found in naturally occurring proteins and are listed in paragraph 48, table 3. Those amino acid sequences containing at least one D-amino acid are not intended to be embraced by this definition. Any amino acid sequence that contains post-translationally modified amino acids may be described as the amino acid sequence that is initially translated using the symbols shown in paragraph 48, table 3, with the modified positions, for example, hydroxylations or glycosylations, being described as set forth in paragraph 48, table 4, but these modifications shall not be shown explicitly in the amino acid sequence. Any peptide or protein that can be expressed as a sequence using the symbols in paragraph 48, table 3, in conjunction with a description elsewhere to describe, for example, abnormal linkages, cross-links (for example, disulfide bridge) and end caps, non-peptidyl bonds, etc., is embraced by this definition;

(v) “sequence identifier” is a unique integer that corresponds to the SEQ ID NO assigned to each sequence in the listing;

(vi) “numeric identifier” is a three-digit number which represents a specific data element;

(vii) “language-neutral vocabulary” is a controlled vocabulary used in the sequence listing that represents scientific terms as prescribed by

sequence database providers (including scientific names, qualifiers and their controlled-vocabulary values, the symbols appearing in paragraph 48, tables 1, 2, 3 and 4, and the feature keys appearing in paragraph 48, tables 5 and 6);
(viii) “competent Authority” is the International Searching Authority that is to carry out the international search on the international application, or the International Preliminary Examining Authority that is to carry out the international preliminary examination on the international application, or the designated/elected Office before which the processing of the international application has started.

Sequence Listing

2. The sequence listing as defined in paragraph 1(i) shall, where it is filed together with the application, be placed at the end of the application. This part shall be entitled “Sequence Listing” or “Sequenzprotokoll” begin on a new page and preferably have independent page numbering. The sequence listing forms an integral part of the description; it is therefore unnecessary, subject to paragraph 35, to describe the sequences elsewhere in the description.
3. Where the sequence listing as defined in paragraph 1(i) is not contained in the application as filed but is a separate document furnished subsequently to the filing of the application (see paragraph 36), it shall be entitled “Sequence Listing” or “Sequenzprotokoll” and shall have independent page numbering. The original numbering of the sequences (see paragraph 4) in the application as filed shall be maintained in the subsequently furnished sequence listing.
4. Each sequence shall be assigned a separate sequence identifier. The sequence identifiers shall begin with 1 and increase sequentially by integers. If no sequence is present for a sequence identifier, the code 000 should appear under numeric identifier <400>, beginning on the next line following the SEQ ID NO. The response for numeric identifier <160> shall include the total number of SEQ ID NOs, whether followed by a sequence or by the code 000.
5. In the description, claims or drawings of the application, the sequences represented in the sequence listing shall be referred to by the sequence identifier and preceded by “SEQ ID NO:”.
6. Nucleotide and amino acid sequences should be represented by at least one of the following three possibilities:
(i) a pure nucleotide sequence
(ii) a pure amino acid sequence
(iii) a nucleotide sequence together with its corresponding amino acid

sequence.
For those sequences disclosed in the format specified in option (iii), above, the amino acid sequence must be disclosed separately in the sequence listing as a pure amino acid sequence with a separate integer sequence identifier.

Nucleotide Sequences

Symbols to be used

7. A nucleotide sequence shall be presented only by a single strand, in the 5′-end to 3′-end direction from left to right. The terms 3′ and 5′ shall not be represented in the sequence.

8. The bases of a nucleotide sequence shall be represented using the one-letter code for nucleotide sequence characters. Only lower case letters in conformity with the list given in paragraph 48, table 1, shall be used.

9. Modified bases shall be represented as the corresponding unmodified bases or as “n” in the sequence itself if the modified base is one of those listed in paragraph 48, table 2, and the modification shall be further described in the feature section of the sequence listing, using the codes given in paragraph 48, table 2. These codes may be used in the description or the feature section of the sequence listing but not in the sequence itself (see also paragraph 31). The symbol “n” is the equivalent of only one unknown or modified nucleotide.

Format to be used

10. A nucleotide sequence shall be listed with a maximum of 60 bases per line, with a space between each group of 10 bases.

11. The bases of a nucleotide sequence (including introns) shall be listed in groups of 10 bases, except in the coding parts of the sequence. Leftover bases, fewer than 10 in number at the end of non-coding parts of a sequence, should be grouped together and separated from adjacent groups by a space.

12. The bases of the coding parts of a nucleotide sequence shall be listed as triplets (codons).

13. The enumeration of the nucleotide shall start at the first base of the sequence with number 1. It shall be continuous through the whole sequence in the direction 5′ to 3′. It shall be marked in the right margin, next to the line containing the one-letter codes for the bases, and giving the number of the last base of that line. The enumeration method for nucleotide sequences set forth above remains applicable to nucleotide sequences that are circular in configuration, with the exception that the designation of the first nucleotide of the sequence may be made at

the option of the applicant.

14. A nucleotide sequence that is made up of one or more non-contiguous segments of a larger sequence or of segments from different sequences shall be numbered as a separate sequence, with a separate sequence identifier. A sequence with a gap or gaps shall be numbered as a plurality of separate sequences with separate sequence identifiers, with the number of separate sequences being equal in number to the number of continuous strings of sequence data.

Amino Acid Sequences

Symbols to be used

15. The amino acids in a protein or peptide sequence shall be listed in the amino to carboxy direction from left to right. The amino and carboxy groups shall not be represented in the sequence.

16. The amino acids shall be represented using the three-letter code with the first letter as a capital and shall conform to the list given in paragraph 48, table 3. An amino acid sequence that contains a blank or internal terminator symbols (for example, “Ter” or “*” or “.”) may not be represented as a single amino acid sequence, but shall be presented as separate amino acid sequences (see paragraph 21).

17. Modified and unusual amino acids shall be represented as the corresponding unmodified amino acids or as “Xaa” in the sequence itself if the modified amino acid is one of those listed in paragraph 48, table 4, and the modification shall be further described in the feature section of the sequence listing, using the codes given in paragraph 48, table 4. These codes may be used in the description or the feature section of the sequence listing but not in the sequence itself (see also paragraph 31). The symbol “Xaa” is the equivalent of only one unknown or modified amino acid.

Format to be used

18. A protein or peptide sequence shall be listed with a maximum of 16 amino acids per line, with a space provided between each amino acid.

19. Amino acids corresponding to the codons in the coding parts of a nucleotide sequence shall be placed immediately under the corresponding codons. Where a codon is split by an intron, the amino acid symbol should be given below the portion of the codon containing two nucleotides.

20. The enumeration of amino acids shall start at the first amino acid of the sequence, with number 1. Optionally, the amino acids preceding the mature protein, for example pre-sequences, pro-sequences, pre-pro-sequences and signal sequences, when present, may have negative

numbers, counting backwards starting with the amino acid next to number 1. Zero (0) is not used when the numbering of amino acids uses negative numbers to distinguish the mature protein. It shall be marked under the sequence every five amino acids. The enumeration method for amino acid sequences set forth above remains applicable for amino acid sequences that are circular in configuration, with the exception that the designation of the first amino acid of the sequence may be made at the option of the applicant.

21. An amino acid sequence that is made up of one or more non-contiguous segments of a larger sequence or of segments from different sequences shall be numbered as a separate sequence, with a separate sequence identifier. A sequence with a gap or gaps shall be numbered as a plurality of separate sequences with separate sequence identifiers, with the number of separate sequences being equal in number to the number of continuous strings of sequence data.

Other Available Information in the Sequence Listing

22. The order of the items of information in the sequence listings shall follow the order in which those items are listed in the list of numeric identifiers of data elements as defined in paragraph 47.

23. Only numeric identifiers of data elements as defined in paragraph 47 shall be used for the presentation of the items of information in the sequence listing. The corresponding numeric identifier descriptions shall not be used. The provided information shall follow immediately after the numeric identifier while only those numeric identifiers for which information is given need appear on the sequence listing. Two exceptions to this requirement are numeric identifiers <220> and <300>, which serve as headers for “Feature” and “Publication Information,” respectively, and are associated with information in numeric identifiers <221> to <223> and <301> to <313>, respectively. When feature and publication information is provided in the sequence listing under those numeric identifiers, numeric identifiers <220> and <300>, respectively, should be included, but left blank. Generally, a blank line shall be inserted between numeric identifiers when the digit in the first or second position of the numeric identifier changes. An exception to this general rule is that no blank line should appear preceding numeric identifier <310>. Additionally, a blank line shall precede any repeated numeric identifier.

Mandatory Data Elements

24. The sequence listing shall include, in addition to and immediately preceding the actual nucleotide and/or amino acid sequence, the following

items of information defined in paragraph 47 (mandatory data elements):

<110>	Applicant name
<120>	Title of invention
<160>	Number of SEQ ID NOs
<210>	SEQ ID NO: x
<211>	Length
<212>	Type
<213>	Organism
<400>	Sequence

Where the name of the applicant (numeric identifier <110>) is written in characters other than those of the Latin alphabet, it shall also be indicated in characters of the Latin alphabet either as a mere transliteration or through translation into English.

The data elements, except those under numeric identifiers <110>, <120> and <160>, shall be repeated for each sequence included in the sequence listing. Only the data elements under numeric identifiers <210> and <400> are mandatory if no sequence is present for a sequence identifier (see paragraph 4, above, and SEQ ID NO: 4 in the example depicted in the end of this Standard).

25. In addition to the data elements identified in paragraph 24, above, when a sequence listing is filed at the same time as the application to which it pertains or at any time prior to the assignment of an application number, the following data element shall be included in the sequence listing:

<130>	Reference number

26. In addition to the data elements identified in paragraph 24, above, when a sequence listing is filed in response to a request from a competent Authority or at any time following the assignment of an application number, the following data elements shall be included in the sequence listing:

<140>	Current patent application
<141>	Current filing date

27. In addition to the data elements identified in paragraph 24, above, when a sequence listing is filed relating to an application which claims the priority of an earlier application, the following data elements shall be included in the sequence listing:

<150>	Earlier patent application
<151>	Earlier application filing date

28. If “n” or “Xaa” or a modified base or modified/unusual L-amino acid is used in the sequence, the following data elements are mandatory:

<220>	Feature
<221>	Name/key
<222>	Location
<223>	Other information

29. If the organism (numeric identifier <213>) is “Artificial Sequence” or “Unknown,” the following data elements are mandatory:

<220>	Feature
<223>	Other information

Optional Data Elements

30. All data elements defined in paragraph 47, not mentioned in paragraphs 24 to 29, above, are optional (optional data elements).

Presentation of Features

31. When features of sequences are presented (that is, numeric identifier <220>), they shall be described by the "feature keys" set out in paragraph 48, tables 5 and 6.

Free Text

32. "Free text" is a wording describing characteristics of the sequence under numeric identifier <223> (Other information) which does not use language-neutral vocabulary as referred to in paragraph 1(vii).

33. The use of free text should be limited to a few short terms indispensable for the understanding of the sequence. It should not exceed four lines with a maximum of 65 characters per line for each given data element. Any further information shall be included in the main part of the description in the language thereof.

34. Any free text may be in the German or the English language.

35. Where the sequence listing part of the description contains free text, any such free text shall be repeated in the main part of the description in the language thereof. It is recommended that the free text in the language of the main part of the description be put in a specific section of the description called "Sequence Listing Free Text".

Subsequently Furnished Sequence Listing

36. Any sequence listing which is not contained in the application as filed but which is furnished subsequently shall not go beyond the disclosure of the sequences indicated in the application. The subsequently furnished sequence listing shall be accompanied by a statement confirming that fact. This means that a sequence listing furnished subsequently to the filing of the application shall contain only those sequences that have been contained in the application as filed.

37. Any sequence listing not contained in the application as filed does not form part of the disclosure of the invention. It is possible for a sequence listing contained in the application as filed to be corrected under Sec. 11(3) by remedying the defects.

Computer Readable Form of the Sequence Listing

38. A copy of the sequence listing contained in the application shall also be submitted in computer readable form.

39. Any sequence listing in computer readable form submitted in addition to the written sequence listing shall be identical to the written sequence listing and shall be accompanied by a statement that “the information recorded in computer readable form is identical to the written sequence listing.”

40. The entire printable copy of the sequence listing shall be contained within one electronic file preferably on a single diskette or any other electronic medium that is acceptable to the German Patent and Trade Mark Office. The file shall be encoded using IBM Code Page 437, IBM Code Page 932 or a compatible code page. A compatible code page, as would be required for, for example, Japanese, Chinese, Cyrillic, Arabic, Greek or Hebrew characters, is one that assigns the Roman alphabet and numerals to the same hexadecimal positions as do the specified code pages.

41. The following media types and formats shall be acceptable for machine-readable sequence listings:

Physical Medium	Type	Format
CD-R	120 mm Recordable Disk	ISO 9660
DVD-R	120 mm DVD-Recordable Disk (4.7 GB)	complying with ISO 9660 or OSTA UDF (1.02 or higher)
DVD+R	120 mm DVD-Recordable Disk (4.7 GB)	complying with ISO 9660 or OSTA UDF (1.02 or higher)

42. The computer readable version may be created by any means. However, it shall correspond to the formats indicated by the German Patent and Trade Mark Office. It should preferably be created by dedicated special software such as PatentIn.

43. File compression is acceptable when using physical data carriers, so long as the compressed file is in a self-extracting format that will decompress on an operating system (MS Windows) that is acceptable to the German Patent and Trade Mark Office. Likewise files relating as regards their contents may be compressed in a non-self-extracting format, if the archive file exists in ZIP format in the version of 13 July 1998 and neither contains other ZIP archives nor a directory structure.

44. The physical data carrier shall have a label permanently affixed thereto on which has been hand-printed, in block capitals or typed, the name of the applicant, the title of the invention, a reference number, the date on which the data were recorded, the computer operating system.

45. If the physical data carrier is submitted after the date of filing of an application, the labels shall also include the filing date of the application and the application number. Corrections or amendments

relating to the sequence listing shall be submitted in writing and in machine-readable form.

46. Any correction of the printed version of the sequence listing which is submitted under PCT Rules 13ter 1(a)(i) or 26.3, any rectification of an obvious error in the printed version which is submitted, based on PCT Rule 91, or any addition which was integrated into the printed version of the sequence listing under PCT Article 34, shall additionally be submitted in an enhanced version of the sequence listing in a machine-readable form including any such additions.

47. Numeric identifiers

Only numeric identifiers as defined below may be used in sequence listings submitted in applications. The text of the data element headings given below shall not be included in the sequence listings. Numeric identifiers of mandatory data elements, that is, data elements which must be included in all sequence listings (see paragraph 24 of this Standard: items 110, 120, 160, 210, 211, 212, 213 and 400) and numeric identifiers of data elements which must be included in circumstances specified in this Standard (see paragraphs 25, 26, 27, 28 and 29 of this Standard: items 130, 140, 141, 150 and 151, and 220 to 223) are marked by the symbol “M”. Numeric identifiers of optional data elements (see paragraph 30 of this Standard) are marked by the symbol “O”.

Admissible Numeric Identifiers			
Numeric Identifier	Numeric Identifier Description	Mandatory (M) or Optional (O)	Comment
<110>	Applicant name	M	where the name of the applicant is written in characters other than those of the Latin alphabet, the same shall also be indicated in characters of the Latin alphabet either as a mere transliteration or through translation into English
<120>	Title of invention	M	
<130>	Reference number	M, In the circumstances specified in paragraph 25 of this Standard	see paragraph 25 of this Standard
<140>	Current patent application	M, In the circumstances	see paragraph 26 of this Standard; the current patent application shall be identified, in the following order, by the two-letter

		specified in paragraph 26 of this Standard	code indicated in accordance with WIPO Standard ST.3 and the application number (in the format used by the industrial property Office with which the current patent application is filed) or, for an international application, by the international application number
<141>	Current filing date	M, In the circumstances specified in paragraph 26 of this Standard	see paragraph 26 of this Standard; the date shall be indicated in accordance with WIPO Standard ST.2 (CCYY MM DD)
<150>	Earlier patent application	M, In the circumstances specified in paragraph 27 of this Standard	see paragraph 27 of this Standard; the earlier patent application shall be identified, in the following order, by the two-letter code indicated in accordance with WIPO Standard ST.3 and the application number (in the format used by the industrial property Office with which the earlier patent application was filed) or, for an international application, by the international application number
<151>	Earlier application filing date	M, In the circumstances specified in paragraph 27 of this Standard	see paragraph 27 of this Standard; the date shall be indicated in accordance with WIPO Standard ST.2 (CCYY MM DD)
<160>	Number of SEQ ID NOs	M	
<170>	Software	O	
<210>	Information for SEQ ID NO: x	M	response shall be an integer representing the SEQ ID NO shown
<211>	Length	M	sequence length expressed in number of bases or amino acids
<212>	Type	M	type of molecule sequenced in SEQ ID NO: x, either DNA, RNA or PRT; if a nucleotide sequence contains both DNA and RNA fragments, the value shall be “DNA”; in addition, the combined DNA/RNA molecule shall be further described in the

			<220> to <223> feature section
<213>	Organism	M	Genus Species (that is, scientific name) or “Artificial Sequence” or “Unknown”
<220>	Feature	M, In the circumstances specified in paragraphs 28 and 29 of this Standard	leave blank; see paragraphs 28 and 29 of this Standard; description of points of biological significance in the sequence in SEQ ID NO: x (may be repeated depending on the number of features indicated)
<221>	Name/key	M, In the circumstances specified in paragraph 28 of this Standard	see paragraph 28 of this Standard; only those keys as described in table 5 or 6 of paragraph 48 shall be used
<222>	Location	M, In the circumstances specified in paragraph 28 of this Standard	see paragraph 28 of this Standard; - from (number of first base/amino acid in the feature) - to (number of last base/amino acid in the feature) - bases (numbers refer to positions of bases in a nucleotide sequence) - amino acids (numbers refer to positions of amino acid residues in an amino acid sequence) - whether feature is located on the complementary strand to that filed in the sequence listing
<223>	Other information	M, In the circumstances specified in paragraphs 28 and 29 of this Standard	see paragraphs 28 and 29 of this Standard; any other relevant information, using language neutral vocabulary, or free text (in German or English); any free text is to be repeated in the main part of the description in the language thereof (see paragraph 35 of this Standard); where any modified base or modified/unusual L-amino acid appearing in paragraph 48, tables 2 and 4, is in the sequence, the symbol associated with that base or amino acid from paragraph 48, tables 2 and 4, should be used
<300>	Publication information	O	leave blank; repeat section for each relevant publication
<301>	Authors	O	

<302>	Title	O	title of publication
<303>	Journal	O	journal name in which data published
<304>	Volume	O	journal volume in which data published
<305>	Issue	O	journal issue number in which data published
<306>	Pages	O	journal page numbers on which data published
<307>	Date	O	journal date on which data published; if possible, the date shall be indicated in accordance with WIPO Standard ST.2 (CCYY MM DD)
<308>	Database accession number	O	accession number assigned by database including database name
<309>	Database entry date	O	date of entry in database; the date shall be indicated in accordance with WIPO Standard ST.2 (CCYY MM DD)
<310>	Document number	O	document number, for patent type citations only; the full document shall specify, in the following order, the two-letter code indicated in accordance with WIPO Standard ST.3, the publication number indicated in accordance with WIPO Standard ST.6, and the kind-of-document code indicated in accordance with WIPO Standard ST.16
<311>	Filing date	O	document filing date, for patent-type citations only; the date shall be indicated in accordance with WIPO Standard ST.2 (CCYY MM DD)
<312>	Publication date	O	document publication date; for patent-type citations only; the date shall be indicated in accordance with WIPO Standard ST.2 (CCYY MM DD)
<313>	Relevant residues in SEQ ID NO: x: from to	O	
<400>	Sequence	M	SEQ ID NO: x should follow the numeric identifier and should appear on the line preceding the sequence (see example)

48. Nucleotide and amino acid symbols and feature table

Table 1 List of Nucleotides		
Symbol	Meaning	Origin of Designation
a	a	adenine

g	g	guanine
c	c	cytosine
t	t	thymine
u	u	uracil
r	g or a	purine
y	t/u or c	pyrimidine
m	a or c	amino
k	g or t/u	keto
s	g or c	strong interactions, 3H-bonds
w	a or t/u	weak interactions, 2H-bonds
b	g or c or t/u	not a
d	a or g or t/u	not c
h	a or c or t/u	not g
v	a or g or c	not t, not u
n	a or g or c or t/u, unknown, or other	any

Table 2
List of Modified Nucleotides

Symbol	Meaning
ac4c	4-acetylcytidine
chm5u	5-(carboxyhydroxymethyl)uridine
cm	2’-O-methylcytidine
cmnm5s2u	5-carboxymethylaminomethyl-2-thiouridine
cmnm5u	5-carboxymethylaminomethyluridine
d	dihydrouridine
Fm	2’-O-methylpseudouridine
Gal q	beta,D-galactosylqueuosine
Gm	2’-O-methylguanosine
I	inosine
i6a	N6-isopentenyladenosine
m1a	1-methyladenosine
m1f	1-methylpseudouridine
m1g	1-methylguanosine
m1i	1-methylinosine
m22g	2,2-dimethylguanosine
m2a	2-methyladenosine
m2g	2-methylguanosine
m3c	3-methylcytidine
m5c	5-methylcytidine
m6a	N6-methyladenosine
m7g	7-methylguanosine
Mam5u	5-methylaminomethyluridine
Mam5s2u	5-methoxyaminomethyl-2-thiouridine
Man q	beta,D-mannosylqueuosine
Mcm5s2u	5-methoxycarbonylmethyl-2-thiouridine
Mcm5u	5-methoxycarbonylmethyluridine
Mo5u	5-methoxyuridine
Ms2i6a	2-methylthio-N6-isopentenyladenosine
Ms2t6a	N-((9-beta-D-ribofuranosyl-2-methylthiopurine-6-yl)carbamoyl)threonine
Mt6a	N-((9-beta-D-ribofuranosylpurine-6-yl)N-methylcarbamoyl)threonine

Mv	uridine-5-oxyacetic acid-methylester
o5u	uridine-5-oxyacetic acid(v)
Osyw	wybutoxosine
P	pseudouridine
Q	queuosine
s2c	2-thiocytidine
s2t	5-methyl-2-thiouridine
s2u	2-thiouridine
s4u	4-thiouridine
T	5-methyluridine
t6a	N-((9-beta-D-ribofuranosylpurine-6-yl)carbamoyl)threonine
Tm	2’-O-methyl-5-methyluridine
Um	2’-O-methyluridine
Yw	wybutosine
X	3-(3-amino-3-carboxy-propyl)uridine,(acp3)u

Table 3
List of Amino Acids

Symbol	Meaning
Ala	Alanine
Cys	Cysteine
Asp	Aspartic Acid
Glu	Glutamic Acid
Phe	Phenylalanine
Gly	Glycine
His	Histidine
Ile	Isoleucine
Lys	Lysine
Leu	Leucine
Met	Methionine
Asn	Asparagine
Pro	Proline
Gln	Glutamine
Arg	Arginine
Ser	Serine
Thr	Threonine
Val	Valine
Trp	Tryptophan
Tyr	Tyrosine
Asx	Asp or Asn
Glx	Glu or Gln
Xaa	unknown or other

Table 4
List of Modified and Unusual Amino Acids

Symbol	Meaning
Aad	2-Aminoadipic acid
BAad	3-Aminoadipic acid
BAla	beta-Alanine, beta-Aminopropionic acid
Abu	2-Aminobutyric acid
4Abu	4-Aminobutyric acid, piperidinic acid
Acp	6-Aminocaproic acid
Ahe	2-Aminoheptanoic acid

Aib	2-Aminoisobutyric acid
BAib	3-Aminoisobutyric acid
Apm	2-Aminopimelic acid
Dbu	2,4 Diaminobutyric acid
Des	Desmosine
Dpm	2,2′-Diaminopimelic acid
Dpr	2,3-Diaminopropionic acid
EtGly	N-Ethylglycine
EtAsn	N-Ethylasparagine
Hyl	Hydroxylysine
AHyl	allo-Hydroxylysine
3Hyp	3-Hydroxyproline
4Hyp	4-Hydroxyproline
Ide	Isodesmosine
AIle	allo-Isoleucine
MeGly	N-Methylglycine, sarcosine
MeIle	N-Methylisoleucine
MeLys	6-N-Methyllysine
MeVal	N-Methylvaline
Nva	Norvaline
Nle	Norleucine
Orn	Ornithine

Table 5
List of Feature Keys Related to Nucleotide Sequences

Key	Description
Allele	a related individual or strain contains stable, alternative forms of the same gene which differs from the presented sequence at this location (and perhaps others)
Attenuator	(1) region of DNA at which regulation of termination of transcription occurs, which controls the expression of some bacterial operons; (2) sequence segment located between the promoter and the first structural gene that causes partial termination of transcription
C_region	constant region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; includes one or more exons depending on the particular chain
CAAT_signal	CAAT box; part of a conserved sequence located about 75 bp up-stream of the start point of eukaryotic transcription units which may be involved in RNA polymerase binding; consensus=GG (C or T) CAATCT
CDS	coding sequence; sequence of nucleotides that corresponds with the sequence of amino acids in a protein (location includes stop codon); feature includes amino acid conceptual translation
conflict	independent determinations of the “same” sequence differ at this site or region
D-loop	displacement loop; a region within mitochondrial DNA in which a short stretch of RNA is paired with one strand of DNA, displacing the original partner DNA strand in this region; also used to describe the displacement of

	a region of duplex DNA by a single stranded nucleic acid in the reaction catalyzed by RecA protein
D-segment	diversity segment of immunoglobulin heavy chain, and T-cell receptor beta chain
enhancer	a cis-acting sequence that increases the utilization of (some) eukaryotic promoters, and can function in either orientation and in any location (upstream or downstream) relative to the promoter
exon	region of genome that codes for portion of spliced mRNA; may contain 5'UTR, all CDSs, and 3'UTR
GC_signal	GC box; a conserved GC-rich region located upstream of the start point of eukaryotic transcription units which may occur in multiple copies or in either orientation; consensus=GGGCGG
gene	region of biological interest, coding nucleic acid
iDNA	intervening DNA; DNA which is eliminated through any of several kinds of recombination
intron	a segment of DNA that is transcribed, but removed from within the transcript by splicing together the sequences (exons) on either side of it
J_segment	joining segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains
LTR	long, directly repeating sequence at both ends of a defined sequence, of the sort typically found in retroviruses
mat_peptide	mature peptide or protein coding sequence; coding sequence for the mature or final peptide or protein product following post-translational modification; the location does not include the stop codon (unlike the corresponding CDS)
misc_binding	site in nucleic acid which covalently or non-covalently binds another moiety that cannot be described by any other Binding key (primer_bind or protein_bind)
misc_difference	feature sequence is different from that presented in the entry and cannot be described by any other Difference key (conflict, unsure, old_sequence, mutation, variation, allele, or modified_base)
misc_feature	region of biological interest which cannot be described by any other feature key; a new or rare feature
misc_recomb	site of any generalized, site-specific or replicative recombination event where there is a breakage and reunion of duplex DNA that cannot be described by other recombination keys (iDNA and virion) or qualifiers of source key (/insertion_seq, /transposon, /proviral)
misc_RNA	any transcript or RNA product that cannot be defined by other RNA keys (prim_transcript, precursor_RNA, mRNA, 5'clip, 3'clip, 5'UTR, 3'UTR, exon, CDS, sig_peptide, transit_peptide, mat_peptide, intron, polyA_site, rRNA, tRNA, scRNA, and snRNA)
misc_signal	any region containing a signal controlling or altering gene function or expression that cannot be described by other Signal keys (promoter, CAAT_signal, TATA_signal, -35_signal, -10_signal, GC_signal, RBS, polyA_signal, enhancer, attenuator, terminator, and

	rep_origin)
misc_structure	any secondary or tertiary structure or conformation that cannot be described by other Structure keys (stem_loop and D-loop)
modified_base	the indicated nucleotide is a modified nucleotide and should be substituted for by the indicated molecule (given in the mod_base qualifier value)
mRNA	messenger RNA; includes 5′ untranslated region (5′UTR), coding sequences (CDS, exon) and 3′ untranslated region (3′UTR)
mutation	a related strain has an abrupt, inheritable change in the sequence at this location
N_region	extra nucleotides inserted between rearranged immunoglobulin segments
old_sequence	the presented sequence revises a previous version of the sequence at this location
polyA_signal	recognition region necessary for endonuclease cleavage of an RNA transcript that is followed by polyadenylation; consensus=AATAAA
polyA_site	site on an RNA transcript to which will be added adenine residues by post-transcriptional polyadenylation
precursor_RNA	any RNA species that is not yet the mature RNA product; may include 5′ clipped region (5′clip), 5′ untranslated region (5′UTR), coding sequences (CDS, exon), intervening sequences (intron), 3′ untranslated region (3′UTR), and 3′ clipped region (3′clip)
prim_transcript	primary (initial, unprocessed) transcript; includes 5′ clipped region (5′clip), 5′ untranslated region (5′UTR), coding sequences (CDS, exon), intervening sequences (intron), 3′ untranslated region (3′UTR), and 3′ clipped region (3′clip)
primer_bind	non-covalent primer binding site for initiation of replication, transcription, or reverse transcription; includes site(s) for synthetic, for example, PCR primer elements
promoter	region on a DNA molecule involved in RNA polymerase binding to initiate transcription
protein_bind	non-covalent protein binding site on nucleic acid
RBS	ribosome binding site
repeat_region	region of genome containing repeating units
repeat_unit	single repeat element
rep_origin	origin of replication; starting site for duplication of nucleic acid to give two identical copies
rRNA	mature ribosomal RNA; the RNA component of the ribonucleoprotein particle (ribosome) which assembles amino acids into proteins
S_region	switch region of immunoglobulin heavy chains; involved in the rearrangement of heavy chain DNA leading to the expression of a different immunoglobulin class from the same B-cell
satellite	many tandem repeats (identical or related) of a short basic repeating unit; many have a base composition or other property different from the genome average that allows them to be separated from the bulk (main band) genomic DNA

scRNA	small cytoplasmic RNA; any one of several small cytoplasmic RNA molecules present in the cytoplasm and (sometimes) nucleus of a eukaryote
sig_peptide	signal peptide coding sequence; coding sequence for an N-terminal domain of a secreted protein; this domain is involved in attaching nascent polypeptide to the membrane; leader sequence
snRNA	small nuclear RNA; any one of many small RNA species confined to the nucleus; several of the snRNAs are involved in splicing or other RNA processing reactions
source	identifies the biological source of the specified span of the sequence; this key is mandatory; every entry will have, as a minimum, a single source key spanning the entire sequence; more than one source key per sequence is permissible
stem_loop	hairpin; a double-helical region formed by base-pairing between adjacent (inverted) complementary sequences in a single strand of RNA or DNA
STS	Sequence Tagged Site; short, single-copy DNA sequence that characterizes a mapping landmark on the genome and can be detected by PCR; a region of the genome can be mapped by determining the order of a series of STSs
TATA_signal	TATA box; Goldberg-Hogness box; a conserved AT-rich septamer found about 25 bp before the start point of each eukaryotic RNA polymerase II transcript unit which may be involved in positioning the enzyme for correct initiation; consensus = TATA (A or T) A (A or T)
terminator	sequence of DNA located either at the end of the transcript or adjacent to a promoter region that causes RNA polymerase to terminate transcription; may also be site of binding of repressor protein
transit_peptide	transit peptide coding sequence; coding sequence for an N-terminal domain of a nuclear-encoded organellar protein; this domain is involved in post-translational import of the protein into the organelle
tRNA	mature transfer RNA, a small RNA molecule (75 - 85 bases long) that mediates the translation of a nucleic acid sequence into an amino acid sequence
unsure	author is unsure of exact sequence in this region
V_region	variable region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for the variable amino terminal portion; can be made up from V_segments, D_segments, N_regions, and J_segments
V_segment	variable segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for most of the variable region (V_region) and the last few amino acids of the leader peptide
variation	a related strain contains stable mutations from the same gene (for example, RFLPs, polymorphisms, etc.) which differ from the presented sequence at this location (and possibly others)
3'clip	3'-most region of a precursor transcript that is clipped off during processing
3'UTR	region at the 3' end of a mature transcript (following

	the stop codon) that is not translated into a protein
5’clip	5’-most region of a precursor transcript that is clipped off during processing
5’UTR	region at the 5’ end of a mature transcript (preceding the initiation codon) that is not translated into a protein
-10_signal	pribnow box; a conserved region about 10 bp upstream of the start point of bacterial transcription units which may be involved in binding RNA polymerase; consensus = TAtAaT
-35_signal	a conserved hexamer about 35 bp upstream of the start point of bacterial transcription units; consensus = TTGACa or TGTTGACA

Table 6
List of Feature Keys Related to Protein Sequences

Key	Description
CONFLICT	different papers report differing sequences
VARIANT	authors report that sequence variants exist
VARSPLIC	description of sequence variants produced by alternative splicing
MUTAGEN	site which has been experimentally altered
MOD_RES	post-translational modification of a residue
ACETYLATION	N-terminal or other
AMIDATION	generally at the C-terminal of a mature active peptide
BLOCKED	undetermined N- or C-terminal blocking group
FORMYLATION	of the N-terminal methionine
GAMMA-CARBOXYGLUTAMIC ACID HYDROXYLATION	of asparagine, aspartic acid, proline or lysine
METHYLATION	generally of lysine or arginine
PHOSPHORYLATION	of serine, threonine, tyrosine, aspartic acid or histidine
PYRROLIDONE CARBOXYLIC ACID	N-terminal glutamate which has formed an internal cyclic lactam
SULFATATION	generally of tyrosine
LIPID	covalent binding of a lipidic moiety
MYRISTATE	myristate group attached through an amide bond to the N-terminal glycine residue of the mature form of a protein or to an internal lysine residue
PALMITATE	palmitate group attached through a thioether bond to a cysteine residue or through an ester bond to a serine or threonine residue
FARNESYL	farnesyl group attached through a thioether bond to a cysteine residue
GERANYL-GERANYL	geranyl-geranyl group attached through a thioether bond to a cysteine residue
GPI-ANCHOR	glycosyl-phosphatidylinositol (GPI) group linked to the alpha-carboxyl group of the C-terminal residue of the mature form of a protein
N-ACYL DIGLYCERIDE	N-terminal cysteine of the mature form of a prokaryotic lipoprotein with an amide-linked fatty acid and a glyceryl group to which two fatty acids are linked by ester linkages

DISULFID	disulfide bond; the ‘FROM’ and ‘TO’ endpoints represent the two residues which are linked by an intra-chain disulfide bond; if the ‘FROM’ and ‘TO’ endpoints are identical, the disulfide bond is an interchain one and the description field indicates the nature of the cross-link
THIOLEST	thiolester bond; the ‘FROM’ and ‘TO’ endpoints represent the two residues which are linked by the thiolester bond
THIOETH	thioether bond; the ‘FROM’ and ‘TO’ endpoints represent the two residues which are linked by the thioether bond
CARBOHYD	glycosylation site; the nature of the carbohydrate (if known) is given in the description field
METAL	binding site for a metal ion; the description field indicates the nature of the metal
BINDING	binding site for any chemical group (co-enzyme, prosthetic group, etc.); the chemical nature of the group is given in the description field
SIGNAL	extent of a signal sequence (prepeptide)
TRANSIT	extent of a transit peptide (mitochondrial, chloroplastic, or for a microbody)
PROPEP	extent of a propeptide
CHAIN	extent of a polypeptide chain in the mature protein
PEPTIDE	extent of a released active peptide
DOMAIN	extent of a domain of interest on the sequence; the nature of that domain is given in the description field
CA_BIND	extent of a calcium-binding region
DNA_BIND	extent of a DNA-binding region
NP_BIND	extent of a nucleotide phosphate binding region; the nature of the nucleotide phosphate is indicated in the description field
TRANSMEM	extent of a transmembrane region
ZN_FING	extent of a zinc finger region
SIMILAR	extent of a similarity with another protein sequence; precise information, relative to that sequence is given in the description field
REPEAT	extent of an internal sequence repetition
HELIX	secondary structure: Helices, for example, Alpha-helix, 3(10) helix, or Pi-helix
STRAND	secondary structure: Beta-strand, for example, Hydrogen bonded beta-strand, or Residue in an isolated beta-bridge
TURN	secondary structure Turns, for example, H-bonded turn (3-turn, 4-turn or 5-turn)
ACT_SITE	amino acid(s) involved in the activity of an enzyme
SITE	any other interesting site on the sequence
INIT_MET	the sequence is known to start with an initiator methionine
NON_TER	the residue at an extremity of the sequence is not the terminal residue; if applied to position 1, this signifies that the first position is not the N-terminus of the complete molecule; if applied to the last position, it signifies that this position is not the C-terminus of the complete molecule; there is no

	description field for this key
NON_CONS	non consecutive residues; indicates that two residues in a sequence are not consecutive and that there are a number of unsequenced residues between them
UNSURE	uncertainties in the sequence; used to describe region(s) of a sequence for which the authors are unsure about the sequence assignment

Example:

<110> Smith, John; Smithgene Inc.

<120> Example for a sequence listing

<130> 01 - 00001

<140> PCT/EP98 / 00001

<141> 1998-12-31

<150> US 08 / 999,999

<151> 1997-10-15

<160> 4

<170> PatentIn Version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

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<221> CDS

<222> (279) ... (389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

<400> 1

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tgatgtggca  attgctggca  gtgccacagg  cttttcagcc  aggcttaggg    tgggttccgc        180
cgcggcgcgg  cggcccctct  cgcgctcctc  tcgcgcctct  ctctcgctct    cctctcgctc        240
ggacctgatt  aggtgagcag  gaggaggggg  cagttagc    atg  gtt  tca  atg  ttc  agc  296
                                               Met  Val  Ser  Met  Phe  Ser
                                               1                  5
ttg  tct  ttc  aaa  tgg  cct  gga  ttt  tgt  ttg  ttt  gtt  tgt  ttg  ttc  caa  344
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Leu  Ser  Phe  Lys  Trp  Pro  Gly  Phe  Cys  Leu  Phe  Val  Cys  Leu  Phe  Gln
                  10                      15                      20
tgt  ccc  aaa  gtc  ctc  ccc  tgt  cac  tca  tca  ctg  cag  ccg  aat  ctt       389
Cys  Pro  Lys  Val  Leu  Pro  Cys  His  Ser  Ser  Leu  Gln  Pro  Asn  Leu
          25                      30                      35
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Annex 2 (resp. Sec. 12) Standards for the Filing of Drawings

A. Paper filing

1. The drawings shall be on sheets with the following minimum margins:
top 2.5 cm
left side 2.5 cm
right side 1.5 cm
bottom 1.0 cm
The area used for drawings may not exceed 26.2 cm x 17 cm; the area used for the drawing of the abstract may be 8.1 cm x 9.4 cm when presented in an upright position, or 17.4 cm x 4.5 cm when presented sideways.

2. Drawings shall be executed with sufficient contrast in durable, black, sufficiently dense and dark, uniformly thick and clearly delineated lines and strokes without colourings.

3. For illustrating the invention, in addition to views and sectional views, perspectives and exploded views may be used. Cross-sections shall be indicated by hatching which should not impede the clear reading of the reference signs and leading lines.

4. The scale of the drawings and the distinctness of their graphical execution shall be such that all details can be distinguished without difficulty, after electronic data capture (scanning), in a linear reduction in size to two-thirds. If, as an exception, the scale is given on a drawing, it shall be represented graphically.

5. The lines in the drawings shall be drawn with the aid of drafting instruments rather than freehand. The numbers and letters used in the drawings shall not be less than 0.32 cm of height. For the lettering of drawings, the Latin and, where customary, the Greek alphabets shall be used.

6. The same sheet of drawings may contain several figures. The different figures shall be arranged without wasting space while remaining clearly separated from one another, preferably in an upright position, and shall be numbered consecutively in Arabic numerals. Drawings concerning the state of the art are admissible if the understanding of the invention is thereby facilitated; however, they shall be clearly marked as “Stand der Technik” (state of the art). Where figures on two or more sheets form in effect a single complete figure, the figures on the several sheets shall be so arranged that the complete figure can be assembled without concealing any part of the partial figures. All elements of a figure shall be in the same scale, except where the use of different scales is indispensable for the clarity of the figure.

7. Reference signs not mentioned in the description and claims shall not

appear in the drawings, and vice versa. The same shall apply mutatis mutandis to the abstract and its drawing.

8. The drawings shall not contain text matter, except, when absolutely indispensable, a single word or words such as “water”, “steam”, “open”, “closed”, “section on AB”, and, in the case of electric circuits and block schematic or flow sheet diagrams, a few short catchwords indispensable for understanding.

B. Electronic filing

9. The following image file formats are admissible for the electronic filing of patent applications with the German Patent and Trade Mark Office:

Image File Format	Compression	Colour Depth	Description
TIFF	no compression or LZW or Fax group 4	1 bit/p or (black and white)	maximum size: A4 and resolution: 300*300 dpi corresponding to 2480*3508 pixels (width*height)
TIFF	no compression or LZW or Fax group 4	8 bit/p grayscale (256 shades of grey)	maximum size: A4 and resolution: 150*150 dpi corresponding to 1240*1754 pixels (width*height)
JPEG	individual compression	24 bit/p	maximum size: A4 and resolution: 150*150 dpi accepts shades of grey only
PDF	no compression	black and white admissible only	the following typefaces (fonts) are allowed: - Times (serif font, proportional) - Helvetica (without serifs, proportional) - Courier - Symbol (symbols) Colour graphics not admissible Use restrictions possible for PDF files at file level by means of cryptographic means (encryption, deactivation of printing options) are not admissible