Internal distribution code:

(A) [-] Publication in OJ
(B) [-] To Chairmen and Members
(C) [-] To Chairmen
(D) [X] No distribution

Datasheet for the decision of 16 July 2019

Case Number: T 0375/15 - 3.3.04

Application Number: 07712678.7

Publication Number: 1991563

IPC: C07K14/11, A61K39/145

Language of the proceedings: EN

Title of invention:
Peptide sequences and compositions

Patent Proprietor:
Peptcell Limited

Opponent:
Immune Targeting Systems (ITS) Limited

Headword:
Peptide sequences/PEPTCELL

Relevant legal provisions:
EPC Art. 100(c), 123(2), 123(3)
RPBA Art. 13(1)

This datasheet is not part of the Decisior
It can be changed at any time and without notic

Keyword:
Main request, auxiliary requests I to V, VIB, VII-IX, XIV: extension of subject-matter (yes)
auxiliary request XV: extension of scope (yes)
auxiliary requests X to XIII, XVIA, XVIB: admitted (no)

Decisions cited:
T 1511/07

Catchword:

This datasheet is not part of the Decisior
It can be changed at any time and without notic

Europäisches Patentamt
European Patent Office
Office européen des brevets

Beschwerdekammern

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 0375/15 - 3.3.04

D E C I S I O N
of Technical Board of Appeal 3.3.04
of 16 July 2019

Appellant I: (Patent Proprietor)	Peptcell Limited 100 Fetter Lane London EC4A 1BN (GB)
Representative:	Alt, Michael Bird & Bird LLP Maximiliansplatz 22 80333 München (DE)
Appellant II: (Opponent)	Immune Targeting Systems (ITS) Limited London Bioscience Innovation Centre 2 Royal College Street London NW1 0NH (GB)
Representative:	J A Kemp 14 South Square Gray's Inn London WC1R 5JJ (GB)
Decision under appeal:	**Interlocutory decision of the Opposition Division of the European Patent Office posted on 22 December 2014 concerning maintenance of the European Patent No. 1991563 in amended form**

Composition of the Board:

Chair	M. Blasi
Members:	R. Morawetz
	B. Claes

Summary of Facts and Submissions

I. The appeals by the patent proprietor (appellant I) and the opponent (appellant II) lie from the opposition division's interlocutory decision according to which European patent No. 1 991 563 as amended in the form of auxiliary request VII, and the invention to which it relates, were found to meet the requirements of the EPC. The patent, entitled "*Peptide sequences and compositions*", derives from European patent application No. 07 712 678.7, which was filed as international application under the PCT. The latter was published as WO 2007/091030 (document D14 in these proceedings; "application as filed" or "application").

Claims 1 to 4 as granted read as follows:

"1. A polypeptide consisting of up to 40 amino acids, which polypeptide comprises a sequence having at least 95% homology with SEQ ID 1:

SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP

wherein, the polypeptide is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele, and is immunogenic to a plurality of influenza virus strains.

2. A polypeptide according to claim 1, which polypeptide comprises a cytotoxic T lymphocyte (CTL) epitope.

3. A polypeptide according to any preceding claim, consisting of up to 35 amino acid residues.

4. A polypeptide composition comprising one or more polypeptides as defined in any preceding claim, further comprising one or more polypeptides having no more than 100 amino acids, the polypeptides comprising: a sequence having at least 85% homology with any of SEQ ID 2-6; or comprising two or more epitopes having 7 amino acids or more, each epitope having at least 85% homology with a sub-sequence of any of SEQ ID 2-6 that has the same length as the epitope:

SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS
SEQ ID 3 DLIFLARSALILRGSVAHKSC
SEQ ID 4 PGIADIEDLTLLARSMVVVRP
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF."

II. One opposition was filed against the patent as a whole under Article 100(a) EPC on the grounds of lack of novelty (Article 54 EPC) and lack of inventive step (Article 56 EPC) and under Article 100(b) EPC and Article 100(c) EPC.

III. In the decision under appeal, the opposition division held that the ground for opposition under Article 100(c) EPC prejudiced the maintenance of the patent as granted; that the set of claims of auxiliary requests I and II, filed on 15 November 2013, auxiliary requests III and IV, filed on 19 December 2013, and auxiliary requests V and VI, filed during the oral proceedings and resubmitted with the letter dated 14 March 2014, infringed the requirements of Article 123(2) EPC; and that the set of claims of auxiliary request VII, filed during the oral proceedings before the opposition division and resubmitted with the letter dated 14 March 2014, met

the requirements of the EPC.

IV. In their statement of grounds of appeal, appellant I maintained the claim requests considered in the decision under appeal (main request and auxiliary requests I to VII) and submitted arguments as regards the allowability of the main request and auxiliary requests I to VI.

Claim 1 of **auxiliary requests I and II** is identical to claim 1 of the main request (claims as granted, see section I).

Claim 1 of **auxiliary requests III and IV** is identical and reads as follows:

"1. A polypeptide consisting of up to 35 amino acids, which polypeptide comprises a sequence having at least 95% homology with SEQ ID 1:

SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP

wherein, the polypeptide is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele, and is immunogenic to a plurality of influenza virus strains."

Claim 3 of **auxiliary request V** reads as follows:

"3. A polypeptide composition comprising at least the following polypeptides:
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide comprising a sequence having at least 95% homology with

SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 1 as defined in claim 1
[DLEALMEWLKTRPILSPLTKGILGFVFTLTVP];
wherein each of said polypeptides consists of up to 35 amino acids, is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 3 of auxiliary request VI (renumbered as **auxiliary request VI A** during oral proceedings) reads as follows:

"3. A polypeptide composition comprising at least the following polypeptides:
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide comprising a sequence having at least 95% homology with

SEQ ID 1 as defined in claim 1
[DLEALMEWLKTRPILSPLTKGILGFVFTLTVP];

wherein each of said polypeptides consists of up to 35 amino acids, is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of **auxiliary request VII** reads as follows:

"1. A polypeptide consisting of up to 35 amino acids, which polypeptide comprises a sequence having 100% homology with SEQ ID 1:

SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP

wherein, the polypeptide is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele, and is immunogenic to a plurality of influenza virus strains."

V. In their statement of grounds of appeal, appellant II submitted arguments as to, *inter alia*, why the subject-matter of claim 1 of auxiliary request VII extended beyond the content of the application as filed (Article 123(2) EPC).

VI. In reply to appellant II's statement of grounds of appeal, appellant I submitted sets of claims of auxiliary requests VIII to X and arguments as regards the allowability of auxiliary requests VII to X.

Claim 1 of **auxiliary request VIII** reads as follows:

"1. A polypeptide composition comprising at least the following polypeptides: a polypeptide comprising a

sequence having at least 95% homology with
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides consists of up to 35 amino acids, is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of **auxiliary request IX** reads as follows:

"1. A polypeptide composition comprising at least the following polypeptides:
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ
a polypeptide comprising a sequence having at least 95% homology with
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide comprising a sequence having at least 95%

homology with
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides consists of up to 35 amino acids, is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of auxiliary request X (renumbered as **auxiliary request XIV** in oral proceedings) differs from claim 1 of auxiliary request IX in that the percentages of homology have been limited to "*at least 100% homology*".

VII. In reply to appellant I's statement of grounds of appeal, appellant II submitted arguments as to why the subject-matter of claim 1 of the main request and auxiliary requests I to VI extended beyond the content of the application as filed (Article 123(2) EPC).

VIII. The board summoned the parties to oral proceedings as requested by the parties and issued a communication pursuant to Article 15(1) RPBA informing of its preliminary opinion on the case. As regards the main request and auxiliary requests I to VII, the board indicated that it "*is inclined to agree with appellant II that the application as filed provides no basis for the specific combination of SEQ ID NO: 1 with the length of the polypeptide (i.e. either "up to 40 amino acids" or "up to 35 amino acids") and the degree of homology (i.e. either "at leat 95%" or "100% homology")*" (see point 11 of the communication).

IX. In response to the board's communication, appellant I submitted by letter of 20 May 2019 sets of claims of an amended auxiliary request VI (renumbered auxiliary request VI B in oral proceedings and subsequently

withdrawn) and auxiliary requests XI to XIV (renumbered in oral proceedings, see below) and, *inter alia*, arguments in favour of the admittance of these claim requests into the proceedings and for a basis in the application as filed (Article 123(2) EPC). Further arguments as regards the allowability of auxiliary requests V to VII were also submitted.

Claim 1 of auxiliary request XI (renumbered as **auxiliary request X** in oral proceedings) reads as follows:

"1. A polypeptide composition comprising at least the following polypeptides:
a polypeptide having at least 95% homology with SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide having at least 95% homology with SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide having at least 95% homology with SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide having at least 95% homology with SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of auxiliary request XII (renumbered as **auxiliary request XI** in oral proceedings) reads as follows:

"1. A polypeptide composition comprising at least the following polypeptides:
a polypeptide according to SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide according to

SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide according to
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide according to
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of auxiliary request XIII (renumbered as **auxiliary request XII** in oral proceedings) reads as follows:

"1. A polypeptide composition comprising at least the following polypeptides:
a polypeptide having at least 95% homology with
SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS
a polypeptide having at least 95% homology with
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
a polypeptide having at least 95% homology with
SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
a polypeptide having at least 95% homology with
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ
a polypeptide having at least 95% homology with
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide having at least 95% homology with
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of auxiliary request XIV (renumbered as **auxiliary request XIII** in oral proceedings) reads as follows:

"1. A polypeptide composition comprising at least the following polypeptides:
a polypeptide according to
SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS;
a polypeptide according to
SEQ ID 3 DLIFLARSALILRGSVAHKSC;
a polypeptide according to
SEQ ID 4 PGIADIEDLTLLARSMVVVRP;
a polypeptide according to
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ;
a polypeptide according to
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
a polypeptide according to
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

X. In the course of the oral proceedings held before the board, appellant I renumbered auxiliary request VI considered in the decision under appeal as auxiliary request VI A; auxiliary request VI filed by letter dated 20 May 2019 as auxiliary request VI B and subsequently withdrew the latter; renumbered auxiliary requests XI to XIV filed with the reply to appellant II's appeal as auxiliary requests X to XIII and auxiliary request X as auxiliary request XIV, respectively. Furthermore, appellant I filed sets of claims of auxiliary requests XV, XVI A and XVI B.

Claim 1 of **auxiliary request XV** reads as follows:

"1. A polypeptide composition comprising the following polypeptides:
the polypeptide
SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS
the polypeptide
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
the polypeptide
SEQ ID 4 PGIADIEDLTLLARSMVVVRP,
the polypeptide
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ
the polypeptide
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
the polypeptide
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

Claim 1 of **auxiliary request XVI A** differs from claim 1 of auxiliary request XV in that the expression "*the following polypeptides*" in lines 1 to 2 has been amended to read "*the following separate polypeptides*".

Claim 1 of **auxiliary request XVI B** reads as follows:

"1. A polypeptide composition comprising the following separate polypeptides:
the separate polypeptide
SEQ ID 2 LLYCLMVMYLNPGNYSMQVKLGTLCALCEKQASHS
the separate polypeptide
SEQ ID 3 DLIFLARSALILRGSVAHKSC,
the separate polypeptide
SEQ ID 4 PGIADIEDLTLLARSMVVVRP,

the separate polypeptide
SEQ ID 5 LLIDGTASLSPGMMMGMFNMLSTVLGVSILNLGQ
the separate polypeptide
SEQ ID 6 IIGILHLILWILDRLFFKCIYRLF; and
the separate polypeptide
SEQ ID 1 DLEALMEWLKTRPILSPLTKGILGFVFTLTVP;
wherein each of said polypeptides is immunogenic in a vertebrate expressing a major histocompatibility complex (MHC) allele and is immunogenic to a plurality of influenza virus strains."

At the end of the oral proceedings, the Chair announced the board's decision.

XI. Appellant I's arguments submitted in writing and during the oral proceedings may be summarised as follows:

Main request (claims as granted) - claim 1

Amendments (Article 100(c) EPC)

While appellant I initially submitted that, the second and fourth paragraph on page 51 of the application as filed together disclosed six different combinations of length and homology, among them the claimed combination, they later argued and maintained during the oral proceedings that these two paragraphs read together on page 51 disclosed two possible combinations, namely a homology of "*at least 95%*" combined with a length of "*up to 40 amino acids*" or a length of "*up to 35 amino acids*".

"*at least 95% homology*"

Page 51, second paragraph, disclosed the homology of "*at least 95%*", which was identical to the homology of

"*95% or more*" as the most preferred embodiment for the following reasons.

Firstly, "[a]*ccording to the opposition division for the skilled person in the field of biotechnology when considering a list of more preferred embodiments of increasing percentages of homology it is implicit that 100% homology is the most preferred embodiment*" (see statement of grounds of appeal, point 12).

Secondly, the skilled person would have recognised from the application as a whole that the core of the invention was consensus sequences, not naturally occurring sequences (see page 13, last paragraph; page 14, first full paragraph; page 20, third paragraph; page 50, last paragraph; page 51, first paragraph). The skilled person would therefore clearly have regarded sequences as being more preferred the higher their homology was to the respective reference sequence (here SEQ ID 1).

Thirdly, since 100% homology was already identity, 95% homology would have been understood by the skilled person to be the most preferred homology value disclosed in the application.

"*up to 40 amino acids*"

The fourth paragraph on page 51 disclosed only two upper limits regarding the peptide length, namely 40 amino acids and 35 amino acids. Although the upper limit of 40 amino acids was not the most preferred, it was mentioned as being preferred.

Page 20, third paragraph, of the application disclosed that "*preferably sequences homologous to SEQ ID 1 are*

*embedded within 40 amino acids of influenza A M1 protein, namely within residues **36-75** of an influenza A M1 protein*" (emphasis in the original; see statement of grounds of appeal, point 9.).

They cited decisions T 783/09 and T 607/05 in support of their case.

Auxiliary requests I and II - claim 1

Amendments (Article 123(2) EPC)

The arguments provided for the subject-matter of claim 1 of the main request applied.

Auxiliary requests III and IV - claim 1
Auxiliary requests V and VI A - claim 3
Auxiliary requests VIII and IX - claim 1

Amendments (Article 123(2) EPC)

The subject-matter of the claims represented the combination of the most preferred features and was supported by claim 1 as filed in combination with claim 15 as filed and page 51, first paragraph, which disclosed a homology of "*95% or more*" as the most preferred embodiment.

Claim 15 as filed had to be read as "*consists*" of up to 35 amino acids.

Auxiliary request VII - claim 1

Amendments (Article 123(2) EPC)

The subject-matter of claim 1 was directly and

unambiguously disclosed by claims 1, 12 and 15 in the application as filed, and the case law of decision T 1511/07 did not need to be invoked because no features constituted selections from lists.

"*consisting of up to 35 amino acids*"

Claim 15 in the application as filed specified 35 amino acids as the preferred upper limit of the length of the peptide. The lower limit of claim 15 was not applicable because SEQ ID 1 was 32 amino acids long. This left the upper limit of 35 amino acids. The term "*comprising*" had to be read as "*consisting*".

Although not required, additional support for a preferred upper size limit of the polypeptide of 35 amino acids was also found in the application on page 51, fourth paragraph, where the most preferred length had been disclosed to be "*from 20-35 amino acids*".

"*having 100% homology*"

Claim 15 of the application as filed referred to all previous claims, including claim 12. Claim 12 specified that the homology was "*substantially 100%*". The opposition division correctly concluded that "*substantially 100% always includes 100% per se as implicitly being more preferred over minute deviations from the 100%*" (see the reply to appellant II's statement of grounds of appeal, point 7). Sequence identity was already encompassed within the meaning of claim 12. Furthermore, it was common general knowledge that sequence identity was always more preferred over any sequence deviating from an authentic sequence.

A further basis for 100% homology could be found on

page 51, second paragraph, of the application.

"*SEQ ID 1*"

SEQ ID 1 was most preferred. It was always mentioned first throughout the application as filed. Nothing in the application indicated that SEQ ID 1 was less preferred.

Auxiliary requests X to XIII

Admittance into the proceedings (Article 13(1) RPBA)

These requests were filed in view of the preliminary opinion of the board issued with the summons. They addressed a new issue since the opposition division had concluded that the patent as amended on the basis of auxiliary request VII complied with the EPC requirements, and they were filed at the earliest opportunity.

The wording of the claims was clear. The amendments involved only deletions which did not change the reading of the claims. The claims of auxiliary requests X to XIII no longer recited a maximum length of the polypeptides, instead, the length of each polypeptide was limited by reference to its SEQ ID NO. Accordingly, the earlier claim feature "*no more than 100 amino acids*" was redundant and could be omitted.

Claim 1 of auxiliary requests X and XII specified that each polypeptide had at least 95% homology with the respective SEQ ID NO. The polypeptides were all shorter than 40 amino acids. A polypeptide having 95% homology to such a polypeptide had less than 40 amino acids.

In claim 1 of auxiliary requests XI and XIII, the polypeptides were limited to the exact sequence identity of the respective SEQ ID NOs. The expression "*according to*" was clear - it could only be interpreted to mean the exact sequence.

Auxiliary request XIV - claim 1

Amendments (Article 123(2) EPC)

Claim 1 was based on a combination of claims 1, 7, 12, 15, 17 and 18 as filed. It represented a combination of the most preferred features (see page 51, second paragraph (homology) and fourth paragraph (size)).

Auxiliary request XV - claim 1

Extension of scope of protection (Article 123(3) EPC)

By reciting "*the*", the claimed polypeptides were separate entities in the composition. Claim 1 thus related to a composition comprising the various polypeptides separately (see also page 52, second paragraph, last sentence of the application, and claims 17 and 18 as filed).

Auxiliary requests XVI A and XVI B

Admittance into the proceedings (Article 13(1) RPBA)

The requests aimed to address the issues identified by the board as regards auxiliary request XV. Auxiliary request XVI B was provided in case auxiliary request XV A was considered unclear.

Basis for the subject-matter of claim 1 was provided on

page 52, second paragraph, last sentence of the application.

XII. Appellant II's arguments submitted in writing and during the oral proceedings may be summarised as follows:

Main request (claims as granted) - claim 1

Amendments (Article 100(c) EPC)

The "*at least 95% homology*" feature and the "*up to 40 amino acids*" feature were not disclosed as the most preferred options within their respective lists. Decision T 1551/07 required a clear convergence of the most preferred embodiments.

"at least 95% homology"

There was no indication in the application, either implicit or explicit, that a level of 95% homology was particularly preferred.

On page 51, second paragraph, the homology percentages were disclosed as equal alternatives and "*95% or more*" homology was not disclosed as more preferred than the others.

In the application in question, it was not implicit that 100% homology was the most preferred embodiment. It was clear from the teaching of the application as a whole that the peptides of the invention could comprise consensus or naturally occurring sequences (see page 14, both full paragraphs; page 17, last three lines; page 20, lines 1 to 2 and 8 to 21; claims 1 and 2). There was no clear indication in the application that

peptides having exact identity with the specified consensus sequences were preferred over peptides having naturally occurring sequences. Therefore, it could not be assumed that 100% homology to the consensus sequences was the most preferred option and hence that 100% homology was preferred from the list of homologies on page 51 of the application.

In addition, pages 21 to 50 of the application listed examples of M1, M2, NP and PB1 proteins by reference to their database entries. The fact (see page 51, fourth paragraph, last three lines) that particularly preferred polypeptides consisted of sequences at defined positions in a specific list of proteins, which might differ from the consensus sequences, indicated that 100% homology with consensus sequences (such as SEQ ID 1) was not the most preferred embodiment.

Exact identity was not disclosed as preferred for SEQ ID 1. On page 51, first paragraph, 60% homology with a consensus sequence was disclosed as preferred.

"*up to 40 amino acids*"

On page 51, fourth paragraph, the most preferred length was "*from 25-35 amino acids*". If any upper limit could be viewed as the most preferred in this passage, it would have been 35 amino acids.

Page 20, third paragraph, of the application did not disclose that "*preferably sequences homologous to SEQ ID 1 are embedded within 40 amino acids of influenza M1 protein*".

Auxiliary requests I and II - claim 1

Amendments (Article 123(2) EPC)

The same arguments as for the subject-matter of claim 1 of the main request applied.

Auxiliary requests III and IV - claim 1
Auxiliary requests V and VI A - claim 3
Auxiliary requests VIII and IX - claim 1

Amendments (Article 123(2) EPC)

The claimed subject-matter was not a combination of the most preferred embodiments. An homology of 95% or more was not disclosed as the most preferred embodiment on page 51, second paragraph.

Claim 15 as filed disclosed "*comprising from 15-35 amino acids*" not "*consisting of 15-35 amino acids*".

Auxiliary request VII - claim 1

Amendments (Article 123(2) EPC)

Convergence of features

There was no clearly intended convergence of the features of claim 1 in the application as filed such that the amendments made to claim 1 resulted in a new combination of features not intended when the application was filed.

(i) There was no indication that SEQ ID 1 was preferred over the other sequences

SEQ ID 1 was always mentioned as part of a list together with SEQ IDs 2 to 6. The only particularly preferred M1 polypeptide disclosed in the application as filed was a polypeptide consisting of residues 36 to 75 of the M1 protein (see page 51, fourth paragraph, last three lines, and page 20, third paragraph, line 10 and page 40). However, SEQ ID 1 comprised only amino acids 38 to 69 of the M1 protein.

(ii) There was no reason to assume that 100% homology was the most preferred embodiment in the application as filed.

(iii) The general disclosure of a most preferred upper limit of 35 amino acid on page 51, fourth paragraph, applied to the peptides in general. It was not a disclosure of the most preferred length for a polypeptide comprising SEQ ID 1. The only exemplified peptide comprising SEQ ID 1, P1, comprised M1 influenza A (M1A) amino acids 36 to 75 (see page 67, first paragraph, and page 80, last paragraph), which was thus longer than the most preferred length of 35 amino acids. It was not, therefore, directly and unambiguously derivable from the application as filed that the upper limit of 35 amino acids was the most preferred embodiment with respect to SEQ ID 1.

Basis in the claims of the application as filed

The combination of claims 1, 12 and 15 of the application as filed did not provide basis for the subject-matter of claim 1.

Firstly, there was no dependent claim which recited that the polypeptide was SEQ ID 1.

Secondly, claim 12 recited that the homology was "*substantially 100%*". The opposition division considered that "*substantially 100% also includes 100% per se as implicitly being more preferred over minute deviations from the 100% criterion*" (see statement of grounds of appeal, point 4.28). This was not the case here. There was no clear indication that sequences having exact identity with the specified consensus sequences were preferred to peptides having naturally occurring sequences. Therefore, there was no reason to assume that 100% homology to the consensus sequences was the most preferred option and hence that 100% homology was preferred to "*substantially 100%*".

Thirdly, claim 15 specified a polypeptide "*comprising from 15-35 amino acids*". The opposition division considered that "*comprising*" included "*consisting of*" as implicitly being more preferred (see statement of grounds of appeal, point 4.29). However, while claim 15 encompassed polypeptides consisting of 15 to 35 amino acids, there was no reason to assume that polypeptides consisting of 15 to 35 amino acids were preferred over polypeptides comprising 15 to 35 amino acids in the context of SEQ ID 1 because the only exemplified peptide comprising SEQ ID 1 (P1) was longer than 35 amino acids (see page 67, paragraph 1).

Auxiliary requests X to XIII

Admittance into the proceedings (Article 13(1) RPBA)

These requests should not be admitted into the proceedings. The board's communication did not raise any new issues. The board merely relied on issues which had already been raised by appellant II at the appeal stage, namely in appellant II's statement of grounds of

appeal and appellant II's reply to appellant I's statement of grounds of appeal. The requests could have been filed in reply to appellant II's appeal and were thus filed late.

The requests were *prima facie* not clearly allowable as the claims lacked clarity within the meaning of Article 84 EPC. It was not clear whether the upper limit was implicit in the expression "*a polypeptide having at least 95% homology with SEQ ID 3*" in auxiliary requests X and XII, i.e. whether the polypeptide had the same length as SEQ ID 3 or could also be a longer polypeptide that comprised a sequence that had 95% homology with SEQ ID 3.

Also, the expression "*a polypeptide according to*" in auxiliary requests XI and XIII was unclear. It was not clear whether it meant the exact sequence or also longer sequences in the context of the claim.

Auxiliary request XIV - claim 1

Amendments (Article 123(2) EPC)

The claimed subject-matter resulted from a selection from two lists disclosed on page 51, second and fourth paragraphs.

Auxiliary request XV - claim 1

Extension of scope of protection (Article 123(3) EPC)

It was not clear that the six polypeptides were separate. Claim 1 used the wording "*comprising*". If claim 1 was understood such that all polypeptides SEQ IDs 1 to 6 were comprised in one large polypeptide then

the length of the resulting polypeptide was longer than 100 amino acids. A polypeptide comprising SEQ ID 1, 2 and 5 was longer than 100 amino acids. In the granted claims, 100 amino acids was the maximum length of the polypeptide.

Auxiliary requests XVI A and XVI B

Admittance into the proceedings (Article 13(1) RPBA)

Page 52, second paragraph, last sentence, of the application disclosed "*the composition contains all of SEQ ID 1-6 either each in a separate peptide or several in a smaller number of peptides*". It did not disclose a composition containing exactly SEQ ID 1 to 6. The application disclosed many polypeptides comprising SEQ ID 1 to 6 but not being exactly SEQ ID 1 to 6 (see page 17 and the examples).

XIII. Appellant I requested that the decision under appeal be set aside and that the patent be maintained as granted (main request), i.e. that the opposition be rejected, or, alternatively, that the patent be maintained in amended form on the basis of one of the sets of claims of the following auxiliary requests, in the following order:
auxiliary requests I or II, filed on 15 November 2013
auxiliary requests III or IV, filed on 19 December 2013
auxiliary request V, filed on 14 March 2014
auxiliary request VI A, filed as auxiliary request VI on 14 March 2014
auxiliary request VII, filed on 14 March 2014 (i.e. amounting to a request that appellant II's appeal be dismissed)
auxiliary requests VIII to IX, filed on 16 September 2015

auxiliary requests X to XIII, filed as auxiliary requests XI to XIV on 20 May 2019
auxiliary request XIV, filed as auxiliary request X on 16 September 2015
auxiliary request XV, XVI A, XVI B, filed during the oral proceedings

XIV. Appellant II requested that the decision under appeal be set aside and that the patent be revoked in its entirety.

Reasons for the Decision

1. The appeals comply with Articles 106 to 108 and Rule 99 EPC and are therefore admissible.

Main request (claims as granted) - claim 1

Amendments (Article 100(c) EPC)

2. The application as filed underlying the patent in suit concerns a polypeptide that is capable of eliciting a cytotoxic T lymphocyte (CTL) immune response in vertebrates against a plurality of influenza strains and/or a plurality of individuals expressing differing HLAs (see page 12, second paragraph). After analysis of all known influenza virus strain sequences across all species, consensus sequences were developed (see page 14, second paragraph). These sequences are referred to in the application as filed by their SEQ ID NOs as SEQ ID 1 to SEQ ID 6 (see page 12, fourth paragraph). The amino acid sequence of SEQ ID 1 (see page 12, fourth paragraph) corresponds to amino acids 38 to 69 of the M1 Influenza A (M1A) consensus sequence

(see page 18, lines 1 to 2).

3. Claim 1 of the main request (see section I) is directed to a polypeptide consisting of up to 40 amino acids that comprises a sequence having at least 95% homology with the consensus sequence SEQ ID 1 and is immunogenic to a plurality of influenza virus strains.

4. The opposition division held that the combination of a homology of "*at least 95%*" and a length of "*up to 40 amino acids*" was not directly and unambiguously derivable from the application as filed (see decision under appeal, Reasons, point 18.1.11).

5. Appellant I contested this finding of the decision under appeal and submitted that the second and fourth paragraph on page 51 of the application as filed provide a basis for the combination of these features.

6. On page 51, second paragraph, the application as filed discloses as regards the percent (%) homology of a first polypeptide sequence to a second polypeptide sequence that "[i]*n the present invention, it is preferred that the polypeptide homology to the defined sequences is 75% or more, 85% or more, 95% or more or 100% (or substantially 100%)".*

7. On page 51, fourth paragraph, the application as filed discloses that "[t]*ypically, the polypeptide comprises between 7 and 100 amino acids, and preferably from 8-50 amino acids. The size should not be so great that useful epitopes suffer from competition with non-protective epitopes in the immune system (for this reason full proteins are not included), nor should the size be so small that only a very narrow range of*

protection is offered. More preferred ranges are from 8-40 amino acids, 15-40 amino acids and 15-35 amino acids. The most preferred length is from 20-35 amino acid residues".

8. It is apparent from the preceding points that the passages relied on by appellant I disclose ranges relating to the homology of a first polypeptide to a second polypeptide as well as ranges relating to the size of the polypeptide, respectively.

9. It is established jurisprudence of the boards of appeal that the standard for assessing compliance with the requirements of Article 123(2) EPC is the standard set out in decision G 2/10 (OJ EPO 2012, 376, see Reasons, point 4.3), also known as the "gold standard". Furthermore, it is established jurisprudence that the content of an application must not be considered a reservoir from which features pertaining to separate sections of the application can be combined to artificially create a particular combination. The combination of an individual range from a first list with another individual range from a second list of ranges and relating to a different feature is not considered disclosed in the application as filed unless there is a clear pointer to such a combination. The indication that ranges are especially preferred is considered a clear indication for the intended parallel convergence of the ranges of the two lists, and the combination of these two especially preferred ranges is considered to satisfy the requirements of Article 123(2) EPC (see Case Law of the Boards of Appeal of the European Patent Office, 8th edition 2016, sections II.E.1 and II.E.1.4.2, and e.g. decision T 1511/07, Reasons, point 2.2).

10. Thus, when assessing whether the claimed subject-matter is disclosed in the application as filed, the relevant question is whether a skilled person would derive — directly and unambiguously, using common general knowledge, and seen objectively and relative to the date of filing — from the whole of the application as filed that the range of "*at least 95% homology*" and the range of "*up to 40 amino acids*" are especially preferred.

"*at least 95% homology*"

11. It is evident from point 6 above that the range of *"95% or more*" homology is not explicitly mentioned as being preferred over the other homology ranges or as being the "most preferred" homology value. Rather, the various ranges of homology are presented as equal alternatives and nothing in the paragraph in question points to *"95% or more*" homology as being particularly preferred.

12. Appellant I submitted that (i) according to the opposition division, it was implicit that 100% homology was the most preferred embodiment; (ii) the gist of the invention entailed consensus sequences and therefore that sequences closer to the consensus sequences were more preferred and (iii) since 100% homology was identity, the skilled person would have understood that 95% was the most preferred homology value.

13. It is established jurisprudence of the boards of appeal that subject-matter implicitly disclosed to the skilled person, using common general knowledge, in the application as filed as a whole relates solely to matter which is not explicitly mentioned but is a clear and unambiguous consequence of what is explicitly

mentioned (*ibid.*, section II.E.1.3.3).

14. On page 51, fourth paragraph, last three lines, the application as filed discloses that "[i]*t is particularly preferred that the polypeptide consists of (or substantially consists of) a sequence selected from the sequences at the positions defined above in the specific list of proteins set out above*".

15. This list referred to on page 51, fourth paragraph, recites the actual sequences of M1, M2, NP and PB1 influenza proteins by reference to their database entries (see page 21, line 3 to page 50, line 34). In the board's opinion, the fact that particularly preferred polypeptides consist of actual proteins with sequences which may differ from the consensus sequences would indicate to the skilled person that identity (100% homology) to a consensus sequences is not the most preferred option in the context of the application in question.

16. The board thus considers that it would not be implicit for the skilled person, when considering the list of increasing percentages of homology on page 51, second paragraph, that 100% homology is the most preferred embodiment for polypeptides being homologous to consensus sequences such as SEQ ID 1.

17. As regards an alleged preference for consensus sequences in the application as filed (see point 12 above), the board notes that on page 13, last paragraph, the application discloses that "[t]*he present inventors have found that the above sequences comprise a plurality of CTL epitopes, which may afford protection against influenza for a wide variety of vertebrates in a population*" and further that "*the*

epitopes within these sequences that provide protection are highly likely to be present in unchanged form in new strains".

18. On page 14, first full paragraph, the application as filed discloses "[t]*he sequences are thus consensus sequences developed from the above analysis. Despite being consensus sequences, the sequences in some cases correspond exactly to natural sequences in some of the known influenza virus strains*" and "[i]*t will be apparent to the skilled person that the invention extends not only to the consensus sequences and their epitopes, but also to the corresponding actual sequences in any influenza strains. Thus, sequences with some homology to the consensus sequences are also within the scope of the invention*".

19. On page 20, third paragraph, the application as filed discloses "[t]*hus the specific sequences homologous to SEQ ID 1-6 described above are preferably the ones at the appropriate positions within the following proteins. Similarly, the sequences of the present invention defined by the residue positions within proteins from any influenza strain, namely residues 36-75 of M1 protein (especially influenza A M1), (...) are preferably those within the following specific proteins".*

20. On page 51, first paragraph, the application as filed discloses as regards the homology with the consensus sequences that in "*further preferred embodiments the polypeptide may comprise one or more sequences as described above and having at least 60% homology with a consensus sequence over known human influenza virus strains*". A similar disclosure is found on page 50, last paragraph, and on page 17, last three lines, of

the application.

21. In the board's opinion, none of the passages relied on by appellant I (see points 17 to 20) indicate explicitly that consensus sequences are preferred over natural sequences or that polypeptides having identical sequences with consensus sequences are preferred over naturally occurring sequences. Indeed, as set out above, natural sequences are explicitly disclosed as being preferred (see points 14 and 15), and according to page 51, first paragraph, of the application, at least 60% homology with a consensus sequence - not 100% - is explicitly disclosed as being preferred (see point 20). Therefore, appellant I's argument that consensus sequences are preferred - and therefore that 100% homology to the consensus sequences is the most preferred option from the list of homologies on page 51 of the application - is not found persuasive.

22. Appellant I's further argument that the skilled person would have known that if the homology reached 100%, the polypeptide would be identical to the reference sequence and that therefore within the homology values given in the application, clearly 95% homology would have been understood as the most preferred homology value consequently also fails.

23. The board concludes from the above that the application as filed does not disclose the homology range *"of 95% or more*" as the most preferred over any other homology range in the context of a polypeptide being homologous to a consensus sequence such as SEQ ID 1.

"*up to 40 amino acids*"

24. It is evident from point 7 above that the most preferred upper length of a polypeptide is explicitly disclosed to be 35 amino acids and not 40 amino acids.

25. As regards appellant I's reliance on page 20, third paragraph, this passage does not disclose (see point 19 above) that "*preferably sequences homologous to SEQ ID 1 are embedded within 40 amino acids of influenza M1 protein, namely within residues 36-75 of an influenza A M1 protein*" as alleged by appellant I (see section XI). Rather, it discloses (i) sequences that are homologous to SEQ ID 1 and (ii) sequences defined by residue positions within specific proteins.

26. The board concludes that the application as filed does not disclose the length range "*up to 40 amino acids*" as most preferred over any other length range.

27. The board considers that the findings in decisions T 783/09 and T 607/05 are not applicable to this case. In decision T 783/09 (see Reasons, points 5.7 to 6.2), the reference to particularly preferred combinations of features was explicitly disclosed in the application as filed, resulting in a list of 44 qualitatively equal elements, of which 41 could be deleted. In decision T 607/05 (see Reasons, point 10), the combination of features was allowed because they were considered not to be isolated single embodiments selected from a list of alternatives. As pointed out above (see points 11 to 23), in this case none of the homology percentages is characterised as being preferred, let alone as being the most preferred, and 95% is selected from a list of alternative homology values.

28. The board concludes from the above that the subject-matter of claim 1 which results from the combination of the features "*at least 95% homology*" and "*up to 40 amino acids*" – neither of which is disclosed in the application as filed as especially preferred – and the further features recited in claim 1 defines a new subgroup of polypeptides not directly and unambiguously disclosed in the application as filed. Thus, this subject-matter extends beyond the content of the application as filed. Therefore, the ground for opposition under Article 100(c) EPC prejudices the maintenance of the patent as granted.

Auxiliary requests I and II

Amendments (Article 123(2) EPC) – claim 1

29. These claims are identical to claim 1 of the main request (see section IV) and the reasoning set out above for the subject-matter of claim 1 of the main request thus applies in the same manner. This was not disputed by appellant I.

30. The subject-matter of claim 1 of auxiliary requests I and II thus extends beyond the content of the application as filed. Therefore, the requirements of Article 123(2) EPC are not fulfilled.

Auxiliary requests III, IV – claim 1
Auxiliary requests V and VI A – claim 3
Auxiliary requests VIII and IX – claim 1

Amendments (Article 123(2) EPC)

31. The subject-matter of these claims comprises a combination of the "*at least 95%*" homology *feature with*

the "*consisting of up to 35 amino acids*" length feature (see sections IV and VII).

32. For all these claims, appellant I submitted that the subject-matter resulted from a combination of the most preferred features based on claims 1 and 15 of the application as filed and page 51, second paragraph, of the application, which disclosed that a percentage of *"at least 95%"* homology was the most preferred value.

33. In the board's judgement, appellant I's argument fails already because a percentage *"of 95% or more" homology* is not disclosed as the most preferred range of homology in the application as filed for a polypeptide homologous to a consensus sequence such as SEQ ID 1 (see points 11 to 23 above).

34. Whether or not claim 15 of the application as filed provides a basis for the "*consisting of up to 35 amino acids*" length feature need therefore not be considered (see, however, points 44 to 49 below).

35. The subject-matter of claim 1 of auxiliary requests III, IV, VIII and IX and the subject-matter of claim 3 of auxiliary requests V and VI A comprise subject-matter which extends beyond the content of the application as filed. Therefore, the requirements of Article 123(2) EPC are not fulfilled.

Auxiliary request VII - claim 1

Amendments (Article 123(2) EPC)

36. The claim is directed to a polypeptide consisting of up to 35 amino acids that comprises a sequence having at least 100% homology with SEQ ID 1 and is immunogenic to

a plurality of influenza virus strains.

37. The opposition division held that claim 1 fulfilled the requirements of Article 123(2) EPC because it considered (i) that both the 100% homology and the 35 amino acid limit were disclosed on page 51 in the application as filed as the most preferred embodiments of the list of homologies and the list of upper limits of the peptide length, respectively. Moreover, it (ii) held that the combination of claims 1, 12 and 15 of the application as filed provided explicit basis for the subject-matter of claim 1 (see decision under appeal, Reasons, points 33.1 to 33.6).

38. Appellant II disputes that (i) there is any clearly intended convergence of the features of claim 1 in the application as filed and (ii) that the claims as filed disclose the subject-matter of claim 1.

(i) Basis in the description as filed

39. The application as filed discloses on page 51, fourth paragraph, that "[t]*he most preferred length is from 20-35 amino acid residues".*

40. The board notes that SEQ ID 1 is not mentioned in this paragraph (see point 6 above). The skilled person reading the fourth paragraph on page 51 of the application as filed at the filing date would have also been aware that the only exemplified peptide comprising SEQ ID 1, the P1 peptide, was defined as amino acids 36 to 75 of the M1A protein and was thus longer than 35 amino acids (see page 67, first paragraph, and page 80, last paragraph).

41. It is not, therefore, in the board's opinion, directly and unambiguously derivable from the application as filed on page 51, fourth paragraph, that the upper limit of 35 amino acids is the most preferred embodiment with respect to a polypeptide comprising SEQ ID 1.

42. As set out above, the application as filed does not disclose "*100% homology*" as the most preferred embodiment in the list of homologies on page 51, second paragraph (see points 11 to 22), either.

43. The board therefore agrees with appellant II that there is no clearly intended convergence of the features of claim 1 of auxiliary request VII in the description as filed.

(ii) Basis in the claims of the application as filed

"consisting of up to 35 amino acids"

44. Claim 15 of the application as filed is directed to "*a polypeptide according to any preceding claim comprising from 15-35 amino acid residues*".

45. The opposition division considered that "*comprising*" included "*consisting of*" as implicitly being more preferred and thus claim 15 as providing the basis for the peptide "*consisting of up to 35 amino acids*" (see decision under appeal, Reasons, point 33.6).

46. The board does not concur with the opposition division's view. Whether the skilled person would construe the term "*comprising*" as encompassing "*consisting of*" depends on the context in which the

term is disclosed.

47. In the context of SEQ ID 1, the skilled person would be aware that (i) the sequence of SEQ ID 1 corresponds to amino acids 38 to 69 of the M1A consensus sequence and consists of 32 amino acids and that (ii) the only exemplified peptide comprising SEQ ID 1, the P1 peptide, is defined as amino acids 36 to 75 of the M1A protein (see page 67, first paragraph, and page 80, last paragraph) and is thus longer than 35 amino acids.

48. Therefore, a polypeptide comprising SEQ ID 1 and consisting of 35 amino acids is not disclosed in the application as filed, while a polypeptide comprising SEQ ID 1 and comprising 35 amino acids is disclosed in the application as filed. Therefore, in the board's opinion, the skilled person would not construe the term "*comprising*" in claim 15 of the application as filed to mean "*consisting of*" in the context of a polypeptide comprising a sequence having at least 60% homology with SEQ ID 1 as defined in claim 1 of the application as filed.

"*at least 100% homology with SEQ ID 1*"

49. Claim 12 of the application as filed is directed to "*a polypeptide according to any preceding claim, wherein the homology is substantially 100%*".

50. The opposition division considered that "*substantially 100% also includes 100% per se as implicitly being more preferred over minute deviations from the 100% criterion*" (see decision under appeal, Reasons, point 33.6).

51. The board does not concur with the opposition division's view and refers to points 13 to 21 above. In the context of this application, the explicit teaching in the application as filed does not support the opposition division's conclusion that, implicitly, identity to the consensus sequences is preferred over minute deviations from the consensus sequences.

52. In summary, neither the description nor the claims of the application as filed - as advanced by appellant I - provide a basis for the combination of the "*up 35 amino acids*" feature and the "*at least 100% homology*" feature with SEQ ID 1. Whether SEQ ID 1 is disclosed in the application as filed as the most preferred sequence thus need not be decided.

53. The subject-matter of claim 1 of auxiliary request VII comprises subject-matter which extends beyond the content of the application as filed. Therefore, the requirements of Article 123(2) EPC are not fulfilled.

Auxiliary requests X to XIII

Admittance into the proceedings (Article 13(1) RPBA)

54. These requests were filed as auxiliary requests XI to XIV in response to the board's communication (see section X). Appellant I submitted that these requests should be admitted into the proceedings because they addressed a new objection. Appellant I argued in their defence that they could not have foreseen that the board would find that claim 1 of auxiliary request VII failed the requirements of Article 123(2) EPC since the opposition division had concluded that the patent as amended on the basis of this request complied with the

requirements of the EPC.

55. Appellant II requested that these auxiliary requests not be admitted into the appeal proceedings.

56. The board observes that the objection at issue here, which the amendments made in the claims of auxiliary requests X to XIII aimed to address, was not a new objection but one that had been raised by appellant II in their statement of grounds of appeal (see section VI). Appellant I was thus confronted with this objection upon receipt of appellant II's statement of grounds of appeal.

57. The board's indication that it was inclined to agree with the appellant II's objection (see section IX) could thus not justify the admittance of requests which objectively could and should have been filed earlier during the appeal proceedings.

58. The board further considers that it was not immediately apparent that the suggested amendments resulted in clearly allowable claim requests that did not give rise to new objections at least as regards the requirements of Article 84 EPC for the following reasons.

59. Claim 1 of auxiliary requests X and XII differed from claim 4 of the main request in that the upper length defining the polypeptide had been removed (see section X). It was thus unclear whether polypeptides that were longer than 100 amino acids also fell within the scope of the claims.

60. Claim 1 of auxiliary requests XI and XIII differed from claim 4 of the main request in that the polypeptides of the compositions were defined to be polypeptides

"*according to*", for example, SEQ ID 1. It was unclear whether the newly introduced term "*according to*" defining the polypeptide meant exactly the same sequence or would allow for some deviation from the exact sequence.

61. Therefore, admitting the requests at this stage of the proceedings would not be in keeping with the principle of procedural economy.

62. Accordingly, the board, exercising its discretion pursuant to Article 13(1) RPBA, decided not to admit auxiliary requests X to XIII into the appeal proceedings.

Auxiliary request XIV – claim 1

Amendments (Article 123(2) EPC)

63. The claim (see section VI) is directed to a polypeptide composition, comprising a polypeptide comprising a sequence having at least 100% homology with SEQ ID 1 in which this polypeptide consists of up to 35 amino acids.

64. Appellant I relied on claims 1, 7, 12, 15, 17 and 18, and page 51, second paragraph (homology) and fourth paragraph (size), as providing a basis for the claimed subject-matter.

65. The board considers that the reasoning set out above for the subject-matter of claim 1 of auxiliary request VII (see points 39 to 52) applies *mutatis mutandis*.

66. Claim 1 of auxiliary request XIV comprises subject-matter which extends beyond the content of the application as filed. Therefore, the requirements of Article 123(2) EPC are not fulfilled.

Auxiliary request XV - claim 1

Extension of scope of protection (Article 123(3) EPC)

67. Claim 1 of auxiliary request XV (see section X) relates to a polypeptide composition comprising the polypeptides SEQ ID 1 to SEQ ID 6 while claim 4 as granted relates to a composition comprising polypeptides which have no more than 100 amino acids (see section I).

68. The length of the polypeptide is not explicitly indicated in claim 1 of auxiliary request XV. In the board's judgement, claim 1 cannot be construed such that it exclusively describes a composition comprising polypeptides of SEQ ID 1 to 6 each in separate form as advocated by appellant I. The patent discloses that the composition can contain several of the sequences, e.g. 3 combined in a larger peptide (see paragraph [0046], corresponding to page 52, second paragraph, of the application as filed). A peptide containing, for example, SEQ ID 1, 2 and 5 is longer than 100 amino acids. Therefore, claim 1 of auxiliary request XV covers compositions not covered by the claims as granted.

69. Thus, claim 1 of auxiliary request XV extends the scope of protection conferred by the claims beyond the protection conferred by the claims of the granted patent. Therefore, the requirements of

Article 123(3) EPC are not fulfilled.

Auxiliary requests XVI A and XVI B

Admittance into the proceedings - Article 13(1) RPBA

70. These requests were filed during the oral proceedings (see section X) after the board expressed its view that claim 1 of auxiliary request XV extended the scope of protection and thus at a very late stage in the appeal proceedings.

71. The board considered that it was not immediately apparent that the suggested amendments resulted in a clearly allowable claim request that did not give rise to new objections at least as regards the requirements of Article 123(2) EPC for the following reasons.

72. Claim 1 of auxiliary request XVI A differs from claim 1 of auxiliary request XV in that the expression "*the following polypeptides*" in lines 1 to 2 had been amended to read "*the following separate polypeptides*".

73. Appellant I relied on page 52, second paragraph, last sentence of the application as filed as providing a basis for the claimed subject-matter.

74. The application as filed discloses on page 52, second paragraph, last sentence, that "[i]*t is particularly preferred that the composition contains all of the sequences of SEQ ID 1-6 either each in a separate peptide or several in a smaller number of peptides (e.g. 3 combined in one larger peptide and the other three 3* [sic] *in another larger peptide, etc.)*".

75. However, it is apparent from the preceding paragraph that this passage does not disclose that each separate peptide consists exactly of SEQ ID 1 to 6. The application discloses many polypeptides comprising SEQ ID 1 to 6 but not being exactly SEQ ID 1 to 6 (see page 17, second paragraph). Also, in example 1, SEQ ID 1 is comprised within a larger peptide not being exactly SEQ ID 1. The subject-matter of claim 1 of auxiliary request XVI A thus appeared not to comply with the requirements of Article 123(2) EPC and therefore not to be *prima facie* clearly allowable.

76. The amendments carried out in auxiliary request XVI B were meant to address any potential clarity problems of auxiliary request XVI A and did not overcome the problem identified above for claim 1 of auxiliary request XVI A. Therefore, the subject-matter of claim 1 of auxiliary request XVI B also appeared not to comply with the requirements of Article 123(2) EPC and therefore not to be *prima facie* clearly allowable.

77. Thus, admitting these requests at this stage of the proceedings would not be in keeping with the principle of procedural economy.

78. Accordingly, the board, exercising its discretion pursuant to Article 13(1) RPBA, decided not to admit auxiliary requests XVI A and XVI B into the appeal proceedings.

Conclusion

79. All claim requests forming part of or having been admitted into the appeal proceedings, respectively, fail the requirements of Article 123(2) or (3) EPC. Accordingly, the patent cannot be maintained in amended

form on the basis of any of these requests. Therefore, in the absence of another allowable claim request, the patent has to be revoked.

Order

For these reasons it is decided that:

1. The decision under appeal is set aside.

2. The patent is revoked.

The Registrar: The Chair:

I. Aperribay M. Blasi

Decision electronically authenticated