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Datasheet for the decision of 26 November 2008

Case Number: T 1624/07 - 3.3.04

Application Number: 00939232.5

Publication Number: 1181317

IPC: C07K 14/705

Language of the proceedings: EN

Title of invention:
An integrin heterodimer and an alpha subunit thereof

Applicant:
Cartela R & D AB

Opponent:
-

Headword:
Integrin alpha 11/CARTELA

Relevant legal provisions:
EPC Art. 54, 56

Relevant legal provisions (EPC 1973):
-

Keyword:
"Main request claim 1 - novelty (yes), inventive step (yes)"

Decisions cited:
T 0506/95

Catchword:
-

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Case Number: T 1624/07 - 3.3.04

D E C I S I O N
of the Technical Board of Appeal 3.3.04
of 26 November 2008

Appellant: Cartela R & D AB
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Decision under appeal: **Decision of the Examining Division of the European Patent Office posted 8 May 2007 refusing European application No. 00939232.5 pursuant to Article 97(1) EPC 1973.**

Composition of the Board:

Chairman: U. Kinkeldey
Members: G. Alt
R. Moufang

Summary of Facts and Submissions

I. This is an appeal against the examining division's decision to refuse the European patent application No. 00939232.5 pursuant to Article 97(1) EPC 1973. The application was filed as an international application under the PCT and published as WO 00/75187 with the title "An integrin heterodimer and an alpha subunit thereof".

II. Claims 1 and 22 to 25 of the published application read:

"1. A recombinant or isolated integrin subunit α11 comprising essentially the amino acid sequence shown in SEQ ID No. 1, and homologues and fragments thereof.

22. A fragment of an integrin subunit αll, which integrin subunit αll comprises essentially the amino acid sequence shown in SEQ ID NO: 1, said fragment being a peptide chosen from the group comprising peptides of the cytoplasmic domain, the I-domain and the extracellular extension region.

23. A fragment according to claim 22, said fragment being a peptide from the cytoplasmic domain comprising essentially the amino acid sequence KLGFFRSARRRREPGLDPTPKVLE.

24. A fragment according to claim 22, which is a peptide comprising essentially the amino acid sequence of the extracellular domain, from about amino acid No. 804 to about amino acid no. 826 of SEQ ID No. 1.

25. A fragment according to claim 22, which is a peptide comprising essentially the amino acid sequence of the I-domain, from about amino acid No. 159 to about amino acid no. 355 of SEQ ID No. 1."

III. Claim 1 of the main request before the examining division read as follows:

"1. A recombinant or isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1, and fragments thereof, wherein the fragments are selected from the group consisting of

a peptide from the cytoplasmic domain comprising the amino acid sequence KLGFFRSARRRREPGLDPTPKVLE,

a peptide comprising the amino acid sequence of the extracellular domain, from amino acid no. 804 to amino acid no. 826 of SEQ ID No. 1, and

a peptide comprising the amino acid sequence of the I-domain, from amino acid no. 159 to amino acid no. 355 of SEQ ID No. 1."

The subject-matter of claims 6, 8, 10, 11, 13, 15, 19 and 22 related to a process of producing the product according to claim 1, to an isolated polynucleotide or oligonucleotide encoding the product of claim 1, to a vector comprising said polynucleotide or oligonucleotide, to a cell containing said vector, to a cell generated by process steps (a) to (c) of claim 6 and wherein the polynucleotide or oligonucleotide has been stably inserted into the cell genome, to a process of producing a recombinant integrin heterodimer, to a binding entity binding to the product of claim 1 and to the use of this entity to detect cells or tissues expressing an integrin subunit α11.

IV. The only reason given in the decision under appeal for the refusal of the application was that the subject-matter of claims 1, 6, 8, 10, 11, 13, 15, 19 and 22 lacked an inventive step. The examining division was of the opinion that document D1 was the closest prior art (bibliographic data see below in point VII) and not document D2 (bibliographic data see below in point VII) because document D1 identified the clones A3321 and A33108 which were used by the inventors for the full-length cloning process of the nucleic acid encoding the claimed integrin. The examining division held that starting from document D1 the provision of the full-length clone could be achieved by routine methods.

V. The board sent a communication informing the appellant that claims 1, 8 and 13 of the main request before it (and which corresponded to the request refused by the examining division, see section III above) seemed to lack clarity. In particular it was noted that it was not clear whether the term "fragments thereof" referred to the expression "integrin subunit α11" or to the expression "SEQ ID No. 1".

VI. Oral proceedings before the board took place on 26 November 2008.

The board raised the question whether the subject-matter of claim 1 could be considered as novel over the disclosure of the protein αmt in document D2 given the statement in the application on page 25, lines 32 to 37 that "[b]ased on similar SDS-PAGE migration patterns, similar behaviour under reducing conditions, association with β1 integrin chain, and up-regulation

during in vitro differentiation of human fetal myoblasts, the present data show that **the α11 integrin is identical with αmt**." (emphasis added).

The appellant filed a new main and three auxiliary requests.

Claim 1, which is the only claim of the main request amended with respect to the previous main request, read:

"1. A recombinant or isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1
or
fragments of the amino acid sequence shown in SEQ ID No. 1, wherein the fragments are selected from the group consisting of

a peptide from the cytoplasmic domain comprising the amino acid sequence KLGFFRSARRRREPGLDPTPKVLE

a peptide comprising the amino acid sequence of the extracellular domain, from amino acid no. 804 to amino acid no. 826 of SEQ ID No. 1, and

a peptide comprising the amino acid sequence of the I-domain, from amino acid no. 159 to amino acid no. 355 of SEQ ID No. 1."

At the end of the oral proceedings the board announced its decision.

VII. The following documents are cited in this decision:

D1: International Journal of Cancer, vol. 66, 1996, pages 571-577, Genini, M. et al.

D2: Developmental Dynamics, vol. 204, 1995, pages 57-65, Gullberg, D. et al.

AD8: Molecular Biology of the Cell, vol. 8, September 1997, pages 1723-1734, Ziober, B.L. et al.

Sequence alignments of clone A3321 and clone A33108, respectively, with SEQ ID No. 1; submitted with the letter dated 15 December 2006

Declaration Dr Gullberg dated 5 April 2006

Second declaration Dr. Gullberg filed with letter dated 17 September 2007

Declaration Dr Velling dated 5 April 2006

Declaration Dr Johansson dated 17 September 2007

Declaration Dr Andersson dated 13 November 2006

VIII. The appellant's arguments in writing and at the oral proceedings, in so far as they are relevant to the present decision, may be summarised as follows:

Main Request

Articles 84 and 123(2) EPC

The amended claim 1 had a basis in the description as filed. Moreover, the claim was clear.

Novelty

The disclosure in Figure 3 of document D2 of a protein band in an SDS-gel termed "αmt" did not destroy the novelty of the subject-matter of claim 1. Due to the lack of explicit sequence information, it was not derivable from document D2 whether αmt comprised the sequence of SEQ ID No. 1. Moreover, even if it was assumed that this was so, the disclosure in document D2 was not novelty-destroying because it did not disclose the isolation of the protein in an enabling manner.

Inventive step

Document D2 was the closest prior art document since it related to the same purpose as the invention. The claimed α11 integrin could not be considered as obvious because its cloning could not be achieved by routine methods.

Reasons for the Decision

Main Request

Articles 84 and 123(2) EPC

1. Amended claim 1 of the main request relates to a "recombinant or isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1" and to three specifically characterized "fragments of the amino acid sequence shown in SEQ ID No 1.", i.e. a peptide from the cytoplasmic domain comprising the amino acid sequence KLGFFRSARRRREPGLDPTPKVLE, a peptide comprising the amino acid sequence of the extracellular domain, from amino acid no. 804 to amino acid no. 826 of SEQ ID No. 1, and a peptide comprising the amino acid sequence of the I-domain, from amino acid no. 159 to amino acid no. 355 of SEQ ID No. 1.

2. The embodiment in claim 1 of a "recombinant or isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1" has a basis in claim 1 as filed (see section II above). A "peptide from the cytoplasmic domain comprising the amino acid sequence KLGFFRSARRRREPGLDPTPKVLE" is recited in claim 23 of the application as filed (see section II above) and an alignment with SEQ ID No. 1 demonstrates that it is indeed a fragment of SEQ ID No. 1. Fragments defined by the features by which the remaining two fragments of claim 1 are characterized are referred to in claims 24 and 25 of the application as filed.

The board has no objections pursuant to Article 84 EPC with regard to claim 1.

Therefore, claim 1 fulfils the requirements of Articles 84 and 123(2) EPC.

Novelty

3. Document D2 discloses an integrin α chain, designated "αmt", which is upregulated in differentiated human fetal myotube cells compared to proliferating myoblast cells (page 58, first column, second full paragraph). The document inter alia reports about an immunodepletion assay with the myotube cells, anti-integrin chain β1 antibodies and anti-integrin chain α1, α3, α4, α5 and αv antibodies. For the assay the cells were iodinated and subsequently lysed to solubilise the proteins. Iodination of a protein indicates that it was located on the cell surface. The solubilised proteins were then first contacted with the anti-β1 integrin chain antibody resulting in a fraction of proteins capable of forming dimers with the β1 integrin chain. The obtained β1-binding fraction was reacted with antibodies to α1, α3, α4, α5 and αv integrin α chains thus precipitating the mentioned α chains from the fraction. The remaining fraction was reacted with the same set of antibodies for a more complete depletion of the mentioned α chains. Finally, the remaining extract was again contacted with the anti-β1 integrin antibody, thus generating a precipitate containing all remaining proteins capable of binding to the integrin β1 chain. The extracts of all the four precipitation rounds were loaded on an SDS gel and electrophoresis was performed.

Figure 3 of document D2 presents the results of the immunodepletion assay. Lane d shows the separation of proteins present in the extract after the last precipitation step as disclosed above. Two distinct protein bands are visible, one being designated "αmt" the other "β1".

4. The present application cites the publication D2 as reference (38)(page 31 of the application). It is stated on page 4, lines 3 to 8 of the application that the cloning and further characterization of the protein "αmt" disclosed in reference document (38), i.e. document D2 in the present proceedings, is the objective underlying the application. The following is furthermore stated on page 25: "Based on similar SDS-PAGE migration patterns, similar behaviour under reducing conditions, association with β1 integrin chain, and upregulation during in vitro differentiation of human fetal myoblasts, the present data show that αll integrin is identical with αmt."

4.1 This latter statement has prompted the board to consider whether or not the protein named "αmt" shown in lane d of Figure 3 (see point 3 above) falls under the definition in claim 1 of an "isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1" and therefore could be considered as novelty-destroying for the subject-matter of claim 1.

4.2 Document D2 does not explicitly disclose any nucleic sequence coding for or amino acid sequence of αmt. Also the properties of αmt reported in document D2 such as PAGE migration pattern, behaviour under reducing

conditions, association with βl integrin chain, the developmental status or the relationship of αmt to the protein class of α integrin chains do not per se convey any specific sequence information.

4.3 Furthermore, αmt disclosed in document D2 and α11 of the present application were detected in different tissues from different human beings of a different developmental stage, i.e. the cell line in which αmt was detected was derived from a clone originating from the thigh muscle of a 73-day-old aborted human foetus (page 62, second column), whereas the cDNA for α11 was isolated from adult human uterus cells (page 20 of the application).

4.4 The skilled person knows that the sequence of a gene encoding a particular protein may be subject to variation. Due to the degeneracy of the genetic code some of these nucleic acid variations do not cause any change in the amino acid sequence. Some however do, although they may remain silent with regard to the functional properties of the protein. Consequently, even two integrin molecules which might be considered to be "identical" on the basis of functional or physical parameters may be structurally different.

4.5 In particular with regard to integrins, a further degree of complexity is added by the alternative splicing of integrin-coding genes which may give rise to different integrin isoforms in the different tissues in which the gene is expressed and by the dependence of the expression of integrins on the developmental status

of the cell (for example document AD8, page 1724, first column).

4.6 Thus, given these circumstances and seeing the different sources from which the integrin named "αmt" in document D2 and the integrin named "α11" of the present application were obtained, a structural difference between the two compounds cannot be excluded. Or, in other words, on the evidence before the board it is not certain that the amino acid sequence of SEQ ID No. 1 is present in αmt.

4.7 However, the novelty of claimed subject-matter is only affected by a prior art disclosure, if on the evidence on file, it is clear and unambiguous that the subject-matter disclosed in the prior art has all the features as the claimed subject-matter (Case Law of the Boards of Appeal, 5th edition 2006, I,C.2.1, 10th paragraph and I.C.4.1.1(a), third paragraph).

4.8 Thus, while - as derivable from the application (see point 4 above) - a molecular biologist would consider the integrin αmt and the integrin of the application to be identical, although a structural non-identity cannot be excluded, the board cannot come to such conclusion in view of the standards developed by the case law cited above.

4.9 Therefore, since there is no evidence that clearly and unambiguously establishes that αmt has the specific feature of the subject-matter of claim 1 namely that it comprises "the amino acid sequence shown in SEQ ID No. 1", the protein αmt shown in Figure 3 of document

D2 cannot be considered as destroying the novelty of the subject-matter in claim 1 as far as it related to an "isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1."

4.10 Hence, the further issues of whether or not the protein in Figure 3 can be considered as an "isolated" integrin α chain and whether or not document D2 discloses an enabling isolation process for αmt need not be addressed.

4.11 The board furthermore considers that document D2 does not disclose any specific fragments of the protein αmt.

4.12 Therefore, in summary, the board concludes that the subject-matter of claim 1 is not anticipated by the disclosure in document D2.

5. Document D1 discloses cDNAs that are expressed in human primary myoblasts, but the expression of which is down-regulated in neoplastic counterpart cells, i.e. embryonal rhabdomyosarcoma cells. According to Table III and page 574, first column of document D1, the sequence of two of these cDNAs, A3321 having a length of 356 base pairs and A33108 having a length of 192 base pairs is partially identical with parts of the nucleic acid sequence encoding known integrins.

5.1 It is apparent from sequence alignments submitted by the appellant during examining proceedings that clone A3321 aligns with SEQ ID No. 1 of the present application at nucleic acid positions 298 to 642 (corresponding to amino acid positions 70 to 184) and that clone A33108 aligns with SEQ ID No. 1 at nucleic

acid positions 1485 to 1717 (corresponding to amino acid positions 466 to 543; note added by the board: the number of base pairs of clone A33108 shown in the sequence alignment is slightly higher than that indicated for the clone with the same name in document D1). Thus, none of the proteins corresponding to the nucleic acid fragments A3321 and A33108 of document D1 has the characteristics by which the proteins in claim 1 are defined. This is also true with regard to the protein last-mentioned in the claim, i.e. a peptide comprising from amino acid 159 to 355 of SEQ ID No. 1, because clone A3321 only partly overlaps with this fragment.

5.2 Thus, the subject-matter of claim 1 is considered to be novel over the disclosure in document D1.

Inventive step

6. In assessing whether or not a claimed invention meets the requirements of Article 56 EPC the boards of appeal apply the "problem and solution approach" which requires as a first step the determination of the closest prior art with regard to the invention as presented in the description and the claims.

The closest prior art document

7. It has been held by the boards that, generally, the closest prior art document fulfils at least the criterion that it is directed to the same objective or purpose as the invention (Case Law of the Boards of Appeal, 5th edition 2006, I.D.3.1 and 3.4, first and second paragraphs).

7.1 In general terms, the present application is related to an integrin β1 chain-related integrin α chain protein.

7.2 The appellant considered document D2 and the examining division document D1 as the closest prior art document.

7.3 Document D1 has already been considered in the context of novelty (see points 5 and 5.1 above). It discloses the isolation of cDNAs related to 48 different genes which are expressed in human primary myoblasts (cell line A33) but not in embryonal rhabdomyosarcoma cells (cell line RD) (first paragraph of section "Results"). The aim of the study is to identify proteins which might play a role in tumour development (see for example the first sentence of the last paragraph of document D1).

7.4 In particular, document D1 discloses the two cDNA clones A3321 and A33108 (see also points 5 and 5.1 above) which according to Table III and page 574, first column of document D1 have 57% identity in their 356 base pairs in the region between residues 280 and 630 human integrin alpha-2 and 62.5% identity in their 192 base pairs between residues 1840 and 2030 of rat integrin alpha-1, respectively. It is suggested that the two cDNAs could represent parts of new isoforms of the two known integrin alpha subunits with which they are partially identical.

7.5 Document D2 discloses an integrin α chain termed "αmt" and some of its properties, inter alia that it is associated with the β1 chain of integrins (see point 3 above).

7.6 Thus, as to document D1, firstly, it relates to the elucidation of skeletal muscle tumour development.

7.7 Secondly, as stated in Dr Gullberg's and Dr Velling's declarations (points 9 and 10 and point 9, respectively), the two integrin-related cDNA clones disclosed in document D1 are very short (356 and 192 base pairs, respectively) when compared to the average full length integrin alpha sequences (around 4 to 7 kilo bases, see Dr Gullberg's second declaration, point 18) and the stated sequence identities to known integrins are relatively low (57% and 62.5%). Furthermore, as submitted by Dr Johansson in points 9 to 11 of his declaration, at the priority date of the application a scientist working in the field of integrin research would have anyhow doubted the existence of any new integrins due to "the sharp drop in the rate of discovery of new members in spite of improved knowledge, reagents and methods" and also due to "odd reports of "integrin-like" proteins/sequences from various sources". Therefore, in the board's view, the skilled person would have had doubts whether the full-length sequences related to the two clones A3321 and A33108 indeed encoded integrin α chains.

7.8 The fact that the sequences of A3321 and A33108 actually have a high percentage of sequence identity with parts of SEQ ID No. 1 of the present application (98.5% and 98.3%; see the title of the sequence

alignments; see also point 5.1 above) was not known at the priority date of the application and could therefore not have been taken into account by the skilled person when interpreting the disclosure of document D1 (for example decision T 506/95, point 4.1, second paragraph of the reasons).

7.9 In contrast, document D2 relates to a specific integrin β1 chain-related integrin α chain protein, i.e. to the same subject as the application.

7.10 Thus, not only for that reason, but also, in the board's view, since the skilled person would not have considered the speculative disclosure in document D1 (see point 7.7 above) as a promising starting point, the board considers that document D2 represents the closest prior art document.

Problem to be solved

8. According to the specification of the present application the problem to be solved would be the cloning and further characterization of the integrin α-chain disclosed in document D2 (page 4, lines 3 to 8 or page 19, lines 21 to 24).

9. However, this formulation of the problem needs qualification, since the board has come to the conclusion that on the evidence on file a structural identity between αmt disclosed in document D2 and the claimed integrin, α11, cannot be unambiguously established (see points 4.2 to 4.9 above).

10. Given that the amino acid sequences of functionally identical proteins may differ (see point 4.4 above), the board considers that the objective technical problem underlying the application is the isolation of the integrin α chain disclosed in document D2 or a variant thereof.

10.1 In the light of the data disclosed in the application, as for example the SDS-PAGE migration pattern, behaviour under reducing conditions, association with the β1 integrin chain, and up-regulation during in vitro differentiation of human fetal myoblasts and given the corresponding data in document D2, the board is satisfied that the above stated problem is solved by the claimed subject-matter.

Obviousness

11. Document D2 suggests four methods for the isolation of αmt in the paragraph bridging the two columns on page 61.

(a) isolation from fetal week 10 muscle myotubes;

(b) immuno-affinity purification from rat or mouse embryos with an anti-β1 integrin antibody;

(c) immuno-affinity purification from G6 muscle cells with anti-αmt antibodies;

(d) screening of a cDNA library from G6 myotubes.

12. In the board's view, prima facie, any one of these methods is to be regarded as a routine method which the skilled person might consider when attempting to isolate the integrin α chain disclosed in document D2 or a variant thereof.

12.1 However, with regard to method (a) above, document D2 discloses that this method will present problems because of limited availability of the fetal week 10 muscle tissue (page 61, first column, last paragraph). Currently, there is no evidence before the board that the skilled person, in contrast to the authors of document D2, had a possibility to obtain sufficient quantities of that tissue for characterization and cloning a gene and the encoded protein.

12.2 With regard to method (b) mentioned above, document D2 discloses that "attempts to perform immunoaffinity purification on anti-β1 integrin columns from rat or mouse embryos will also present problem [sic] since $\alpha_{mt}\beta$1 has similar molecular weight as α2β1 and α9β1."(page 61, second column, second paragraph).

12.3 Moreover, with regard to method (c) it is indicated in document D2 that "initial attempts have generated muscle specific monoclonal antibodies but no antibodies reactive with α_{mt}"(page 61, second column, second paragraph).

12.4 Finally, with regard to the isolation by screening a cDNA library from G6 myotubes (method (d) above), it is stated in the present application on page 19, line 21 et seq.:

"In order to determine the nature of the integrin chain that we had previously characterized on human fetal muscle cells and named αmt (38) a number of approaches were used. Applying PCR with mRNA from fetal muscle cells as template together with degenerate primers to conserved regions of integrin α subunits (43) we amplified cDNA for α1, α4, α5, α6 and αv integrin chains (data not shown), **but failed to amplify the novel integrin.**" (emphasis added).

12.5 The failure to isolate αmt DNA from a cell line of fetal muscle cells is confirmed by Dr. Gullberg in the declaration dated 5 April 2006, point 16:

"16. [...]. Several attempts to isolate the gene using standard cloning techniques proved unsuccessful. For example, applying PCR with mRNA from human fetal muscle cells (myoblasts) as a template together with degenerate primers to conserved regions of known integrin alpha subunits failed to amplify the alpha-11 gene. In fact, we were never able to succeed in cloning the alpha-11 gene from a myoblast library."

12.6 Hence, on the evidence before it, the board concludes that the skilled person would not have been able isolate the integrin α chain disclosed in document D2 or a variant thereof when relying on the screening of a cDNA library made from a cell line of fetal muscle cells.

12.7 For the board it follows from the observations in points 11 to 12.6 above that the skilled person would not have tried methods (a) to (c) above because, due to the limited availability of starting material (method

(a)) or in view of the discouraging statements in document D2 itself (methods (b) and (c)), he/she would not have expected to succeed in isolating the integrin α chain disclosed in document D2 or a variant thereof on their basis. In contrast, the skilled person would have tried method (d), but, as shown by the evidence on file, would have failed to isolate the integrin α chain disclosed in document D2 or a variant with its help. Therefore, the board concludes that the subject-matter of claim 1 as far as it relates to an "isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1" cannot be considered as obvious on the light of any one of the methods disclosed in document D2.

13. A further question is whether or not the subject-matter of claim 1 is obvious in the light of a combination of document D2 with document D1.

13.1 Document D1 suggests that the full-length DNA related to clones A3321 and A33108 encodes **isoforms** of those known integrin α chains with which clones A3321 and A33108 are disclosed in document D1 to have partial sequence identity, i.e. integrins α1 and α2 (page 574, first column, first paragraph; (see point 7.4 above). In contrast, document D2 proposes that "αmt" is an integrin which is **not related to any of the known integrins**, i.e. it is a considered as a "hitherto unidentified integrin α-chain on myotubes" (see the penultimate sentence of the abstract; see also the first paragraph of the section "Discussion"). Hence, in the board's view, the skilled person would not have

seen any link between the two clones disclosed in document D1 and the integrin disclosed in document D2.

13.2 Moreover, the skilled person would have doubts whether the full-length sequences pertaining to clones A3321 and A33108 encoded integrin α chains at all (see point 7.7 above).

13.3 The potential usefulness of these two clones was not known to the skilled person at the priority date, because the high sequence identity of these clones with the sequence shown in SEQ ID No. 1 turned only out later (see point 7.8 above).

13.4 Finally, in the board's view, an indication that the skilled person would not have considered that there is a relation between the clones A3321 and A33108 and the integrin chain disclosed in document D2 might be derived from the fact that a period of three years elapsed between the publication of document D1 and the priority date of the application which, as submitted by Dr Anderson, has to be considered as long because at that time integrin research was very competitive. Dr Andersson states in point 10 of his declaration:

"[I]ntegrin research has over the last 10-20 years been a very competitive field. Consequently, if it had been a routine, trivial task to identify new integrin subunits based on the information in the paper of Genini and co-workers (note added by the board: document D1), then it is very unlikely that it would have taken more than one year for someone in the in the field of integrin search to succeed. In fact, it took Gullberg and co-workers three years to do so,

indicating that in practice the cloning of the integrin alpha-11 was not straightforward."

13.5 Therefore, in the board's judgement, the skilled person would not have used the two clones A3321 and A33108 disclosed in document D1 for the isolation of the integrin α chain disclosed in document D2 or a variant thereof.

13.6 Thus, the board concludes that the subject-matter of claim 1 as far as it relates to a "recombinant or isolated integrin subunit α11 comprising the amino acid sequence shown in SEQ ID No. 1" is not obvious in view of a combination of the disclosure in documents D2 and D1.

13.7 A fortiori, the conclusion reached in points 12.7 and 13.6 above applies to the provision of the peptide fragments of the amino acid sequence of SEQ ID No. 1 according to claim 1.

Procedural issues

14. The present decision deals with the patentability of claim 1 of the main request. An examination of the patentability of the remaining claims of this request is still needed.

Order

For these reasons it is decided that:

1. The decision under appeal is set aside.

2. The case is remitted to the department of first instance for further prosecution on the basis of the Requests filed at the oral proceedings.

The Registrar: The Chair:

P. Cremona U. Kinkeldey