

**UNITED STATES PATENT AND TRADEMARK OFFICE**

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**BEFORE THE BOARD OF PATENT APPEALS  
AND INTERFERENCES**

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*Ex parte* PAUL BARTEL

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Appeal 2008-2711  
Application 10/122,573  
Technology Center 1600

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Decided: July 2, 2008

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Before DONALD E. ADAMS, DEMETRA J. MILLS, and JEFFREY N.  
FREDMAN, *Administrative Patent Judges*.

FREDMAN, *Administrative Patent Judge*.

**DECISION ON APPEAL**

This is an appeal under 35 U.S.C. § 134 involving claims to an isolated protein complex, which the Examiner has rejected as lacking an adequate description in the Specification, as failing to enable the full scope of the claims and as inherently anticipated. We have jurisdiction under 35 U.S.C. § 6(b). We affirm.

*Background*

“In contrast with the traditional view of protein function, which focuses on the action of a single protein molecule, a modern expanded view of protein function defines a protein as an element in an interaction network” (Spec. 3). The Specification discloses that by “identifying interacting proteins, a better understanding of disease pathways and the cellular processes that result in diseases may be achieved, and important regulators and potential drug targets in disease pathways can be identified (Spec. 4). The Specification separately notes that the “yeast two-hybrid system can be employed to identify proteins that interact with a specific known protein involved in a disease pathway” (Spec. 6).

Appellants teach that the “apoptosis regulator Bcl-XL (“BCL-XL”) interacts with translationally-controlled tumor protein 1 (“TCTP”, also known as IgE-dependent histamine-releasing factor or HRF)” (Spec. 6).

*Statement of the Case*

*The Claims*

Claims 39-48 are on appeal. We will focus on claim 39 which is representative and reads as follows:

39. An isolated protein complex comprising a first protein interacting with a second protein, wherein said first protein is selected from:
- (a) BCL-XL, or a fragment thereof that interacts with TCTP;
  - (b) a first polypeptide having an amino acid sequence at least 75% identical to that of (a), and that interacts with TCTP;
- or
- (c) a first fusion protein comprising (a) or (b); and wherein said second protein is selected from:

- (i) TCTP, or a fragment thereof that interacts with BCL-XL;
- (ii) a second polypeptide having an amino acid sequence at least 75% identical to that of (i), and that interacts with BCL-XL; or
- (iii) a second fusion protein comprising (i) or (ii).

*The prior art*

The Examiner relies on the following prior art reference to show unpatentability:

Yang<sup>1</sup> et al. *An N-terminal region of translationally controlled tumor protein is required for its antiapoptotic activity*. 24 *Oncogene* 4778 (2005).

Walensky et al. *Novel chemically stabilized helices of the BCL-2 family induce apoptosis of leukemia cells*. 102 *Blood* 5A (2003).

Gachet et al. *The growth-related, translationally controlled protein P23 has properties of a tubulin binding protein and associates transiently with microtubules during the cell cycle*. 112 *J. Cell Sci.* 1257 (1999).

*The Issues*

The rejections as presented by the Examiner are as follows:

- A. Claims 39-48 stand rejected under 35 U.S.C. § 112, first paragraph, as failing to comply with the written description requirement.

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<sup>1</sup> Consonant with to 37 C.F.R. § 41.39(b)(2)(2006), Appellants have addressed the Yang reference, newly cited in the Examiner's answer, in the Reply Brief filed March 19, 2007, thereby maintaining the appeal.

B. Claims 39-48 stands rejected under 35 U.S.C. § 112, first paragraph, as being nonenabled for the full scope of the claims.

C. Claims 39-48 stands rejected under 35 U.S.C. § 102(b), as being anticipated by Gachet.

*A. Written Description rejection*

The Examiner rejected claims 39-48 under 35 U.S.C. § 112, first paragraph, on the basis that the “genus of proteins complexes are highly variant because the genus is not characterized by a functional attribute of the complex which would serve to identify members of the genus from those which are not part of the genus” (Ans. 4). The Examiner contends that the “disclosure of the complex of Bcl-xL and TCTP does not adequately describe the claimed genus of proteins complexes because the claimed genres encompasses protein complexes which differ in both structure and function from the Bcl-xL-TCTP complex.” (Ans. 4).

Appellant argues that, like the RNA polymerase in *Invitrogen*, “the modified Bcl-xL protein in Claim 39 is defined by both structural (sequence identity to native Bcl-xL protein, or Bcl-xL fragment) and functional features (interacting with TCTP protein)” (App. Br. 9). Appellant notes that “both Bcl-xl and TCTP were well known proteins in the art at the time of filing” (App. Br. 9). Appellant further contends that “the PTO's own Written Description Guidelines teach that a single species of polypeptide, disclosed through a combination of structural and functional attributes, is sufficient to describe a genus of related, variant polypeptides” (App. Br. 10). Appellant also argues that the “Examiner's allegation that binding is not a

functional attribute (Final Office Action at paragraph 4, p. 4) has no basis in law or fact. *Invitrogen* did not limit what type of functional information, when combined with structural characteristics, would be sufficient to describe a genus invention” (App. Br. 11).

In view of these conflicting positions, we frame the description issue before us as follows:

Does Appellant’s Specification contain a written description sufficient to show they had possession of their claimed invention at the time the application was filed, as required by Federal Circuit precedent?

*Findings of Fact*

1. The Specification teaches that “apoptosis regulator Bcl-XL (“BCL-XL”) interacts with translationally-controlled tumor protein 1 (“TCTP”, also known as IgE-dependent histamine-releasing factor or HRF)” (Spec. 6:17-19).

2. The Specification teaches that “homologues, derivatives, and fragments of BCL-XL and of TCTP may also be used in forming protein complexes” (Spec. 7:2-4).

3. The Specification refers to the specific Genbank accession numbers which teach the amino acid sequences of BCL-XL and TCTP (*see* Spec. 20, Table 1).

4. The Specification provides no correlation between specific structural domains of either BCL-XL or TCTP and any functional activities of the proteins including protein binding (*see* Spec. 108).

*A. Discussion of Written Description rejection*

We agree with the Examiner that the Specification does not adequately describe the claimed protein complex as broadly claimed. Describing a claim to a protein complex requires describing the compounds used in the complex.

It is well settled that

the inventor cannot lay claim to that subject matter unless he can provide a description of the compound sufficient to distinguish infringing compounds from non-infringing compounds, or infringing methods from non-infringing methods. As the district court observed, “[t]he claimed method depends upon finding a compound that selectively inhibits PGHS-2 activity. Without such a compound, it is impossible to practice the claimed method of treatment.”

*University of Rochester v. G.D. Searle & Co.*, 358 F.3d 916, 926 (Fed. Cir. 2004).

Claim 39 is broadly drawn to not only to a complex of the BCL-XL and TCTP proteins, for which the sequences are known (FF 1, 3), but also encompasses the genus of complexes in which fragments of unknown size and sequence of the BCL-XL and TCTP proteins form the complex (FF 2). Additionally, the claim encompasses proteins with only 75% identity to some BCL-XL or some TCTP, without a specific delineation of what starting sequence is being used for the 75% identity comparison (*see* claim 39). The Specification therefore must adequately describe that genus of compounds.

The written description requirement can be met by disclosing “complete or partial structure, other physical and/or chemical properties,

functional characteristics when coupled with a known or disclosed correlation between function and structure, or some combination of such characteristics.” *Enzo Biochem, Inc. v. Gen-Probe Inc.*, 323 F.3d 956, 964, (Fed. Cir. 2002).

In this case, the Specification references the complete sequence of the BCL-XL and TCTP proteins (*see* FF 3). However, the Specification does not describe any of the specific structural features of BCL-XL which give rise to the function of TCTP binding. In fact, the Specification fails to identify which region, or regions, within the 216 amino acid BCL-XL protein are involved in TCTP binding.

The present case is therefore analogous to *Rochester*. In *Rochester*, the patent claimed a method of selectively inhibiting the enzyme PGHS-2 (also known as COX-2) by “administering a non-steroidal compound that selectively inhibits activity of the PGHS-2 gene product to a human.” *Rochester*, 358 F.3d at 918. The patent “describes in detail how to make cells that express either COX-1 or COX-2, but not both . . . , as well as ‘assays for screening compounds, including peptides, polynucleotides, and small organic molecules to identify those that inhibit the expression or activity of the PGHS-2 gene product.’” *Rochester*, 358 F.3d at 927.

The court held that even if a DNA sequence might support a claim to hybridizing nucleic acids, the “same is not necessarily true in the chemical arts more generally. Even with the three-dimensional structures of enzymes such as COX-1 and COX-2 in hand, it may even now not be within the ordinary skill in the art to predict what compounds might bind to and inhibit them.” *Rochester*, 358 F.3d at 925.

The concern is even more acute in the current case, where unlike in *Rochester*, where the claims involved only the use of the natural COX-2 molecule, here the claims encompass any protein that is 75% similar to the 216 amino acid BCL-XL protein or that is 75% similar to the 172 amino acid TCTP protein.

Appellants have not provided any identification of a single region or multiple regions within the BCL-XL protein which are involved in TCTP binding. Appellants have not provided any identification of critical residues in the BCL-XL which are essential to HCV E2 binding.

As in *Rochester*, the present application discloses the assay for screening BCL-XL and TCTP interaction but fails to provide BCL-XL regions other than the wild type which bind to wild type TCTP (FF 3).

As the district court pointed out: Tellingly, . . . what plaintiff's experts' [sic] do not say is that one of skill in the art would, from reading the patent, understand what compound or compounds-which, as the patent makes clear, are necessary to practice the claimed method-would be suitable, nor would one know how to find such a compound except through trial and error . . . . Plaintiff's experts opine that a person of ordinary skill in the art would understand from reading the '850 patent what method is claimed, but it is clear from reading the patent that one critical aspect of the method-a compound that selectively inhibits PGHS-2 activity-was hypothetical, for it is clear that the inventors had neither possession nor knowledge of such a compound.

*Rochester*, 358 F.3d at 925-926.

Just as in *Rochester*, it is hypothetical which amino acid modifications of BCL-XL will share the claimed activity of binding to TCTP. In the

Specification, there is no possession or knowledge of any such specific compound which will form the claimed complex.

Appellant argues that *Invitrogen* supports a finding of that the written description is satisfied because “the Federal Circuit recognized that (1) the sequences of the RT gene family were known at the time of filing, and (2) the specification also discloses methods and data of testing that the enzyme produced by the listed sequence has the claimed features” (App. Br. 8).

We think that *Invitrogen* is readily distinguished from the current case because in *Invitrogen*, there was “an article by Johnson et al., 83 Proc. Nat'l Acad. Sci. USA 7648-52, 7651 (1986), established a sufficiently known correlation between RNase H activity in RT (function) and the RT gene made by deletion mutation (structure) to satisfy the PTO test for written description.” *Invitrogen Corp. v. Clontech Laboratories, Inc.*, 429 F.3d 1052, 1072 (Fed. Cir. 2005). Along with the known nucleotide sequences and the known significant homologies between reverse transcriptases, *Invitrogen* also relies upon the correlation between function and structure that was also known in the prior art. No such correlation has been disclosed for BCL-XL or for TCTP. The Examiner points out that knowledge of the structure and separability of the DNA polymerase and RNase H activities was disclosed in *Invitrogen* (Ans. 11).

Appellants cite two papers in Exhibits (App. Br. 10) as evidence that sequences of TCTP and BCL-XL are known from other species, but neither Cheng nor Bhisutthibhan discloses any correlation between any function of either TCTP and BCL-XL and structure, much less the binding function necessary to form the complex of BCL-XL and TCTP.

It is the absence of any knowledge of structural elements within BCL-XL or TCTP which mediate the complex formation that fails the *Enzo* description test. Here, as many as ¼ of the amino acids in either or both of BCL-XL and TCTP may be altered based upon the 75% identity language. However, the Specification lacks possession of any method, other than trial and error, to determine whether the alterations will impact the binding to form the complex (Ans. 4). We find that in the absence of knowledge of which structural elements of BCL-XL are involved in TCTP binding, there is no possession of which subset of BCL-XL or TCTP molecules in the immense genus encompassed by the 75% similarity language will retain the binding function.

We note that the revised Written Description guidelines have changed the analysis from that discussed by Appellant (see App. Br. 10). The March 2008 revision discusses the situation where 95% variants of a protein with function are claimed,

[t]here is no teaching in the specification regarding which 5% of the structure can be varied while retaining the ability of the protein to catalyze the reaction A->B. Further, there is no art-recognized correlation between any structure (other than SEQ ID NO: 3) and the activity of catalyzing A->B, based on which those of ordinary skill in the art could predict which amino acids can vary from SEQ ID NO: 3 without losing the catalytic activity. Consequently, there is no information about which amino acids can vary from SEQ ID NO: 3 in the claimed genus of proteins and still retain the catalytic activity.

(Written Description guidelines at 35, in Example 10 (available at <http://www.uspto.gov/web/menu/written.pdf> (last visited May 19, 2008))).

The revised Written Description guidelines conclude that the claim fails to comply with the written description requirement because of the absence of information correlating any structure with function. We think that this applies directly to the current situation, where the no BCL-XL or TCTP structure which correlates with the binding activity is disclosed and consequently, there is no information about which amino acids can vary and still retain the ability for the protein complex required by claim 39.

We need not address Appellant's argument that "Applicant has fulfilled the requirements of § 101 by asserting a specific, substantial, credible utility that gives the public an immediately useful, powerful new tool in the search for novel therapeutic compounds that potentially could be used for the treatment of cancer" (Rep. Br. 7). No utility rejection is present in the Examiner's answer.

We affirm the rejection of claim 39 under 35 U.S.C. § 112, first paragraph, for lack of adequate written description. Pursuant to 37 C.F.R. § 41.37(c)(1)(vii)(2006), we also affirm the rejection of claims 40-48 under 35 U.S.C. § 112, first paragraph as these claims were not argued separately.

*B. Enablement rejection*

Claims 39-48 stand rejected under 35 U.S.C. § 112, first paragraph, on the basis that the Specification

while being enabling for complexes comprising Bcl-xL and TCTP, complexes comprising fragments of Bcl-xL and TCTP, and complexes comprising Bcl-xL and fragments of TCTP, does not reasonably provide enablement for complexes comprising homologues of Bcl-xL having 80%, 90% or 95% amino acid identity to Bcl-xL, or homologues of TCTP having 80%, 90% or 95% amino acid identity to TCTP.

(Answer 5.) The Examiner reasons that the “specification does not teach which amino acid residues within the disclosed "binding domains" are necessary for the binding of Bcl-xL to TCTP, and thus it would be necessary to first determine the tolerance of the Bcl-xL-TCTP interaction to amino acid substitutions, and deletions within the binding domains” (Ans. 7). The Examiner cites the Ibragimova reference to demonstrate that the unpredictability in factors regarding protein structure and stability (*see* Ans. 7).

Appellants argue that “orthologs of both Bcl-xL and TCTP, i.e., naturally occurring Bcl-xL and TCTP proteins from non-human species, were known in the art at the time of filing. See Exhibits A & B provided herewith” (App. Br. 14). Appellants further contend that “specific examples of protein fragments having the claimed features are disclosed in the Specification” (App. Br. 14). Appellants argue that the “Specification also provides detailed descriptions of various assays for identifying those homologues and fragments possessing such functional features” (App. Br. 14).

Appellant “asserts that only routine experiments are required to make and identify Bcl-xL protein homologues and fragments capable of interacting with TCTP, and TCTP protein homologues and fragments capable of interacting with Bcl-xL” (App. Br. 15).

In view of these conflicting positions, we frame the enablement issue before us as follows:

Would it have required undue experimentation to use the full scope of the claimed BCL-XL and TCTP proteins of claim 39?

*Findings of Fact*

*Breadth of the Claims*

5. The BCL-XL and TCTP proteins of claim 39 are not limited to any specific sequences, but encompass any complexes of proteins with “fragments” of BCL-XL and/or TCTP, and polypeptides “having an amino acid sequence at least 75 % identical to” either BCL-XL and/or TCTP ( *see* Claim 39).

*Presence of Working Examples*

6. The Specification has a single working example of a BCL-XL complex with TCTP (*see* Spec. 20).

*Amount of Direction or Guidance Presented*

7. The Specification does provide guidance on methods of identifying interacting proteins, including the use of immunoaffinity chromatography (Spec. 24:25-31), protein microchips (Spec. 29:14-31), the yeast two hybrid system (Spec. 42:16-25) and antibody based techniques (Spec. 37:10-13).

8. The Specification teaches that “it is particularly desirable to decipher the protein binding sites. Thus, it is important that the mutations introduced only affect protein-protein interaction and cause minimal structural disturbances” (Spec. 68:24-26).

9. The Specification teaches that “[o]nce the pharmacophore has been elucidated, a structural model can be established by a modeling process that may incorporate data from NMR analysis, X- ray diffraction data, alanine scanning, spectroscopic techniques and the like” (Spec. 70:3-5).

*State of the Prior Art and Unpredictability of the Art*

10. Walensky teaches that “Apoptosis is governed by the BCL-2 family of pro- and anti-apoptotic proteins, which form a complex network of checks and balances that dictate cell fate” (Walensky, abstract). Walensky further notes that “BCL-2, for example, is a survival protein whose overproduction can facilitate pathologic cell survival. Anti-apoptotic proteins, such as BCL-2 and BCL-XL, and pro-apoptotic proteins, such as BAK and BAX, share sequence conservation in multiple “BCL-2 homology” (BH) domains” (Walensky, abstract).

11. Cheng, cited as Exhibit A, teaches that “we demonstrated here that amino acid substitutions within the BH3 domain of Bcl-xL had no effect on its death-repressor activity. This suggests that BH3 is not directly involved in the death repressor activity of Bcl-2 homologs” (Chang 693, col. 2).

12. Cheng, cited as Exhibit A, teaches that “[a]lthough the BH3 domains of Bax and Bak facilitate cell death and mediate heterodimerization with BclxL and Bcl-2, the role of BH3 in Bcl-2 and Bcl-xL is not clear” (Chang 693, col. 2).

13. Bhisutthibhan, cited as Exhibit B, discloses an alignment of TCTP protein sequences from multiple organisms (Bhisutthibhan 16194, fig. 3).

14. Yang noted that “previous studies did not identify an interaction between TCTP and BCL-xl (Zhang et al. 2002), presumably due to the differences in the methods and antibodies used” (Yang 4785, col. 1).

*B. Discussion of 112, first paragraph enablement rejection*

We agree with the Examiner that the Specification does not provide sufficient guidance to enable practice of the full scope of the claimed invention without undue experimentation. The nature of the invention places it in the class of invention which the Federal Circuit has characterized as “the unpredictable arts such as chemistry and biology.” *Mycogen Plant Sci., Inc. v. Monsanto Co.*, 243 F.3d 1316, 1330 (Fed. Cir. 2001).

The Specification expressly teaches that the BCL-XL and TCTP polypeptides encompass fragments and proteins with 75% identity thereto. However, the Specification does not teach what activity is required of the complex of BCL-XL and TCTP given the broad claims (FF 5) and the prior art of Walensky and Chang suggest that BCL-XL may have multiple roles (FF 10-12).

While there is a single working example in the Specification (FF 6), the guidance of the Specification focused on methods of screening and provided no disclosure of function protein regions for either BCL-XL or TCTP (FF 7-9).

The prior art demonstrates that no functional region was known for TCTP and that the BH3 region of BCL-XL was unpredictable in its activity, since mutations in the BCL-XL BH3 region had no effect on death repressor activity (FF 11-13). The post filing date art of Yang further supports the unpredictability and difficulties in establishing which regions, if any of TCTP and BCL-XL interact, since Yang notes that prior studies by Zhang had failed to identify the TCTP interaction with BCL-XL (FF 14). This directly supports the “how to use” enablement issue since until the

disclosure by Yang of the functional regions of TCTP and BCL-XL, it would have been unpredictable whether any protein with 75% identity to TCTP or BCL-XL would have formed the claimed complex.

We are not persuaded by Appellant's reliance on *Invitrogen*. The issue in *Invitrogen* was that enablement for the claims was "not limited by the method of achieving the mutation." *Invitrogen*, 429 F3d at 1071. In the current situation, the issue is not whether other methods could be used to obtain the mutation but rather that undue experimentation would have been required to determine which of the 75% or more identical proteins would retain the interaction regions necessary to form the TCTP and BCL-XL complex.

We are also not persuaded by Appellant's argument that "the Specification is replete with explanations of methods for making such homologues and fragments" (App. Br. 14). The enablement concern is not whether modifications of BCL-XL and TCTP can be made, but whether such homologues and fragments will form the complex between the proteins. This undue experimentation is particularly evident given Yang's disclosure that a contemporaneous experimenter, Zhang, did not detect an interaction between TCTP and BCL-XL (FF 14). Additionally, the teaching by Cheng that mutations in the BH3 domain had little functional effect on BCL-XL also support a conclusion of undue experimentation since mutations in BCL-XL were unpredictably related to function, even in conserved domains (FF 11).

We affirm the rejection of claim 39 under 35 U.S.C. § 112, first paragraph. Pursuant to 37 C.F.R. § 41.37(c)(1)(vii)(2006), we also affirm

the rejection of claims 40-48 under 35 U.S.C. § 112, first paragraph as these claims were not argued separately.

*C. 35 U.S.C. § 102(b) rejection over Gachet*

The Examiner contends that “Gachet et al disclose that TCTP is also referred to as P23 . . . Gachet et al disclose that ‘P23: is a cytoplasmic protein that occurs in complexes of 100-150 kDa’ . . . Gachet et al disclose that said complexes were isolated from HeLa cells” (Ans. 10). The Examiner concludes that a “complex comprising detectably labeled TCTP would inherently comprise Bcl-xL” (Ans. 10). The Examiner also notes that “Yang et al (Oncogene, 2005, Vol. 24, pp. 4778-4768) provides evidence that in HeLa cells, TCTP and Bcl-xL are co-localized both in the cytosol and the mitochondria (page 4779, second column, lines 2-18)” (Ans. 15).

Appellant argues that the “Examiner has not shown that Bcl-xL was necessarily present in the complexes isolated in Gachet” (Rep. Br. 16). Appellant contends that “TCTP has at least 7 interacting partners beside Bcl-xL and itself . . . there is strong evidence to show the protein or proteins in the complex with TCTP of Gachet could have been any of eight different proteins besides Bcl-xL, and thus was (were) not necessarily Bcl-xL” (Rep. Br. 16). Appellant argues that the “Examiner's proffered evidence that TCTP and Bcl-xL co-localize in the cytoplasm and mitochondria of HeLa cells falls far short of proving that Bcl-xL was necessarily present in complex with TCTP in Gachet” (Rep. Br. 16).

In view of these conflicting positions, we frame the anticipation issue before us as follows:

Would the TCTP containing complexes of Gachet inherently have comprised BCL-XL?

*Findings of Fact*

15. Gachet teaches that

P23 is eluted over a fairly wide range of fractions starting significantly earlier than the elution of the pure recombinant protein. Calibration of the column showed that the P23 containing fractions correspond to a molecular mass range from about 40 to 150 kDa, whereas pure recombinant P23 elutes at about 40-60 kDa.

(Gachet 1260, col. 2.)

16. Yang teaches that “TCTP and Bcl-xL are partially colocalized in the cytosol” (Yang 4779, col. 2).

17. The Specification teaches that “interactions between BCL-XL and TCTP will result in the formation of protein complexes both *in vitro* and *in vivo* that contain BCL-XL and TCTP” (Spec. 6:21-22).

18. The Specification teaches that the “protein complexes formed under physiological conditions can mediate the functions and biological activities of BCL-XL and TCTP” (Spec. 6:23-24).

*C. Discussion of § 102(b) rejection over Gachet*

We agree with the Examiner that Gachet as evidenced by Yang provides sufficient information for a prima facie case of inherent anticipation. Gachet isolates protein complexes of TCTP (termed P23) from HeLa cells which include TCTP and additional proteins (FF 15). Yang evidences that Bcl-xl is present in HeLa cells in the same cellular compartments as TCTP (FF 16). Appellant’s Specification shows that BCL-

XL and TCTP will form protein complexes under physiological conditions (FF 17-18).

We are not persuaded by Appellants' argument that the Gachet composition is necessarily different than that claimed because "TCTP has at least 7 interacting partners beside Bcl-xl" (Rep. Br. 16). Appellant does not show that these proteins are located in same cellular compartment, the cytosol, as TCTP and Bcl-xl. However, even if we accept Appellant's logic that seven other proteins are present, then the isolated complexes of TCTP must represent competition products with all complexes of all the proteins present in the cellular compartment. *See Atlas Powder Co. v. Ireco, Inc.*, 190 F.3d 1342, 1348 (Fed. Cir. 1999) ("The public remains free to make, use, or sell prior art compositions or processes, regardless of whether or not they understand their complete makeup of the underlying scientific principles which allow them to operate.").

We are not persuaded by Appellant's argument that "skilled artisans, who were most certainly aware of Gachet's findings nevertheless deemed the Bcl-xL- TCTP interaction novel six years after Gachet!" (Rep. Br. 16). This argument fails to address the inherent nature of the interaction, since if Gachet did not look for the interaction with BCL-xl, the mere presence of the complexes isolated from the superose column would not teach the presence of BCL-xl, but "[i]t matters not that those of ordinary skill heretofore may not have recognized these inherent characteristics." *In re Cruciferous Sprout Litigation*, 301 F.3d 1343, 1350 (Fed. Cir. 2002).

In demonstrating that Gachet discloses protein complexes with TCTP that are derived from the same cell type and same cell compartment as BCL-

xl (FF 15-16) and where the Specification admits that these proteins interact under physiological conditions (FF 17-18), we think the Examiner has reasonably shifted the burden to Appellants to demonstrate that TCTP complexes isolated from HeLa cells does not contain BCL-xl. As the court noted in *Best*, “[w]here, as here, the claimed and prior art products are identical or substantially identical, or are produced by identical or substantially identical processes, the PTO can require an applicant to prove that the prior art products do not necessarily or inherently possess the characteristics of his claimed product.” *In re Best*, 562 F.2d 1252, 1255 (CCPA 1977).

We affirm the rejection of claim 39 under 35 U.S.C. § 102(b) over Gachet. Pursuant to 37 C.F.R. § 41.37(c)(1)(vii)(2006), we also affirm the rejection of claims 40-48 under 35 U.S.C. § 112, first paragraph as these claims were not argued separately.

#### CONCLUSION

In summary, we affirm the rejection of claim 39 under 35 U.S.C. § 112, first paragraph, written description and enablement. We also affirm the rejection of claim 39 under 35 U.S.C. § 102(b). Pursuant to 37 C.F.R. § 41.37(c)(1)(vii)(2006), we also affirm the rejection of claims 40-48 as these claims were not argued separately.

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

Appeal 2008-2711  
Application 10/122,573

dm

Myriad Genetics Inc.  
Intellectual Property Department  
320 Wakara Way  
Salt Lake City, UT 84108