

The opinion in support of the decision being entered today
is *not* binding precedent of the Board.

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS
AND INTERFERENCES

Ex parte MICHAEL C. PITMAN, BLAKE G. FITCH,
HANS W. HORN, WOLFGANG HUBER,
JULIA E. RICE, and WILLIAM C. SWOPE

Appeal 2007-0537
Application 10/102,902
Technology Center 1600

Decided: July 23, 2007

Before DONALD E. ADAMS, ERIC GRIMES, and NANCY J. LINCK,
Administrative Patent Judges.

LINCK, *Administrative Patent Judge.*

DECISION ON APPEAL

This is a 35 U.S.C. § 134 appeal in the above-referenced case.¹
We have jurisdiction under 35 U.S.C. § 6(b). We affirm.

¹ The application was filed March 22, 2002. The real party in interest is the assignee, International Business Machines Corporation.

STATEMENT OF THE CASE

The field of the invention is field-based similarity search systems, i.e., three dimensional searching, and methods used to “identify molecules that have a similar function to a molecule known to be active towards a biological target or that elicits a biological response of interest.”

(Specification (hereafter “Spec.”) 1-2, 11.) “Several conventional superposition methods . . . are field-based.” (*Id.* at 5.)

Appellants’ presently claimed system is designed “based on a similarity of fragment pair features” between a “query molecule” and a “candidate molecule” using “context-adaptive scaling” of fragment pair “descriptors” to “tune the weights of the various feature components based on examples relevant to the particular context under investigation.” (*Id.* at 6-7, 17.)

Representative claim 1 reads:

1. A field-based similarity search system, comprising:
 - a database for storing data pertaining to at least one candidate molecule;
 - an input device for inputting data pertaining to a query molecule;
 - a processor which identifies a candidate molecule which is similar to said query molecule by:
 - identifying features of a candidate molecule fragment pair which correspond to features of a query molecule fragment pair; and
 - aligning said candidate molecule fragment pair to said query molecule based on said corresponding features; and
 - a display device for displaying an output of said processor,

wherein said *features of said candidate molecule fragment pair and query molecule fragment pair comprise descriptors, said processor performing context-adaptive scaling of said descriptors.*

(Claim 1 (emphasis added to the disputed clause) (App. Br. 11; Reply Br. 1-4).)

The Examiner has rejected all the pending claims, claims 1-27, under 35 U.S.C. § 103(a) as follows:

Claims 1-4, 6-10, 12-19, 21-23, and 25-26 over Cornilescu et al., *Protein backbone angle restraints from searching a database for chemical shift and sequence homology*, 13 J. Biomolecular NMR 289-302 (1999) (hereafter “Cornilescu”), and Gilhuijs et al., U.S. Patent No. 6,317,617 (issued Nov. 13, 2001) (hereafter “Gilhuijs”);

Claims 1, 11, 14, 20, 24, and 27 over Cornilescu, Gilhuijs, and Atta-ur-Rahman, *Nuclear Magnetic Resonance: Basic Principles* 8-10 (Springer-Verlag 1986) (hereafter “Atta-ur-Rahman”); and

Claim 5 over Cornilescu, Gilhuijs, and Aude et al., *Applications of pyramidal clustering method to biological objects*, 23 Computers & Chemistry 303-15 (1999).

PATENTABILITY UNDER § 103(a)

Claim 1

The patentability of claim 1 turns on the meaning of the claim phrase “features of said candidate molecule fragment pair and query molecule fragment pair comprise descriptors, said processor performing context-adaptive scaling of said descriptors.” More specifically, it turns on the meaning of “features,” “fragment pair,” “context-adaptive scaling,” and

“descriptors.” These are the specific terms Appellants argue are not taught or suggested by the cited prior art. (App. Br. 12-18; Reply Br. 1-4.)

The Examiner primarily relies upon Cornilescu. Cornilescu describes using a computer system and program (TALOS) to compare secondary chemical shift and sequence data for triplets of amino acid residues of unknown proteins with such data for triplets of known proteins. TALOS was developed to search their database for “strings of residues with chemical shift and residue type homology” (Cornilescu 289 (abstract)). Cornilescu’s system was designed based on the recognition that “[c]hemical shifts of backbone atoms in proteins are exquisitely sensitive to local conformation, and homologous proteins show quite similar patterns of secondary chemical shifts.” (*Id.*)

The Examiner equates “triplets of amino acid residues” with “fragment pairs” (Answer 7, 16-18), “chemical shifts” with “features of a fragment pair” or “descriptors” (Answer 17, 19, 20), and “k-values scaling” of the chemical shifts with “context-adaptive scaling” (Answer 19-20).

Thus, the key issue before us is, do the disputed claim terms “fragment pair,” “features” of a fragment pair (or “descriptors”), and “context-adaptive scaling” in claim 1 encompass Cornilescu’s “triplets of amino acid residues,” “chemical shifts,” and “k-values scaling,” respectively?

Findings of Fact

Claim Interpretation

1. The Specification defines “fragment pair” as follows: “A fragment pair consists of two neighboring fragments connected by a rotatable bond at a specific dihedral angle.” (Spec. 21; *see also* Answer 7.) “By this

definition, a protein qualifies as a series of molecular fragment pairs, where each amino acid is separated by a peptide dihedral.” (Answer 7.) Likewise the term “fragment pair” would include adjacent amino acid residues, or triplets, connected by a peptide bond. (*See* Answer 7, 16-18 (A “‘triplet’ constitutes three consecutive amino acid residues in which a center residue [is] connected to two out[er] residues, each ‘outer’ residue and the center residue forming a fragment pair.”).)

2. “Features” of a fragment pair are not defined in the Specification. Thus, we define this term to simply mean “characteristic[s]” (Webster’s Ninth New Collegiate Dictionary (hereafter “Webster’s) 454 (Merriam-Webster Inc. 1990), or, in pattern recognition, “individual measurable properties” (*Wikipedia, The Free Encyclopedia*, “Feature” (retrieved June 28, 2007)),² of the fragment pair. Given this definition, the term “features” includes chemical shifts and amino acid sequences.

3. “Descriptor” is not defined in the Specification. Thus, we define it to mean “something used to identify an item . . . esp. in an information retrieval system.” Webster’s 343. A mathematical representation of a feature, such as a chemical shift or amino acid sequence, would be a “descriptor” under this definition.

4. Appellants equate the terms “descriptor” and “feature,” consistent with our definitions of these two terms. (Spec. 32 (“the CoMMA descriptor X_k . . . may be called a *feature*”) (emphasis in original); *see also* claim 1 (“wherein said features . . . comprise descriptors”).)

² Available at <http://en.wikipedia.org/w/index.php?title=Feature&oldid=130983553>).

5. “Context-adaptive scaling” (claim 1) and “context-adaptive descriptor scaling” (claim 13) are not defined in the Specification. Thus, we define these terms to mean weighting the descriptors (or features) in view of their surroundings. (*See* Webster’s 283 (“context” means “the interrelated conditions in which something exists”) & 55 (“adaptation,” the noun for the adjective “adaptive,” means “adjustment to environmental conditions”).)

6. Our definition of “context-adaptive scaling” and “context-adaptive descriptor scaling” comports with Appellants’ statement that such scaling “helps to allow the user to tune the weights of the various feature components [or descriptors] based on examples relevant to the particular context under investigation.” (Spec. 17.)

7. Appellants have not limited “context-adaptive scaling” to any particular method of weighting the descriptors, or features, in view of their surroundings (*see, e.g.*, claim 1), and thus the term includes “k-values scaling,” used to give weight to a chemical environment (*see* FF 18).

8. Appellants’ extensive use of “may” throughout their Specification does not limit the scope of their claims, i.e., does not require us to narrow our claim interpretation (*see, e.g.*, Spec. *passim*); neither do their “preferred embodiments.” (*See* Spec. 76 (“the invention can be practiced with modification”).)

The Prior Art

9. Cornilescu teaches: “Chemical shifts of backbone atoms in proteins are exquisitely sensitive to local conformation, and homologous proteins show quite similar patterns of secondary chemical shifts. The inverse of this relation is used to search a database for triplets of adjacent residues with secondary chemical shifts and sequence similarity which

provide the best match to the query triplet of interest.” (Cornilescu 289 (Abstract).)

10. Cornilescu uses this information to identify protein backbone angle restraints through sequence homology and similar patterns of secondary chemical shifts for triplets of adjacent residues (i.e., shifts related to secondary, 3-dimensional structure). (E.g, Cornilescu 290 (“if a string of adjacent amino acids shows high similarity in secondary chemical shifts with a string of amino acids in a database, the central residues in the two strings are likely to have similar backbone torsion angles”); *see also* Answer 16.).

11. Cornilescu’s “computer program TALOS was developed to search for strings of residues with chemical shift and residue type homology. The relative importance of the weighting factors attached to the secondary chemical shifts of the five types of resonances relative to that of sequence similarity was optimized empirically.” (Cornilescu 289 (Abstract), *quoted in* Answer 7.)

12. Cornilescu also teaches an alignment step. (Cornilescu 289 (Abstract) (“Tests carried out for proteins of known structure indicate that the root-mean-square difference (rmsd) between the output of TALOS and the X-ray derived backbone angles is about 15 degrees.”), *quoted in* Answer 7. *See also* Cornilescu 293 (Figure 1).)

13. Cornilescu would have suggested to the skilled artisan the use of such data to identify homologous proteins. (Cornilescu 289 (Abstract); *see also* 293 (Fig. 1).)

14. Based on our definition of “fragment pair,” Cornilescu’s amino acid residues qualify as a “series of molecular fragment pairs, where each amino acid is separated by a peptide dihedral.” (Answer 7.)

15. Cornilescu searches “a database for triplets of adjacent residues with secondary chemical shifts and sequence similarity which provide the best match to the query triplet of interest.” (Cornilescu 289 (Abstract); *see also* Answer 16.)

16. Thus, Cornilescu identifies secondary chemical shifts and sequence similarity between triplets of adjacent residues and the query triplet of interest, i.e., “features of a candidate molecule fragment pair which correspond to features of a query molecule fragment pair.” (See claim 1.)

17. Cornilescu’s “database contains . . . chemical shifts for 20 proteins for which a high resolution X-ray structure is available” and is searched “for strings of residues with chemical shift and residue type homology.” (Cornilescu 289 (Abstract); *see also* Answer 6-7.)

18. Cornilescu optimizes empirically the “relative importance of the weighting factors attached to the secondary chemical shifts of the five types of resonances relative to that of sequence similarity.” (*Id.* (citing Table 2 for a listing of such weighting factors, “by which the chemical shift data are scaled”); *see also* Answer 7, 19-20.) Thus, Cornilescu uses “context-adaptive scaling” to give weight to the chemical environment.

19. Gilhuijs, like Cornilescu, relates to “studies of magnetic resonance of biological materials” and discloses standard computer hardware, including means to “display and input results” (Answer 11 (citing Gilhuijs’s Fig. 3).) Thus Gilhuijs’s teachings would have been relevant to further utilizing Cornilescu’s method on a computer.

20. According to the Specification, “features may be considered generalizations of CoMMA descriptors that characterize local regions of the property field by its local moments.” (Spec. 19; *see also* Answer 12.) “Atta-ur-Rahman shows that chemical shifts of compounds” are features (or descriptors) that “have moment-based aspects to them” and are “invariant under coordinate system transformations.” (Answer 12 (citing Atta-ur-Rahman 8-10).)

21. “Cluster analysis of protein sequences for representing distance data has been commonly used by biologists for a long time” (Aude 303 (cited in Answer 13).)

Additional Findings

22. Field-based similarity search methods are known in the art, as are computer systems and methods employing a “database,” an “input device,” a “processor,” and a “display device.” (Spec. 2-5 (citing pages of prior art systems and methods); *see also* Spec. 74 & Fig. 27 (illustrating conventional computer system components).)

23. Numerous methods of molecular superposition, i.e., aligning molecular structures also are known in the art. (*See* Spec. 2, 48-49; Cornilescu 293 (Fig. 1 showing detection of “missing alignments”).)

24. With respect to context-adaptive scaling techniques, “there is a vast repertoire of methods from the disciplines of classification and pattern recognition” to provide such scaling, including “Fisher’s linear discriminant analysis”. (Spec. 34.)

25. The skilled artisan, interested in searching with a computer for homologous proteins, would have had a reason to utilize the teachings of Cornilescu to do so in view of Cornilescu’s express teaching that

“homologous proteins show quite similar patterns of secondary chemical shifts.” (FF 9; see also FFs 10-17.)

26. The skilled artisan, applying Cornilescu’s teachings to search for homologous proteins, would have had a reasonable expectation of identifying such proteins. (*See* FF 9-17.)

27. The skilled artisan, faced with the problem of further implementing Cornilescu’s method on a computer, including the use of NMR to study chemical shifts, would have had reason to look to the general teachings in the prior art, such as those of Gilhuijs.

28. Appellants’ contested and undefined terms “features” and “descriptor,” and “context-adaptive scaling” are sufficiently broad to include Cornilescu’s “chemical shifts” and “amino acid sequences,” and “k-values scaling,” respectively. (FFs 2-7, 9-11, 17-18.)

29. In addition, their broad definition of “fragment pairs” includes Cornilescu’s amino acid residues separated by a dihedral bond. (FFs 10-11, 14-17.)

DISCUSSION

The § 103 Rejection Based on Cornilescu and Gilhuijs

Our decision whether to affirm the rejection of claims 1-4, 6-10, 12-19, 21-23, and 25-26 turns primarily on claim interpretation, more specifically the meaning of the terms “features,” “fragment pair,” “descriptor,” and “context-adaptive scaling.” Except when applicants expressly define their claim terms, “claims are given their broadest reasonable interpretation consistent with the specification. [This] proposition ‘serves the public interest by reducing the possibility that claims, finally allowed, will be given broader scope than is justified,’ . . . and it is

not unfair to applicants, because ‘before a patent is granted the claims are readily amended as part of the examination process’” *In re Hyatt*, 211 F.3d 1367, 1372, 54 USPQ2d 1664, 1667 (Fed. Cir. 2000) (internal citations omitted).

Claim 1

Each of the disputed terms in claim 1, “fragment pair,” “features,” “descriptor,” and “context-adaptive scaling” are taught or suggested by Cornilescu. (See FFs 2-7, 9-11, 14-18, 28 & 29.) While we recognize Cornilescu focuses on identifying similar backbone torsion angles between amino acid residues rather than identifying molecules with similar structures, Cornilescu’s teachings would have suggested to the skilled artisan the use of such data to obtain homologous molecules. (See FFs 9-13.)

Given the scope of the disputed terms, Cornilescu discloses or suggests all of the limitations of claim 1, including the computer hardware (exemplified by Gilhuijs). (FFs 1-19, 22-29.) More specifically, Cornilescu discloses a database with data (1) “pertaining to at least one candidate molecule” (chemical shift and sequence data for triplets of amino acid residues for 20 fully characterized proteins) and (2) “pertaining to a query molecule” (chemical shift and sequence data for a triplet of amino acid residues for Cornilescu’s protein of unknown structure).

Using a computer program (TALOS), Cornilescu “identifies a candidate molecule,” (one or more proteins of known structure) which is “similar to said query molecule” (Cornilescu’s uncharacterized protein). This is accomplished by: “identifying features of a candidate molecule fragment pair” (chemical shifts and sequences for triplets of amino acid

residues for one or more of the 20 known proteins) “which correspond to features of a query molecule fragment pair” (chemical shifts and sequences for a triplet of amino acids residues for the unknown structure); and “aligning said candidate molecule fragment pair to said query molecule based on said corresponding features” (*see* FF 12 (citing Cornilescu 289 (abstract), 293 (Figure 1) (describing differences resulting from such alignment)); FF 23).

Finally, with respect to the disputed claim language (*see* App. Br. 11; Reply Br. 1-4), Cornilescu’s “features of said candidate molecule fragment pair and query molecule fragment pair comprise descriptors” (mathematical representations of chemical shifts and amino acid sequences for computer analysis), which are weighted using “context-adaptive scaling of said descriptors.” (FFs 1-19, 22-29.)

Appellants argue:

In direct contrast to Cornilescu, the claimed invention recognizes the importance of fragment pairs. Indeed, an important feature of an exemplary aspect of the claimed invention **may** include partitioning a molecule into fragments, and using data regarding two of the fragments (e.g. neighboring fragments connected by a rotatable bond) as a basis for a similarity search.

The Application explains that there **may be** significant benefits to using features of fragment pairs (e.g., neighboring fragments connected by a rotatable bond), as a basis for a similarity search. For example, the Application states that a “key” to the invention is that “*it avoids the need to search every conformation of every molecule and apply a similarity metric to the query at each possible alignment. This is done by using selected features from fragment pairs to align them to the query*” (Application at page 15, line 24-page 16, line 5). Nowhere is this recognized by Cornilescu.

Further . . . the total number of conformations in a molecule **may be** significantly more than the conformations in a fragment pair (Application at page 22, lines 7-20). Thus, the claimed invention recognizes that using fragment pair representation **may** require significantly smaller storage than a brute force enumeration (Application at page 22, lines 20-24). Nowhere is this recognized by Cornileseu.

(Reply Br. 1-2 (bolding added for emphasis).)

Appellants' arguments are unavailing, particularly since they do not focus on the claim language or limit the scope of the present claims. (FF 8; see also the permissive language in the passages quoted above.) In any case, Cornileseu *does* recognize the value of using select features of *adjacent* amino acid residues, i.e., secondary chemical shifts and amino acid sequence. (FFs 10, 11, 14-18.) This technique takes into account the effect of surrounding residues on chemical shifts and "avoids the need to search" every characteristic of the adjacent residues in his database to identify other residues with similar backbone torsion angles.

As found by the Examiner,

chemical shifts of the backbone atoms are functions of the molecular properties of the neighboring amino acids as well as the amino acid itself. . . . Since the values of the chemical shifts change between their values in isolated amino acids to their values in proteins, the search with these modified values of chemical shifts are actually searches of fragment pairs of amino acids and not merely a single residue.

(Answer 17.)

This is not a case in which Appellants invented a new computer, or a new search method, or even a new method of molecular superposition (i.e., alignment). (FFs 22-24.) Instead, Appellants are using systems and techniques well known in the art to identify molecules with similar structure

(also a practice well known in the art). (FF 22.) Thus, Appellants' only arguable *claimed* contribution is the use of "fragment pairs" to simplify identifying similar molecules. Given the teachings of Cornilescu, such "fragment pairs" are in the prior art, at least as Appellants have broadly defined this term. (FFs 1, 9, 10, 29.)

Appellants dispute the combination of Cornilescu and Gilhuijs. (App. Br. 11.) According to Appellants, "these references are directed to different problems and solutions" and are "completely *unrelated*." (*Id.* at 11-12 (emphasis Appellants').)

Gilhuijs is relied upon merely for its teachings of standard "computer hardware used to display and input results." (Answer 11 (citing Fig. 3); *see also* FF 19.) In fact, in our view Gilhuijs is merely an example of many such teachings in the art. (FF 27.) In any case, since both Gilhuijs and Cornilescu relate to "studies of magnetic resonance of biological materials," Gilhuijs's teachings would have been relevant to the skilled artisan utilizing Cornilescu's method on a computer. (FF 19.) Thus, the Examiner appropriately combined these two references.

Based on our findings and those of the Examiner, Cornilescu would have taught or suggested the invention of claim 1 to the skilled artisan. Gilhuijs supplements Cornilescu's teaching by providing an example of well known computer hardware, including input and display means. (FF 19.) Thus, we conclude the invention of claim 1 would have been obvious under § 103(a) based on Cornilescu and Gilhuijs.

Independent Claims 13, 14, 15, and 16³

With respect to independent claims 13, 14, 15, and 16, Appellants simply argue the claimed “features are similar to the features discussed above with respect to claim 1.” (App. Br. 18-21.) In response, we have reconsidered the arguments Appellants made with respect to claim 1, and again conclude they are not convincing for the reasons previously given. (See *supra* pp. 10-14.)

Dependent Claims 2-4, 6-10, 12, 17-19, 21-23, and 25-26

With respect to each of these claims, Appellants merely state that the references do not teach or suggest the additional limitation, recite the limitation, and conclude by stating the Examiner’s position is “flawed as a matter of fact and as a matter of law.” (App. Br. 22-29.) Appellants provide no explanation why this is so with respect to any of these claims.⁴ (*Id.*)

The Examiner found each recited limitation met by the references. (Answer 7-11.) We have considered the Examiner’s findings with respect to these limitations. Lacking any argument by Appellants why the Examiner’s findings are flawed, we agree with the Examiner that the references teach or

³ Claims 13 and 16 do not recite “fragment pair” or “features” of a fragment pair. Thus, the only disputed claim term with respect to these two claims appears to be “context-adaptive descriptor scaling.” As previously found, this term is satisfied by Conilescu’s “k-values scaling.” (See *supra* pp. 11-12.)

⁴ In our view, Appellants have not fully complied with 37 C.F.R. § 41.37(c)(1)(vii) which requires more than recitation of an additional claim limitation. Merely stating the references don’t teach or suggest the limitation, coupled with a statement that the Examiner’s position is “flawed,” is not sufficient. Nevertheless, we have considered each recited limitation, and the Examiner’s findings with respect to each.

suggest the recited limitations of claims 2-4, 6-10, 12, 17-19, 21-23, and 25-26.

The § 103 Rejection Based on Cornilescu, Gilhuijs, and Atta-ur-Rahman

Claims 1, 11, 14, 20, 24, and 27 are rejected based on Cornilescu, Gilhuijs, and Atta-ur-Rahman.

With respect to independent claims 1 and 14, Appellants again argue the references do not teach or suggest the claim limitation “features of said candidate molecule fragment pair and query molecule fragment pair comprise descriptors, said processor performing context-adaptive scaling of said descriptors.” For the reasons previously given, we find this claim language taught or suggested by Cornilescu. Thus, we again conclude these claims would have been obvious over Cornilescu and Gilhuijs alone (*see supra* pp. 11-14). We further conclude they would have been obvious over Cornilescu, Gilhuijs, and Atta-ur-Rahman, finding nothing in Atta-ur-Rahman that teaches away from such a combination.

Appellants rely on a different claim phrase with respect to claims 11, 20, 24, and 27: “wherein a feature in said corresponding features comprises a generalization of a comparative molecular moment analysis (CoMMA) descriptor” (claim 11); “wherein said feature comprises a generalization of a comparative molecular moment analysis (CoMMA) descriptor” (claim 20); “wherein said fragment pair features comprise generalizations of comparative molecular moment analysis (CoMMA) descriptors for said fragment pairs” (claim 24); and “wherein said descriptors comprises a set of local, rotationally invariant, moment-based descriptorw for said candidate molecule” (claim 27). (App. Br. 31-33.)

In each case, following recitation of the claim phrase, Appellants argue: The “Examiner’s position is flawed as a matter of fact and as a matter of law. Specifically, neither Cornilescu, nor Gilhuijs, nor Atta-ur-Rahman, nor any alleged combination thereof teaches or suggests this feature [or] each and every element of the claimed invention as recited in [the subject] claim.” (App. Br. 31-34.) Appellants provide no explanation why this is so with respect to any of these claims.⁵ (*Id.*)

The Examiner found each recited limitation met by the references. (Answer 11-12 (referencing Answer 7-11); *see also* FF 20.) We have considered the Examiner’s findings with respect to the recited limitations. Lacking any argument by Appellants why the Examiner’s findings are flawed, we agree with the Examiner that the references would have taught or suggested the recited limitations of claims 1, 11, 14, 20, 24, and 27 to the skilled artisan and would have taught or suggested the subject matter of the claims as a whole.

⁵ Again, in our view, Appellants have not fully complied with 37 C.F.R. § 41.37(c)(1)(vii) which requires more than recitation of an additional claim limitation. Merely stating the references don’t teach or suggest the limitation or all the elements of the claim, coupled with a statement that the Examiner’s position is “flawed,” is not sufficient. Nevertheless, we have considered each recited limitation, and the Examiner’s findings with respect to each.

The Rejection of Claim 5

Claim 5 is rejected under § 103 based on Cornilescu, Gilhuijs, and Aude. “Claim 5 is identical to claim 1 with the additional limitation of cluster analysis to determine molecular structure.” (Answer 13.) Aude teaches that cluster analysis of protein sequences “has been commonly used by biologists for a long time.” (FF 21; Answer 13.) Appellants do not respond to this finding. Rather, they state Aude “merely discloses an application of a pyramidal clustering algorithm for biological objects” without providing any reason why the skilled artisan would not have utilized clustering analysis to determine molecular structure. (App. Br. 35.)

Appellants argue that Aude does not address the deficiencies of Cornilescu and Gilhuijs with respect to the claim limitations that appear in both claims 1 and 5. As we previously found Cornilescu and Gilhuijs teach or suggest these claim limitations, it is unnecessary for us to address this argument again.

Appellants also argue Aude would not have been combined with Cornilescu and Gilhuijs, but do not give any reason. (App. Br. 34.) We agree with the Examiner that the combination is an appropriate one. Thus, based on our findings and those of the Examiner, we conclude the invention of claim 5 would have been obvious in view of the cited references.

CONCLUSION

In summary, given the teachings of the cited references and Appellants’ failure to limit the scope of their claims, we affirm the § 103(a) rejections of all the pending claims.

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No time period for taking any subsequent action in connection with this appeal may be extended under 37 C.F.R. § 1.136(a)(1)(iv)(2006).

AFFIRMED

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MCGINN INTELLECTUAL PROPERTY LAW GROUP, PLLC
8321 OLD COURTHOUSE ROAD
SUITE 200
VIENNA, VA 22182-3817