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Datasheet for the decision of 22 January 2026

Case Number: T 0137/24 - 3.3.08

Application Number: 18728259.5

Publication Number: 3615667

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Language of the proceedings: EN

Title of invention:
Microorganisms and methods for producing cannabinoids and cannabinoid derivatives

Patent Proprietor:
The Regents of the University of California

Opponents:
Dr Schüssler, Andrea
J A Kemp LLP

Headword:
Cannabinoid-producing yeast cells/UC

Relevant legal provisions:
EPC Art. 54, 83, 123(2)

Keyword:
Novelty - (yes)
Sufficiency of disclosure - (yes)
Amendments - allowable (yes)

Decisions cited:
G 0003/14, T 2134/10

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Beschwerdekammern

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Case Number: T 0137/24 - 3.3.08

D E C I S I O N
of Technical Board of Appeal 3.3.08
of 22 January 2026

Appellant: (Opponent 2)	J A Kemp LLP 80 Turnmill Street London Greater London EC1M 5QU (GB)
Representative:	J A Kemp LLP 80 Turnmill Street London EC1M 5QU (GB)
Respondent: (Patent Proprietor)	The Regents of the University of California 1111 Franklin Street, 12th Floor Oakland, CA 94607 (US)
Representative:	Maiwald GmbH Grünstraße 25 40212 Düsseldorf (DE)
Party as of right: (Opponent 1)	Dr Schüssler, Andrea c/o Patent- und Rechtsanwälte Huber + Schüssler Truderinger Strasse 246 81825 München (DE)
Representative:	Schüssler, Andrea Kanzlei Huber & Schüssler Truderinger Strasse 246 81825 München (DE)
Decision under appeal:	**Decision of the Opposition Division of the European Patent Office posted on 27 November 2023 rejecting the opposition filed against European patent No. 3615667 pursuant to Article 101(2) EPC**

Composition of the Board:

Chairwoman	T. Sommerfeld
Members:	A. Schmitt
	A. Bacchin

Summary of Facts and Submissions

I. The appeal of opponent 2 (the appellant) is against the opposition division's decision to reject the opposition filed against European patent No. 3 615 667 (the patent). The patent was granted on the basis of European patent application No. 18 728 259.5, which had been filed as an international application published as WO 2018/200888 (the application) and claiming priority from US application No. 62/491,114 (priority document P1 filed on 27 April 2017) and US application No. 62/569,532 (priority document P2 filed on 7 October 2017, on file as D2).

II. Two oppositions were filed against the patent. The opposition proceedings were based on the grounds for opposition under Article 100(a) EPC in relation to novelty (Article 54 EPC) and inventive step (Article 56 EPC), as well as those under Article 100(b) and (c) EPC.

III. In the decision under appeal, the opposition division found that the none of the grounds of opposition prejudiced the maintenance of the patent. As regards Article 100(a) EPC, it found that the claims as granted were not entitled to priority from P1 but were entitled to priority from P2, and that the claimed subject-matter was novel over, *inter alia*, document D3 and involved an inventive step.

IV. With the statement of grounds of appeal the appellant filed six new documents (D33 to D38) and challenged the opposition division's decision on added matter, sufficiency of disclosure and validity of the claim to priority from P2. They also provided arguments

supporting their view that claims 1 to 3 and 6 to 15 of the patent as granted lacked novelty over the disclosure in document D3 and that the same applied to the claims of auxiliary requests 1 to 3 and 6 to 8 filed in the opposition proceedings. The appellant did not challenge the opposition division's decision on inventive step nor submit any comments on auxiliary request 4 filed during the opposition proceedings.

V. With the reply to the appeal, the patent proprietor (respondent) filed two documents (D39 and D40) and sets of claims of auxiliary requests 1 to 22. Auxiliary requests 1 to 17 are identical to auxiliary requests 1 to 17 filed in the opposition proceedings.

VI. The board summoned the parties to oral proceedings in accordance with their requests. In a communication under Article 15(1) RPBA, it expressed its preliminary opinion that the grounds in Article 100(b) and (c) EPC did not prejudice the maintenance of the patent as granted but that the subject-matter of claim 1 of each of the main request and auxiliary requests 1 to 3 was not novel over the disclosure in document D3. It further remarked that the appellant did not challenge the opposition division's decision on inventive step (Article 56 EPC) and did not raise any objections under Article 54 EPC against the claims of auxiliary request 4.

VII. Neither the appellant nor opponent 1 were represented at the oral proceedings, as previously indicated in writing. During the oral proceedings, the respondent withdrew the main request and auxiliary requests 1 to 3 and declared that auxiliary request 4 was the new main request.

VIII. Claims 1, 7 to 11, 14 and 15 of the main request read as follows:

"1. A genetically modified yeast cell for producing a cannabinoid or a cannabinoid derivative, the genetically modified yeast cell comprising one or more heterologous nucleic acids integrated into a chromosome of the genetically modified yeast cell and encoding a geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or SEQ ID NO: 100, wherein the one or more heterologous nucleic acids encoding the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises one to eight copies of the heterologous nucleic acids."

"7. The genetically modified yeast cell of any one of claims 1-6, wherein the genetically modified yeast cell comprises one or more heterologous nucleic acids encoding a cannabinoid synthase polypeptide, wherein the cannabinoid synthase polypeptide is a tetrahydrocannabinolic acid (THCA) synthase polypeptide or a cannabidiolic acid (CBDA) synthase polypeptide."

"8. The genetically modified yeast cell of claim 7, wherein the THCA synthase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:155 and the CBDA synthase polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:88 or SEQ ID NO:151."

"9. The genetically modified yeast cell of any one of claims 1-8, wherein the genetically modified yeast cell comprises one or more of the following:

a) one or more heterologous nucleic acids encoding a polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative, wherein the polypeptide that generates an acyl-CoA compound or an acyl-CoA compound derivative is an acyl-activating enzyme (AAE) polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:90, SEQ ID NO:92, or SEQ ID NO:149; a fatty acyl-CoA ligase polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:145 or SEQ ID NO:147; or a fatty acyl-CoA synthetase (FAA) polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:169, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, or SEQ ID NO:200;
b) one or more heterologous nucleic acids encoding [...];
c) one or more heterologous nucleic acids encoding [...];
d) one or more heterologous nucleic acids encoding [...];
e) one or more heterologous nucleic acids encoding [...];
f) one or more heterologous nucleic acids encoding [...];
g) one or more heterologous nucleic acids encoding [...];
h) one or more heterologous nucleic acids encoding [...];
i) one or more heterologous nucleic acids encoding [...]; or
j) one or more heterologous nucleic acids encoding [...]."

" 10. A method of producing a cannabinoid or a cannabinoid derivative, the method comprising:

a) culturing a genetically modified yeast cell comprising:
i) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified yeast cell and encoding a geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or SEQ ID NO:100, wherein the one or more heterologous nucleic acids encoding the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises one to eight copies of the heterologous nucleic acids; and
ii) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified yeast cell and encoding a tetraketide synthase (TKS) polypeptide comprising the amino acid sequence of SEQ ID NO:11; and/or
iii) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified yeast cell and encoding an olivetolic acid cyclase (OAC) polypeptide comprising the amino acid sequence of SEQ ID NO:10;
in a suitable medium containing a carboxylic acid; and
b) recovering the produced cannabinoid or cannabinoid derivative."

"11. The method of claim 10, wherein the TKS polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:11 and the OAC polypeptide comprises an amino acid sequence having at least 85% sequence identity to SEQ ID NO:10."

"14. A method of producing a cannabinoid or cannabinoid derivative, the method comprising:
a) culturing a genetically modified yeast cell comprising:

i) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified yeast cell and encoding a geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or SEQ ID NO:100, wherein the one or more heterologous nucleic acids encoding the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises one to eight copies of the heterologous nucleic acids;
ii) one or more heterologous nucleic acids integrated into a chromosome of the genetically modified yeast cell and encoding a tetraketide synthase (TKS) polypeptide comprising an amino acid sequence having at least 85% sequence identity to SEQ ID NO:11;
iii) [...];
iv) [...];
v) [...]; and
vi) [...];
in a suitable medium; and
b) recovering the produced cannabinoid or cannabinoid derivative, wherein, optionally, [...]."

"15. A method of producing a cannabinoid or a cannabinoid derivative, the method comprising use of a genetically modified yeast cell comprising a heterologous nucleic acid integrated into a chromosome of the genetically modified yeast cell and encoding a geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 90% sequence identity to SEQ ID NO:110 or SEQ ID NO:100, wherein the one or more heterologous nucleic acids encoding the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises one to eight copies of the heterologous nucleic acids."

IX. The following documents are referred to in this decision:

D3 WO 2019/071000 A1
D4 US application No. 62/568,355

X. The arguments of the parties relevant to the board's decision are referred to, where necessary, in the Reasons for the Decision.

XI. The parties' requests relevant for the decision are as follows.

The appellant requests that the decision under appeal be set aside and that the patent be revoked.

The respondent requests that the appeal be dismissed and the patent be maintained in amended form on the basis of the set of claims of the main request, filed with the reply to the statement of grounds of appeal as auxiliary request 4.

Opponent 1 did not formulate any requests.

Reasons for the Decision

Appellant not represented at the oral proceedings

1. As announced previously, the appellant was not represented at the oral proceedings (see section VII. above). In accordance with Rule 115(2) EPC and Article 15(3) RPBA, the oral proceedings were continued in the absence of the duly summoned appellant, who was considered to be relying only on their written case.

Main request
Amendments (Article 123(2) EPC)

2. The appellant did not submit any comments under Article 123(2) EPC on former auxiliary request 4, i.e. the current main request (see section IV. above). However, the objections raised on added matter against the claims of the patent as granted are also relevant to the claims of the current main request. These differ from the claims of the patent as granted in that:
(i) the independent claims 1, 10, 14 and 15 comprise the additional feature "*wherein the one or more heterologous nucleic acids encoding the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprises one to eight copies of the heterologous nucleic acids*", and
(ii) the sequence identity to SEQ ID NO:110 or SEQ ID NO:100 is at least 90% instead of at least 85% (see section VIII. for the full wording of claims 1, 10, 14 and 15 of the main request).

Claims 1 to 9

3. Claim 1 of the main request is based on claims 2 and 3 of the application as filed.

4. Claim 2 of the application relates to "[a] *genetically modified host cell for producing a cannabinoid or a cannabinoid derivative, the genetically modified host cell comprising one or more heterologous nucleic acids encoding a geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide comprising an amino acid sequence having at least 65% sequence identity to SEQ ID NO:110*". Claim 3 of the application has the same wording as claim 2 except for the sequence

identification number (SEQ ID NO), which is "*SEQ ID NO:100*".

5. Compared to this disclosure in claims 2 and 3 of the application, claim 1 of the main request contains the four additional features that:
(i) the genetically modified host cell is yeast,
(ii) the geranyl pyrophosphate:olivetolic acid geranyltransferase polypeptide (GOT) polypeptide-encoding nucleic acid is integrated into a chromosome,
(iii) the GOT polypeptide comprises an amino acid sequence having at least 90% (instead of at least 65%) sequence identity to sequence SEQ ID NO:110 or SEQ ID NO:100, and
(iv) the one or more heterologous nucleic acids encoding the GOT polypeptide comprises one to eight copies of the heterologous nucleic acids.

6. The appellant asserted that the combination of features (i), (ii) and (iii) as defined in point 5. above was not disclosed in the application. Instead, each of these features was selected from a list of independent alternatives.

7. The board disagrees. Feature (i) as defined in point 5. above has a basis in claims 39 and 40 of the application. Claim 39 of the application is dependent on any of claims 1 to 38 and defines that "*the genetically modified host cell is a eukaryotic cell*"; claim 40 is dependent on claim 39 and defines that "*the eukaryotic cell is a yeast cell*". Claim 40 of the application therefore singles out the embodiment that the genetically modified host cell as defined in, *inter alia*, claims 2 and 3 of the application is yeast. The same teaching is present in paragraphs [0009], [0010] and [0016] of the application. Therefore, contrary to

the appellant's view, this feature is directly disclosed in the application in combination with the disclosure in claims 2 and 3 of the application and hence was not selected from a list of alternatives.

8. Feature (ii) as defined in point 5. above has an explicit basis in claim 45 of the application by virtue of its dependency of any of claims 1 to 44. Claim 45 teaches that "*at least one or more heterologous nucleic acids is integrated into the chromosome of the genetically modified host*". Since claim 45 is dependent on claim 40, it encompasses the chromosomal integration of a GOT nucleic acid molecule having the amino acid sequence as defined in claims 2 and 3 of the application into a yeast host cell (see point 7. above) and therefore provides a formal basis for the claim comprising features (i) and (ii) as defined in point 5. above, without requiring any selections from lists of features, as asserted by the appellant. The same teaching is present in paragraphs [0016] and [0018] of the application in conjunction with paragraphs [0009] and [0010].

9. The fact that claims 1 to 44 of the application, on which claim 45 depends, disclose further options for heterologous nucleic acids in addition to those disclosed in independent claims 2 and 3, is irrelevant since the combination of claims 2, 3, 39, 40 and 45 of the application, by virtue of their respective dependencies as explained above, directly and unambiguously discloses the claimed subject-matter with respect to features (i) and (ii) as defined in point 5. above. Additionally, as pointed out by the respondent, yeast is used as the host cell in all examples of the application, and the chromosomal integration of a GOT nucleic acid into a yeast host cell is also taught in,

for example, paragraph [948] of Example 3, which also points to this feature combination.

10. Claim 1 of the main request further differs from the disclosure in claims 2, 3, 39, 40 and 45 in that the percentage of the amino acid sequence identity of the sequences recited in the claim is amended from at least 65% to at least 90% (feature (iii) as defined in point 5. above). This feature is disclosed in several paragraphs of the application as filed in a list of increasing amino acid sequence identities to SEQ ID NO:100 or SEQ ID NO:110, starting from at least 65% to at least 99.9% and ending with 100% (e.g. paragraph [00228] of the application). Selecting an amino acid sequence identity from such a list that is higher than the amino acid identity recited in the claims of the application does not constitute a selection from a list of independent alternatives, as asserted by the appellant.

11. Instead, lists of increasing amino acid sequence identities to a given amino acid sequence - here SEQ ID NO:100 or SEQ ID NO:110 - are convergent lists of preferred options from the lowest amino acid sequence identity to the given amino acid sequence (least preferred) to the highest amino acid sequence identity (most preferred). In addition to the identity with the most preferred amino acid sequence, the polypeptide recited in the claim is functionally defined in the claim by its enzymatic activity (a GOT polypeptide). This means that the increase of the amino acid sequence identity to SEQ ID NO:100 or SEQ ID NO:110 from 65% to 90%, as recited in the claim, merely narrows down the GOT polypeptides falling within the definition in the claim, without singling out

specific polypeptides or conferring any new properties to these polypeptides.

12. In line with the considerations set out in decision T 2134/10, second paragraph of point 11 of the Reasons, the selection of a degree of sequence identity with a given (most preferred) amino acid sequence from a convergent list for a functionally defined polypeptide does not single out a particular molecule or confer properties to this molecule that are not disclosed in the application as filed. Feature (iii) as defined in point 3. above therefore has a basis in, for example, paragraph [00228] of the application as filed.

13. As a basis for feature (iv) as defined in point 5. above, the respondent referred to paragraph [00251] of the application. The appellant did not object to this feature having a basis in the application. Since paragraph [00251] of the application discloses that the genetically modified host cell has one, two, three, four, five, six, seven or eight copies of a GOT-encoding heterologous nucleic acid and therefore discloses feature (iv) inserted into claim 1 of the main request, the board has no objection under Article 123(2) EPC to this feature, either.

14. With respect to dependent claims 8 and 9 of the patent as granted (see section VIII. above for the wording of the claims in the current main request), the appellant additionally pointed to the fact that in these claims, not only the sequence identity of the GOT polypeptide but also the sequence identities of further polypeptides had been amended. Each of the sequence identities recited in the claim had been selected from a list of alternatives disclosed individually in the application, a fact that resulted in a combination of

features that was not disclosed in the application as filed.

15. However, as discussed above (see points 10. to 12.), to narrow down the number of functionally defined polypeptides falling within a given definition by selecting a higher sequence identity to a given, most preferred, amino acid sequence is neither a selection from a list of independent alternatives nor confers any undisclosed properties to these polypeptides. The combination of the amended amino acid sequence identities of each of the functionally defined polypeptides recited in claims 8 and 9 therefore does not result in new subject-matter which was not disclosed in the application.

16. Independent claim 1 and its dependent claims 2 to 9 do not contain subject-matter that extends beyond the content of the application as filed (Article 123(2) EPC).

Claims 10 to 15

17. The appellant raised the same argument against claims 10, 11, 14 and 15 of the patent as granted as they had against claims 8 and 9, namely that the amendments of the amino acid sequence identities for each of the multiple polypeptides recited in these claims was the result of multiple selections from multiple lists which resulted in a new combination of features not disclosed in the application as filed. However, for the same reasons as explained above for claims 8 and 9 (see point 15.), this argument cannot be accepted when, as is the case also in claims 10, 11, 14 and 15 of the current main request, functionally defined polypeptides falling within a given definition

are narrowed down by selecting a higher sequence identity to a given, most preferred, polypeptide sequence.

18. The appellant additionally pointed out that claim 11 of the patent as granted "*despite being dependent on claim 10, confusingly seeks to broaden out the sequence identities to encompass sequences with at least 85% identity to SEQ ID NOs 11 and 10*" (section 5.13 of the statement of grounds of appeal). The board considers that claim 11 is indeed unclear due to this inconsistency between claims 10 and 11. However, this is not an issue of added matter but rather of lack of clarity. Since this inconsistency was present in the claims as granted, it cannot be objected to under Article 84 EPC in opposition (G 3/14, Order).

19. Claims 10 to 15 do not contain subject-matter that extends beyond the content of the application as filed (Article 123(2) EPC).

Priority

20. The application claims priority from US applications P1 and P2 (see section I. above). It was uncontested that the application's claim to priority from P1 was not valid. The appellant asserted that the application's claim to priority from P2 was not valid, either.

21. Document D3, cited by the appellant as relevant prior art under Article 54(3) EPC, claims priority from, *inter alia*, document D4 filed on 5 October 2017. Since document D3's claim to priority from document D4 was not contested and is therefore deemed to be valid, the effective filing date of document D3 is 5 October 2017, which is earlier than the filing date of P2

(7 October 2017). Therefore, document D3 is prior art under Article 54(3) EPC for the claimed subject-matter, irrespective of whether the claim to priority from P2 is valid. As no other prior art under Article 54(3) EPC was cited on appeal, the validity of the application's claim to priority from P2 is irrelevant for the present decision and can be left undecided.

Novelty (Article 54(3) EPC) - claim 1
Document D3

22. As uncontested, document D3 is comprised within the state of the art under Article 54(3) EPC (see also point 21. above).

23. The appellant asserted that the subject-matter of, *inter alia*, claim 1 of the patent as granted lacked novelty over the disclosure in document D3 (see section IV. above). However, the appellant did not raise any objections under Article 54 EPC against auxiliary request 4 filed in the opposition proceedings, i.e. against the current main request (see sections IV. and VI. above and point 36 of the board's communication under Article 15(1) RPBA, to which the appellant did not react).

24. Claim 1 of the current main request differs from claim 1 of the patent as granted, *inter alia*, in the feature that the one or more heterologous nucleic acids encoding the GOT polypeptide comprises one to eight copies of the heterologous nucleic acids (see point 2. above).

25. Document D3 discloses, in claims 1, 2, 10 and 25, a genetically modified yeast cell capable of making a cannabinoid comprising a polynucleotide that is at

least 60% identical to SEQ ID NO:2 and that encodes an amino acid sequence that is at least 60% identical to SEQ ID NO:1. SEQ ID NO:2 of document D3 is 100% identical over its entire length to SEQ ID NO:110 of the patent. Document D3 also discloses that the nucleic acid sequence encoding an enzyme including PT "*can be inserted into the genome of the cell/microorganism used*" and that, in some cases, "*the isolated nucleic acid is inserted into the genome at a specific locus, where the isolated nucleic acid can be expressed in sufficient amounts*" (paragraph [000128] of D3).

26. However, document D3 is silent on the number of GOT copies integrated into the yeast chromosome and therefore does not directly and unambiguously teach that the one or more GOT-encoding nucleic acid integrated into a chromosome of the genetically modified yeast cell comprises one to eight copies. In view of this, the board has no objections against the claims of the current main request under Article 54 EPC.

Sufficiency of disclosure (Article 83 EPC)

27. The appellant asserted that the claims of the patent as granted encompassed non-working embodiments because many polypeptide sequences falling under the definition in the claim did not have any enzymatic activity, as evident from Example 5 of the patent in which a number of truncated polypeptides had been tested unsuccessfully. A research project was hence required to test and identify functional polypeptides. Since the patent did not provide any guidance on how the sequences could be changed without losing enzymatic activity, it was an undue burden to find functional polypeptides.

28. However, firstly, since the claims require that the genetically modified yeast cells be suitable for producing a cannabinoid or a cannabinoid derivative and the recited polypeptides are also functionally defined by reference to their enzymatic activity, polypeptides without this enzymatic activity do not fall under the scope of the claims.

29. Secondly, as pointed out in the decision under appeal (paragraph bridging pages 18 and 19), generating polypeptide variants as recited in the claims, such as polypeptides comprising an amino acid sequence that has at least 90% sequence identity to SEQ ID NO:110 or SEQ ID NO:100, and testing them for their enzymatic activity are disclosed in the patent (e.g. paragraphs [0222] to [0230]) and only require the use of techniques that are routine for the skilled person working in the technical field of recombinant enzyme variants. No evidence to the contrary was submitted by the appellant. The board thus concludes that the identification of polypeptide sequences falling under the definitions recited in the claims is not an undue burden for the skilled person.

30. The invention as defined in the claims of the main request is sufficiently disclosed in the patent (Article 83 EPC).

Article 56 EPC

31. In the decision under appeal, the opposition division was of the opinion that none of the appellant's objections raised in the opposition proceedings under Article 56 EPC was persuasive. Since the appellant did not challenge the opposition division's decision with

respect to Article 56 EPC on appeal (section IV. above), the board concludes that the current main request meets the requirements of Article 56 EPC.

Admittance of documents D33 to D40 (Article 12 RPBA)

32. Document D33 to D40 were filed on appeal by the appellant (section IV. above) or the respondent (section V. above), to support an argument with respect to novelty of the claims of the patent as granted over the disclosure in document D3. This argument was irrelevant for the assessment of novelty of the claims of the current main request over the teaching in document D3 because these claims differed from the disclosure in document D3 by an additional, uncontested feature (see points 23. to 26. above). It was therefore not necessary to decide on admittance of documents D33 to D40.

Order

For these reasons it is decided that:

1. The decision under appeal is set aside.

2. The case is remitted to the opposition division with the order to maintain the patent in amended form on the basis of the claims of the main request, filed as auxiliary request 4 with the reply to the statement of grounds of appeal, and a description and drawings to be adapted, if needed.

The Registrar: The Chairwoman:

C. Rodríguez Rodríguez T. Sommerfeld

Decision electronically authenticated