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Datasheet for the decision of 30 November 2023

Case Number: T 0168/19 - 3.3.08

Application Number: 08757278.0

Publication Number: 2158315

IPC: C12N15/09, A61K39/395, C12N15/13, C07K16/00

Language of the proceedings: EN

Title of invention:
Methods of modifying antibodies, and modified antibodies with improved functional properties

Patent Proprietor:
Novartis AG

Opponents:
O1: Strawman Limited
O2: F.Hoffmann-La Roche AG
O3: Vossius & Partner Patentanwälte Rechtsanwälte mbB

Headword:
Modified antibodies/NOVARTIS

Relevant legal provisions:
EPC Art. 56
RPBA Art. 12(4)
RPBA 2020 Art. 13(2), 12(8)

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It can be changed at any time and without notic

Keyword:
Late-filed arguments - admitted (no)
Inventive step - (no)
Late-filed auxiliary requests - request could have been filed in first instance proceedings (yes)

Decisions cited:

Catchword:
-

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Boards of Appeal

Chambres de recours

Boards of Appeal of the
European Patent Office
Richard-Reitzner-Allee 8
85540 Haar
GERMANY
Tel. +49 (0)89 2399-0
Fax +49 (0)89 2399-4465

Case Number: T 0168/19 - 3.3.08

D E C I S I O N
of Technical Board of Appeal 3.3.08
of 30 November 2023

Appellant: (Patent Proprietor)	Novartis AG Lichtstrasse 35 4056 Basel (CH)
Representative:	Grünecker Patent- und Rechtsanwälte PartG mbB Leopoldstraße 4 80802 München (DE)
Respondent I: (Opponent 1)	Strawman Limited Orchard Lea Horns Lane Combe, Witney Oxfordshire OX29 8NH (GB)
Representative:	Vossius & Partner Patentanwälte Rechtsanwälte mbB Siebertstrasse 3 81675 München (DE)
Respondent II: (Opponent 2)	F.Hoffmann-La Roche AG 124 Grenzacherstrasse 4070 Basel (CH)
Representative:	Mewburn Ellis LLP Aurora Building Counterslip Bristol BS1 6BX (GB)
Respondent III: (Opponent 3)	Vossius & Partner Patentanwälte Rechtsanwälte mbB Siebertstrasse 3 81675 München (DE)

Decision under appeal: **Decision of the Opposition Division of the European Patent Office posted on 6 November 2018 revoking European patent No. 2158315 pursuant to Article 101(3)(b) EPC**

Composition of the Board:

Chair T. Sommerfeld
Members: B. Claes
R. Winkelhofer

Summary of Facts and Submissions

I. The appeal lodged by the patent proprietor (appellant) lies from the decision of the opposition division revoking European patent No. 2158315 having the title "*Methods of modifying antibodies, and modified antibodies with improved functional properties*". The patent claims priority from *inter alia* US 60/937112 (US 937112 P), filed on 25 June 2007 (P1).

II. The opposition division decided that the set of claims of auxiliary request 1 met the requirements of Articles 54, 84 and 123(2) EPC, but that the claimed subject-matter lacked an inventive step. Auxiliary requests 2 to 21 were not admitted into the proceedings. The claimed subject-matter of auxiliary requests 22 to 41 was held to lack an inventive step.

III. With the statement of grounds of appeal, the appellant filed a set of claims of a new main request (identical to auxiliary request 1 in the decision under appeal) and five auxiliary requests. The appellant argued that the claimed subject-matter of the main request involved an inventive step.

Claim 1 of the main request reads as follows.

"1. A method of engineering an immunobinder with improved functional properties, the immunobinder comprising (i) a heavy chain variable region, or fragment thereof, of a VH3, VH1a or VH1b family, the heavy chain variable region comprising VH framework residues and/or (ii) a light chain variable region, or fragment thereof, of a Vκ1, Vκ3 or Vλ1 family, the

light chain variable region comprising V_L framework residues, the method comprising:

A) selecting one or more amino acid positions within the V_H framework residues, the V_L framework residues or the V_H and V_L framework residues for mutation;

B) mutating the one or more amino acid positions selected for mutation, and

C) screening the immunobinder for improved functional properties selected from solubility, stability, non-aggregation, expression and/or refolding yield,

a) wherein if the one or more heavy chain amino acid positions selected for mutation are of a human **VH3** family heavy chain variable region, the mutating comprises one or more substitutions selected from the group consisting of:

(iii) threonine (T) or alanine (A) at amino acid position 7 using AHo or Kabat numbering system;

(iv) valine (V) at amino acid position 89 using AHo numbering system (amino acid position 78 using Kabat numbering system); and

(v) arginine (R), glutamine (Q), leucine (L), methionine (M) or phenylalanine (F) at amino acid position 103 using AHo numbering system (amino acid position 89 using Kabat numbering);

b) wherein if the one or more heavy chain amino acid positions selected for mutation are of a human **VH1a** family heavy chain variable region, the mutating comprises one or more substitutions selected from the group consisting of:

(i) glutamic acid (E) at amino acid position 1 using AHo or Kabat numbering system;

(iv) methionine (M) at amino acid position 13 using AHo numbering system (amino acid position 12 using Kabat numbering system);

(v) glutamic acid (E) or glutamine (Q) at amino acid position 14 using AHo numbering system (amino acid position 13 using Kabat numbering system);

(ix) aspartic acid (D) or glutamine (Q) at amino acid position 92 using AHo numbering system (amino acid position 81 using Kabat numbering system);

(x) glycine (G), asparagine (N) or threonine (T) at amino acid position 95 using AHo numbering system (amino acid position 82b using Kabat numbering system); and

(xi) threonine (T), alanine (A), proline (P) or phenylalanine (F) at amino acid position 98 using AHo numbering (amino acid position 84 using Kabat numbering);

c) wherein if the one or more heavy chain amino acid positions selected for mutation are of a human **VH1b** family heavy chain variable region, the mutating comprises one or more substitutions selected from the group consisting of:

(i) glutamic acid (E) at amino acid position 1 using AHo or Kabat numbering system;

(ii) threonine (T), proline (P), valine (V) or aspartic acid (D) at amino acid position 10 using AHo numbering system (amino acid position 9 using Kabat numbering system);

(iv) valine (V), arginine (R), glutamine (Q) or methionine (M) at amino acid position 13 using AHo numbering system (amino acid position 12 using Kabat numbering system);

(v) glutamic acid (E), arginine (R) or methionine (M) at amino acid position 14 using AHo numbering system (amino acid position 13 using Kabat numbering system);

(vi) arginine (R), threonine (T), or asparagine (N) at amino acid position 20 using AHo numbering system

(amino acid position 19 using Kabat numbering system);

(vii) isoleucine (I), phenylalanine (F), or leucine (L) at amino acid position 21 using AHo numbering system (amino acid position 20 using Kabat numbering system);

(viii) lysine (K) at amino acid position 45 using AHo numbering system (amino acid position 38 using Kabat numbering system);

(ix) threonine (T), valine (V) or arginine (R) at amino acid position 47 using AHo numbering system (amino acid position 40 using Kabat numbering system);

(x) lysine (K), histidine (H) or glutamic acid (E) at amino acid position 50 using AHo numbering system (amino acid position 43 using Kabat numbering system);

(xii) lysine (K) at amino acid position 77 using AHo numbering (amino acid position 66 using Kabat numbering);

(xiv) glutamic acid (E), or threonine (T) at amino acid position 82 using AHo numbering system (amino acid position 71 using Kabat numbering system);

(xvi) aspartic acid (D) at amino acid position 87 using AHo numbering system (amino acid position 76 using Kabat numbering system); and

(xvii) asparagine (N) or serine (S) at amino acid position 107 using AHo numbering system (amino acid position 93 using Kabat numbering system);

d) wherein if the one or more light chain amino acid positions selected for mutation are of a human **Vκ1** family light chain variable region, the mutating comprises one or more substitutions selected from the group consisting of:

(i) glutamic acid (E) or isoleucine (I) at amino acid position 1 using AHo or Kabat numbering system;

(ii) valine (V) or isoleucine (I) at amino acid position 3 using AHo or Kabat numbering system;
(v) arginine (R) or isoleucine (I) at amino acid position 47 using AHo numbering system (amino acid position 39 using Kabat numbering system);
(vii) histidine (H), serine (S) or phenylalanine (F) at amino acid position 57 using AHo numbering system (amino acid position 49 using Kabat numbering system);
(viii) phenylalanine (F) at amino acid position 91 using AHo numbering system (amino acid position 73 using Kabat numbering system); and
(ix) valine (V), serine (S), glycine (G) or isoleucine (I) at amino acid position 103 using AHo numbering system (amino acid position 85 using Kabat numbering system);

e) wherein if the one or more light chain amino acid positions selected for mutation are of a human **Vκ3** family light chain variable region, the mutating comprises one or more substitutions selected from the group consisting of:
(i) threonine (T) at amino acid position 2 using AHo or Kabat numbering system;
(ii) threonine (T) at amino acid position 3 using AHo or Kabat numbering system;
(iii) isoleucine (I) at amino acid position 10 using AHo or Kabat numbering system;
(iv) tyrosine (Y) at amino acid position 12 using AHo or Kabat numbering system;
(v) serine (S) at amino acid position 18 using AHo or Kabat numbering system;
(vi) alanine (A) at amino acid position 20 using AHo or Kabat numbering system;
(vii) methionine (M) at amino acid position 56 using AHo numbering system (amino acid position 48 using Kabat numbering system);

(viii) valine (V) or threonine (T) at amino acid position 74 using AHo numbering system (amino acid position 58 using Kabat numbering system);

(ix) asparagine (N) at amino acid position 94 using AHo numbering system (amino acid position 76 using Kabat numbering system);

(x) tyrosine (Y) or serine (S) at amino acid position 101 using AHo numbering system (amino acid position 83 using Kabat numbering system); and

(xi) leucine (L) or alanine (A) at amino acid position 103 using AHo numbering (amino acid position 85 using Kabat numbering);

f) wherein if the one or more light chain amino acid positions selected for mutation are of a human **Vλ1** family light chain variable region, the mutating comprises one or more substitutions selected from the group consisting of:

(i) leucine (L), serine (S) or glutamic acid (E) at amino acid position 1 using AHo or Kabat numbering system;

(ii) alanine (A), proline (P), or tyrosine (Y) at amino acid position 2 using AHo or Kabat numbering system;

(iii) valine (V) at amino acid position 4 using AHo or Kabat numbering system;

(iv) glutamic acid (E) at amino acid position 7 using AHo or Kabat numbering system;

(v) alanine (A) at amino acid position 11 using AHo or Kabat numbering system;

(vi) threonine (T) or serine (S) at amino acid position 14 using AHo or Kabat numbering system;

(vii) histidine (H) at amino acid position 46 using AHo numbering system (amino acid position 38 using Kabat numbering system);

(ix) glutamine (Q) at amino acid position 82 using AHo numbering system (amino acid position 66 using Kabat numbering system);
(x) glycine (G), threonine (T) or aspartic acid (D) at amino acid position 92 using AHo numbering system (amino acid position 74 using Kabat numbering system); and
(xi) valine (V), threonine (T), histidine (H) or glutamic acid (E) at amino acid position 103 using AHo numbering (amino acid position 85 using Kabat numbering)."

IV. Opponents 1 to 3 (respondents I to III) each replied to the appeal.

V. The board summoned the parties to oral proceedings and issued a communication under Article 15(1) RPBA setting out its preliminary appreciation of substantive and legal matters concerning the appeal.

VI. In response to the communication of the board, the appellant made a further submission dated 10 November 2023, including a modified auxiliary request 2. Respondent II responded to this submission.

VII. The following document is cited in this decision.

D1: WO 03/008451

VIII. The arguments of the parties, where relevant to the board's decision, are summarised in the reasons for the decision.

IX. The appellant requested that the decision under appeal be set aside and amended such that the patent be maintained with the set of claims of the main request

(identical to auxiliary request 1 dealt with in the decision under appeal), or alternatively, with the set of claims of one of auxiliary requests 1, 3 to 5, all requests having been submitted with the statement of grounds of appeal, or auxiliary request 2, as filed with the submission dated 10 November 2023.

The respondents requested that the appeal be dismissed and that auxiliary requests 1 to 5 not be admitted and considered in the proceedings. Respondent II further requested that none of the amendments to the appellant's case filed with the submission of 10 November 2023, including auxiliary request 2, be admitted and considered in the proceedings.

Reasons for the Decision

Appellant's submission dated 10 November 2023 - amendment to a party's appeal case (Article 13(2) RPBA)

1. In the communication under Article 15(1) RPBA, the board set out its preliminary opinion, which agreed with the opposition division and disagreed with the appellant, that not all the mutations indicated in claim 1 of the main request were over-represented in the QC library as compared to the germline antibody library (point 15 of the communication; see also, for example, point 16. below).

2. In response, the appellant made a further submission (see section VI.) and argued for the first time that it was not relevant that the claimed substitution mutation to proline (P) at amino acid position 10 in the heavy chain variable region of the VH1b family did not constitute a mutation to an amino acid which was over-

represented in the QC library as compared to a germline antibody library, because proline was in fact over-represented at amino acid position 10 as compared to the mature antibody library ("KDB").

3. In the grounds of appeal, when defending the claimed subject-matter in relation to the relevant part of the decision under appeal and explaining the particulars of the so-called "functional consensus approach" underlying the claimed invention, the appellant explicitly emphasised the final (fourth) step in this approach, i.e. the selection of residues that were over-represented in the QC dataset over the germline dataset for a given position, and added that "*All positions described in present claim 1 are overrepresented in the QC database relative to the same position in the germline databases, as shown in Tables 13 to 18 of the patent*" (point 3.8 of the grounds of appeal, first paragraph on page 11, hereinafter "statement A"). Of note in this context is that a similar statement to statement A was also made on page 3, first full paragraph, of the later submission of the appellant: "*As a matter of fact, all mutations described in Auxiliary Request 1 (= new Main Request) underlying the OD's decision on inventive step are mutations, which have been identified by the inventors as being overrepresented in the QC library over the germline library.*"

4. The appellant subsequently submitted that statement A referred to above was made in the context of the preceding sentence in point 3.8 of the grounds of appeal, i.e. that the appellant "*disagree*[d] *with the Opposition Division's allegation in section 8.9 of the decision under appeal that not all of the positions claimed are overrepresented in the QC database*."

Indeed, in that point of the decision the opposition division had expressed the view that it could "*except* [sic] *such plausible teaching for the mutations which have been found as being over-represented in the QC library compared to a germline and/or mature antibody library in the context of an scFv*" (emphasis added). Hence, according to the appellant, the argument in the submission of 10 November 2023 that it was sufficient for the residue mentioned in the claim to be over-expressed as compared to the mature antibody library alone (as opposed to the germline database) had in fact already been submitted and relied on by the appellant in the grounds of appeal.

5. However, the board is not persuaded by this argument, in view of the explicit emphasis on the selection of residues that were over-represented for a given position in the QC dataset over the germline dataset (as opposed to the mature antibody library), and the unequivocal statement A referred to in point 3. above. As argued by respondent II, the mere statement in point 3.8 of the the grounds of appeal that the appellant disagreed with the conclusions in point 8.9 of the appealed decision is not a reasoned statement. The reasons are given only in the following sentence (statement A) and are restricted to a particular point, which does not include the new line of argument which was then introduced in the submission of 10 November 2023.

6. Accordingly, the new defence is an amendment to the appellant's case as set out in the grounds of appeal. Its admission is governed by Article 13(2) RPBA, which imposes the most stringent limitations on a party wishing to amend their appeal case at an advanced stage of the proceedings and states that any amendment to a

party's appeal case made at this stage of the proceedings will not be taken into account unless there are exceptional circumstances which have been justified with cogent reasons.

7. The appellant has not argued that there were exceptional circumstances justifying the admittance of the new defence into the appeal proceedings (Article 13(2) RPBA), nor has the board identified any such circumstances.

8. Thus, the new line of argument could not be considered in the appeal proceedings (Article 13(2) RPBA).

Main request - claim 1 - inventive step

9. The claimed method (see section III.) allows the engineering of immunobinders with improved functional properties, in particular improved solubility, stability, non-aggregation, expression and/or refolding yield. The method is based on mutating one or more selected amino acid positions within the V_H and/or V_L frameworks, and screening the immunobinder for any of the improved functional properties. The one or more mutations are specific amino acid substitutions at specific positions within the frameworks of specific framework families, namely heavy chain frameworks of the VH3, VH1a and VH1b family, and light chain frameworks of the Vκ1, Vκ3 or Vλ1 family (specified in subsections a) to f) of the claim).

10. The disclosure in document D1 represents the closest prior art. This has not been contested.

11. Similarly to the claimed method, the method disclosed in document D1 aims to improve biophysical properties

such as the stability, expression and/or solubility of immunobinders (e.g. antibodies) by modifying framework residues within a human variable heavy or light chain of a particular subclass (see for example page 4, last full sentence, to page 5, line 6). Example 1 describes the systematic identification of particular amino acid positions and amino acid residues in the framework regions based on a functional consensus testing method. In Example 2, the structure-based improvement of the relevant biophysical properties of immunoglobulin V_H domains is tested.

12. The opposition division found that the claimed method differed from the methods disclosed in the closest prior art only in the nature of the mutations, i.e. the specific positions and/or residues chosen. This finding has not been contested by the appellant, and the board has no reason to disagree.

13. As regards the technical effect of the specific positions and/or residues recited in the claim, the appellant has referred to the particulars of the so-called "functional consensus approach" disclosed in the patent and underlying the claimed invention. The appellant stated that this "functional consensus approach" included i) the generation of a "quality control" (QC) database with sequence data of immunobinders with favourable properties based on sequence data obtained by experimental selection of immunobinders with preferred properties, in particular improved stability and solubility; ii) the grouping of the QC dataset to the different variable domain subclasses; iii) comparing, within each subclass, the frequency of each amino acid between the QC dataset and a germline database or a database of mature antibodies; and iv) the selection of residues that are over-

represented in the QC dataset over the germline dataset for a given position. According to the appellant, the over-representation of the selected residues indicated that the residues contributed to the favourable properties of the immunobinders of the QC dataset, and the claimed method recited these purposefully selected, and thus not arbitrary, subclass-specific mutations. The disclosed purposeful approach was not taught or suggested in the art, so the claimed subject-matter involved an inventive step.

14. The board agrees with the opposition division that, given the particulars of the "functional consensus approach" disclosed in the patent, it can be argued that the objective technical problem resulting from the technical difference (see point 12.) is the provision of a method of engineering an immunobinder, by introducing mutations in the V_H or V_L chains, which has an increased likelihood of improved functional properties selected from solubility, stability, non-aggregation, expression and/or refolding yield. The appellant agreed with the opposition division's formulation of the technical problem in this way.

15. However, the opposition division held that this objective technical problem was not solved by the claimed subject-matter, *inter alia* because not all the mutations indicated in the claim were over-represented in the QC library.

16. Also during the appeal proceedings, the issue of whether all the mutations recited in the claim were indeed over-represented in the QC library, in particular as compared to a germline library, was the subject of dispute; and in this respect the board agrees with the respondents that the claimed

substitution mutation to proline (P) at amino acid position 10 (using the AHo numbering system) in the heavy chain variable region of the VH1b family does not constitute a mutation to an amino acid which is over-represented in the QC library as compared to a germline antibody library (see P1, Appendix G, Figure for position 10). The appellant has not contested this point.

17. One claimed embodiment of claim 1 is the following method.

A method of engineering an immunobinder with improved functional properties, the immunobinder comprising a heavy chain variable region of a **VH1b family**, the heavy chain variable region comprising V_H framework residues, the method comprising:

A) selecting one or more amino acid positions within the V_H framework residues for mutation;

B) mutating the position selected for mutation, and

C) screening the immunobinder for improved functional properties selected from solubility, stability, non-aggregation, expression and/or refolding yield,

wherein the mutating comprises substitution [by] **proline (P)** at amino acid position 10 using AHo numbering system (amino acid position 9 using Kabat numbering system).

Put more simply, this claimed embodiment is a method of engineering an immunobinder having a VH1b region with V_H framework regions by substituting the amino acid at position 10 using the AHo numbering system by proline (P), and screening the immunobinder for improved functional properties selected from solubility,

stability, non-aggregation, expression and/or refolding yield.

18. However, this embodiment of claim 1 in fact negates the general rationale which was relied on by the appellant in the grounds of appeal, based on the "functional consensus approach", i.e. QC database over-representation as compared to a germline antibody library, to justify the formulation of the objective technical problem (see point 14.). In fact, this single mutation embodiment cannot increase the likelihood of improved functional properties selected from solubility, stability, non-aggregation, expression and/or refolding yield, as it is not over-represented in the QC library.

19. For the sake of completeness, in this context it must be added that the appellant's arguments that the claimed subject-matter does indeed solve the technical problem formulated by the opposition division, given that non-working embodiments are eliminated from the claimed subject-matter by virtue of step C) and/or because the claim did not require a 100% guarantee of success, must fail in the face of the particular embodiment above of the claimed method.

20. In view of the foregoing, the board agrees with the opposition division that the objective technical problem formulated above is not solved by every embodiment of the claimed subject-matter, and so the technical problem needs to be reformulated in less ambitious terms.

21. As an alternative formulation to that given in point 14., the appellant suggested the following: the provision of an alternative method to that disclosed in

document D1 of engineering an immunobinder, by introducing mutations in the V_H or V_L chains, which has an increased likelihood of improved functional properties selected from solubility, stability, non-aggregation, expression and/or refolding yield over random substitution.

22. Regardless of whether this alternative formulation is admitted into the appeal proceedings, the reasons given in points 16. and 17. above also apply, leading to the conclusion that this alternative objective technical problem is not solved by every embodiment of the claimed subject-matter, and so here too the technical problem needs to be reformulated in less ambitious terms.

23. The board agrees with the opposition division that under these circumstances the less ambitious problem can be formulated as the provision of alternative positions and/or residues in the V_H or V_L chains of immunobinders for mutation and screening for improved functional properties. The appellant has not contested this point.

24. On the topic of obviousness in assessing inventive step with this reformulated and less ambitious objective technical problem, the appellant did not provide any persuasive arguments that the assessment in the decision under appeal was wrong. Accordingly, there is no reason to depart from the opposition division's assessment that "[t]*he solution to this problem is obvious as the prior art already discloses many of the indicated positions and the screening for improved functional properties. The skilled person would have arbitrarily chosen any of the possible residues to solve the problem of providing an alternative*

immunobinder to be screened. In the absence of a proven advantage of the claimed positions and residues any mutation would have been introduced by the skilled person and screened for improved functional properties." (Point 8.15 of the decision under appeal; Article 15(8) RPBA)

25. Accordingly, the claimed subject-matter lacks an inventive step.

Auxiliary requests 1 to 5 - admittance and consideration - (Article 12(4) RPBA 2007)

26. In addition to former auxiliary request 1 (which is the current main request), in the decision under appeal the opposition division dealt with forty further auxiliary requests, which ultimately were either inadmissible or else not allowable because they did not remedy the issues on inventive step.

27. As regards the appeal, auxiliary requests 1 and 3 to 5 were all submitted with the grounds of appeal, while a first version of auxiliary request 2 was also filed with the grounds of appeal, but then re-filed in "corrected" form with a later submission after sthe ummons to oral proceedings had been issued. All five auxiliary requests are thus new to the proceedings.

28. Admittance of auxiliary requests 1 and 3 to 5 is thus governed by Article 12(4) RPBA 2007, while admittance of auxiliary request 2, regardless of whether it is considered under Article 12(4) RPBA 2007 (as argued by the appellant) or under Article 13(2) RPBA (as argued by the respondents), depends on auxiliary request 2 as filed with the grounds of appeal being found admissible. Hence, admittance of all auxiliary requests

is governed by Article 12(4) RPBA 2007, which gives the board the power to hold inadmissible facts, evidence or requests which could have been presented or were not admitted in the proceedings before the examining or opposition division.

29. Given that the aim of opposition appeal proceedings is to obtain a judicial review of the decision of the opposition division, it follows that the board must take its decision on the basis of the issues in dispute before the opposition division. Article 12(4) RPBA 2007reflects the principle, which can be directly inferred from the above, that the parties have only limited scope to amend the subject of the dispute in appeal proceedings, and serves to ensure compliance with the requirement of fair proceedings and to expedite processing of the case. Indeed, Article 12(4) RPBA 2007 mentions that the board in *inter partes* proceedings has discretion over whether or not to admit facts, evidence or requests which could have been presented by the patent proprietor in opposition proceedings, but were not. The precondition of whether the facts, evidence or requests at issue could have been presented in the opposition proceedings relates to the question of whether the party concerned could have been expected to present them in the opposition proceedings, given the circumstances of the specific case.

30. When filing the auxiliary requests with the grounds of appeal, the appellant did not submit reasons why these could not already have been filed in the opposition proceedings, or why the board should admit these documents into the proceedings at the appeal stage. In particular, the appellant did not argue that the new auxiliary requests were filed in response to any new

reasoning by the opposition division in the decision under appeal to which they had not had time to reply.

31. Therefore, under such circumstances any claim request supposedly supporting the appellant's arguments on inventive step (see point 26.) should have been filed during the opposition proceedings. Consequently, these new auxiliary requests not only could but should have been filed during the opposition proceedings.

32. In response to the board's communication under Article 15(1) RPBA which expressed the board's preliminary view that it would not admit auxiliary requests 1 to 5 into the proceedings (Article 12(4) RPBA 2007), the appellant for the first time submitted arguments on the admittance of the auxiliary requests. No reasons were given why such arguments had not been presented earlier.

33. Since these submissions were filed late, they were not taken into consideration in the board's assessment of admittance of the auxiliary requests under Article 12(4) RPBA 2007.

34. Accordingly, auxiliary requests 1 to 5 could not be considered in the appeal proceedings (Article 12(4) RPBA 2007).

35. Given this situation, there was moreover no possibility of admitting a modified auxiliary request 2 as submitted later in the appeal proceedings (see point 28. above, Article 13(2) RPBA).

Order

For these reasons it is decided that:

The appeal is dismissed.

The Registrar: The Chair:

L. Malécot-Grob T. Sommerfeld

Decision electronically authenticated