Intellectual Property Office

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14 August 2018

PATENTS ACT 1977

APPLICANT	Pacific Biosciences of California, Inc.
ISSUE	Whether patent applications GB1500009.4, GB1803482.7 and GB1807346.0 comply with Section 14(3)
HEARING OFFICER	**C L Davies**

DECISION

Introduction

1 The decision concerns patent application numbers GB1500009.4, GB1803482.7 and GB1807346.0, all entitled "Modified base detection with nanopore sequencing" and all in the name of Pacific Biosciences of California, Inc. GB1500009.4 was filed under the provisions of the Patent Cooperation Treaty (PCT) on 10 June 2013, claiming a priority date of 08 June 2012 from earlier United States application 61/657583 and was initially published as WO2013/185137 on 12 December 2013. On entering the national phase it was republished as GB 2517875 on 04 March 2015. GB1803482.7 (published as GB 2557509) is a divisional application of GB1500009.4 and GB1807346.0 (published as GB2559073) is a divisional of GB1803482.7. Both of the divisional applications are treated as having been filed on the same date as the first application and having the same priority date.

2 The examiner has maintained that each of the applications is non-compliant with Section 14(3) being both classically insufficient and insufficient due to excessive claim breadth. The applicant has not been able to suitably overcome these objections and a hearing was offered to resolve the matter. The hearing took place on 29 June 2018 at the Intellectual Property Office. The applicant was represented by Mr Simon Kiddle of Mewburn Ellis LLP.

3 The outstanding issue is the same in all three applications and consequently each application will stand or fall on the same arguments in relation to Section 14(3). The hearing was concerned predominantly with the first application, GB1500009.4, and this decision will proceed on the basis that the outcome on that application will also apply in respect of both divisional applications.

4 The compliance date on all three applications at the time of the hearing stood at 05 August 2018. At the hearing, the Hearing Officer agreed to exercise discretion to

allow further extensions of the compliance date for the applications and this has now been done, with extended compliance dates standing at 05 October 2018.

The invention

5 The invention is concerned with a method for sequencing a nucleic acid template and identifying modified bases therein. Modified bases are defined as bases that differ from the canonical bases A, C, G and T/U and refer not only to a chemical modification but also to a variation in nucleic acid conformation or composition, interactions of an agent with a nucleic acid, and other perturbations associated with the nucleic acid. The presence and position of the modified base can be determined by identifying a "kinetic signature" of a processive enzyme (such as a polymerase, exonuclease or helicase) that is attached in proximity to a nanopore. A nucleic acid template is threaded through the nanopore and can be sequenced *via* conventional nanopore sequencing methods, wherein the disruption of the ionic current flowing through the pore is characteristic of the nucleotide base present in the pore at any given time. The enzyme is positioned such that a known number of nucleic acid bases in the template is present between the nanopore and the enzyme active site. When the enzyme processes a modified base, the read from the nanopore is disrupted or affected in a manner specific to both the base modification and the enzyme and the type of disruption observed (*i.e.* kinetic signature) can be used to identify the modification. In addition, since the distance between the enzyme and nanopore is known the position of the modified base can also be determined.

6 It should be noted that detection of modified bases is known using nanopore sequencing. In these methods, the presence of a modified base within a nanopore disrupts the current in a manner that allows its direct identification. The method proposed in the present application instead indirectly detects the presence of a modified base which is not present within the nanopore at the point at which it is identified.

The claims

7 This decision is based on the most recent set of claims on GB1500009.4 filed on 27 February 2018. There is one independent claim set out below:

"1. A method for sequencing a nucleic acid template and identifying modified bases therein comprising:

providing a substrate having an upper solution above the substrate and a lower solution below the substrate, the substrate comprising a nanopore connecting the upper solution and lower solution, the nanopore sized to pass a single-stranded nucleic acid;

providing a voltage across the nanopore to produce a measurable current flow through the nanopore;

controlling the rate of translation of a single stranded portion of the template nucleic acid through the nanopore with a processive enzyme associated with a template nucleic acid, wherein the processive enzyme comprises polymerase, exonuclease, or helicase activity;

measuring the current through the nanopore over time as it is translated through the nanopore, wherein such measuring includes measuring the current and measuring the rate of translation;

determining the sequence of a portion of the template nucleic acid as it translates through the nanopore using the measured current over time; and

determining the presence of modified bases in the template nucleic acid by correlating changes in the rate of translation of the nucleic acid through the nanopore to changes in the kinetics of the processive enzyme from the interaction of the modified base with the processive enzyme".

8 For comparison purposes claim 1 on the divisional applications read as follows,

GB1803482.7 (claims filed 05 June 2018):

"1.A method for sequencing a nucleic acid and determining the presence and position of a modified base in a template nucleic acid using a nanopore comprising:

providing a substrate having an upper solution above the substrate and a lower solution below the substrate, the substrate comprising a nanopore connecting the upper solution and lower solution, the nanopore sized to pass a single stranded nucleic acid;

providing a voltage across the nanopore to produce a measurable current flow through the nanoore;

providing, in the upper solution, a polymerase-nucleic acid complex comprising a strand displacing polymerase and a circular nucleic acid template which may have modified bases and providing the components required for nucleic acid synthesis whereby the polymerase produces a nascent strand that passes through the nanopore as the nascent strand is produced;

measuring the current through the nanopore over time as the nascent strand is translated through the nanopore;

determining the sequence of the nascent strand as it translates through the nanopore using the measured current over time, and determining the presence of a modified base in the circular nucleic acid template using a measured change in kinetics of the polymerase, whereby the polymerase proceeds around the circular template, then continues to produce nascent strand such that a sequence in the nascent strand and the presence of a modified base in the circular template is determined more than once, and determining the position of the modified base using a determined value for the number of bases between the active site and the bases within the nanopore."

9 GB1807346.0 (amended claims filed 11 June 2018):

"1. A method for sequencing a nucleic acid template and determining the presence and position of a modified base in a template nucleic acid which may have modified bases using a nanopore comprising:

providing a substrate having an upper solution above the substrate and a lower solution below the substrate, the substrate comprising a nanopore connecting the upper solution and lower sloution, the nanopore sized to pass a single stranded nucleic acid;

providing a voltage across the nanopore to produce a measurable current flow through the nanopore;

controlling the rate of translation of a single stranded portion of the template nucleic acid through the nanopore with a processive enzyme associated with a template nucleic acid, wherein the processive enzyme has an active site and is a polymerase, an exonuclease, or a helicase;

measuring the current through the nanopore over time as it is translated through the nanopore, wherein such measuring includes measuring the current and measuring the rate of translation;

determining a sequence of a portion of the template nucleic acid as it translates through the nanopore using the measured current over time, determining the presence of modified bases in the template nucleic acid by correlating changes in the rate of translation of the nucleic acid through the nanopore to changes in the kinetics of the processive enzyme from the interaction of the modified base with the processive enzyme; and

determining the position of the modified base using a determined value for the number of bases between the active site of the processive enzyme and the bases within the nanopore."

Issue to be decided

10 The issue to be decided is whether the applications comply with Section 14(3).

11 Specifically, the examiner considers that all three applications are both classically insufficient and also insufficient due to excessive claim breadth. Since an objection of classical insufficiency is insurmountable I shall consider this first and move on to insufficiency due to excessive claim breath if necessary.

The relevant law

12 Section 14 of the Act, entitled "Making of Application", sets down a number of requirements for a patent application. Section 14(3) relates to the specification and reads as follows:

13 *"The specification of an application shall disclose the invention in a manner which is clear enough and complete enough for the invention to be performed by a person skilled in the art."*

Arguments and Analysis

14 The purpose of Section 14(3) is to prevent a patentee laying claim to products or processes which the teaching of the patent does not enable the skilled addressee to perform. In all situations sufficiency is a question of fact – does the patent enable

the invention to be worked across the breadth of the claim? If the disclosure of the invention claimed is not clear and complete, then either the application must be refused or the claims restricted to matter that is adequately disclosed. Any deficiencies in the specification cannot be rectified by adding technical matter after filing as this would contravene section 76 of the Act.

15 There is significant case law on this issue. In *Eli Lilly v Human Genome Sciences* [2008] RPC 29 at [239], Kitchen J gave the following summary of the relevant principles to be applied:

"The specification must disclose the invention clearly and completely enough for it to be performed by a person skilled in the art. The key elements of this requirement which bear on the present case are these:

(i) the first step is to identify the invention and that is to be done by reading and construing the claims;

(ii) in the case of a product claim that means making or otherwise obtaining the product;

(iii) in the case of a process claim, it means working the process;

(iv) the sufficiency of the disclosure must be assessed on the basis of the specification as a whole including the description and the claims;

(v) the disclosure is aimed at the skilled person who may use his common general knowledge to supplement the information contained in the specification;

(vi) the specification must be sufficient to allow the invention to be performed over the whole scope of the claim;

(vii) the specification must be sufficient to allow the invention to be so performed without undue burden."

16 In *Zipher Ltd v Markem Systems Ltd* [2009] FSR 1, the objection to classical insufficiency is summed up as follows:

"Classical insufficiency arises where the express teaching of the patent does not enable skilled addressee to perform the invention. This type of insufficiency requires an assessment...of the steps to which it would be necessary for the skilled reader or team to take in following the teaching of the specification and in order to arrive within the claim. Plainly the steps should not include inventive ones. But a patent can also be found insufficient if the steps can be characterised as prolonged research, enquiry or experiment."

17 Whilst in *Biogen Inc v Medeva plc* [1997] RPC 1 it was held that the disclosure must be sufficient to enable the whole width of the claimed invention to be performed, and the disclosure of a single embodiment will not always satisfy the requirement regardless of the width of the claim. Hence, in contrast to classical insufficiency, in insufficiency by excessive claim breadth there may be an enabling disclosure for some portion of the invention, but not for the full breadth of the claims.

18 In considering section 14(3) it is necessary to define the skilled person or team and identify the common general knowledge. In his report the examiner considered that the skilled addressee in this instance is one working in the field of nanopores and nanopore sequencing. Mr Kiddle did not comment on who the skilled person might be but did not disagree with this suggestion. I am therefore happy to proceed on this basis.

19 The common general knowledge of this person extends to the nanopores commonly used in such processes including solid-state pores and biological pores such as alpha-haemolysin and MspA. They would also be aware of the usual method of sequencing nucleic acids using such pores by measuring the change of an ionic current to identify a base (including a modified base) within a nanopore. At the hearing Mr Kiddle agreed that nanopores and nanopore sequencing as a general concept is known and that setting up of nanopore systems was known at the priority date.

20 Whilst processive enzymes are not an essential part of nanopore sequencing methods the skilled person would be aware of those that have been used in sequencing experiments, these generally being exonucleases and polymerases. Exonucleases that would be known to the skilled person, such as *Escherichia coli* exonuclease I (ExoI), have primarily been used to produce 5'-phosphorylated mononucleotides by digestion of a single-stranded nucleic acid strand which are then fed into the nanopore, with luck in the correct order, to obtain the sequence. DNA polymerases that are widely known to modify nucleic acid translocation into a pore include the Klenow fragment of *E. coli* and the phi29 DNA polymerase.

21 At the hearing Mr Kiddle suggested a number of times that the classes of enzymes disclosed in the application (*i.e.* polymerases, exonucleases and helicases) would be known to the skilled person and would be available for them to use in nanopore systems. I agree that these classes of enzymes would generally be known to the skilled person but I do not agree that all of the specific types encompassed by these classes, or even some of the classes themselves, would form part of the common general knowledge of the skilled person in relation to nanopore sequencing. Documents put forward by Mr Kiddle, US2010/0331194 (D2, Turner *et al*.) and US2012/0094278 (D3, Akeson *et al.*), both disclose a wide range of processive enzymes that might be useful in nanopore sequencing although I am not convinced that they would form the common general knowledge. D3 (Akeson *et al.*) exemplifies exonucleases, although these were bound to a single-stranded DNA molecule and not used to produce a single-stranded template from a double-stranded one, whilst D2 (Turner *et al.*) relates predominantly to the use of phi29 DNA polymerase as discussed above. While both of these documents refer to helicases as possible DNA translocating enzymes (and indeed D3 (Akeson *et al.*) even provides some specific examples at paragraph [0029]), these are nothing more than suggestions and I do not consider that they constitute part of the common general knowledge of the skilled person.

22 Next I will construe the claim and identify the invention. Use of the terms "translated" and "translation" in the claims and throughout the application, to describe movement of a nucleic acid strand through a nanopore or the function of an enzyme controlling this process, is slightly confusing given that translation of nucleic acids more usually relates to the synthesis of proteins from a messenger ribonucleic acid. However,

throughout this decision I shall continue to use these terms in the same way that they are used in the application, *i.e.* they may be considered synonyms of transport or translocate.

23 For the most part claim 1 of GB1500009.4, as currently presented, describes a standard method for nanopore sequencing. The part of the claim from the phrase *"...providing a substrate having an upper solution above the substrate..."* through to the phrase *"...determining the sequence of a portion of the template nucleic acid as it translates through the nanopore using the measured current over time..."* provides a substrate comprising a nanopore, provision of a voltage across the nanopore, control of the rate of translation of a single-stranded portion of the template nucleic acid through the nanopore with a processive enzyme and sequencing of a nucleic acid strand based on current measurement over time within the nanopore and, in my opinion, is conventional in the art of nanopore sequencing.

24 As discussed above, use of processive enzymes is known in nanopore sequencing; however, it is clear to me from reading the application that in order for the invention to work as described the enzyme must be attached to, or somehow held in place upon, the nanopore. This attribute of the enzyme is not present in claim 1; there is merely the requirement for a processive enzyme "...associated with a template nucleic acid, wherein the processive enzyme has an active site and is a polymerase, an exonuclease, or a helicase...". The description at paragraph [00119] tells the reader that:

"...the translating enzyme should be fixed in space to ensure that the distance between the base modification event at the enzyme and the bases in the nanopore remain constant."

25 It is suggested that the attachment may be covalent, by affinity or through genetic fusion or alternatively the enzyme can be held in place with the voltage across the nanopore that is used to pull the nucleic acid into the pore (paragraph [00119]) or by the force of the electric field pulling on the nucleic acid strand (paragraph [0048]). At the hearing, Mr Kiddle confirmed that the enzyme would need to be fixed in space using the "...electrical point..." or to be tethered physically.

26 The description at paragraph [0049] further teaches that:

"By controlling the force on the nucleic acid strand 106 (e.g. by controlling the applied voltage), the number of bases 120 between the active site of the enzyme and nanopore will remain relatively constant throughout the process. Where the number of bases between the enzyme and the nanopore is constant, the rate of passage through the nanopore will be equivalent to the rate of nucleic acid synthesis by the polymerase enzyme."

27 It would therefore appear that the applied voltage is adjusted to apply a force to the nucleic acid such that the rate of translation of the nucleic acid through the pore is substantially equivalent to the rate of processing the nucleic acid by the enzyme. Note also paragraph [0039] where it is confirmed that the translating enzyme controls the rate of transport of the nucleic acids.

28 Whilst I have had difficulty interpreting paragraphs [0039] and [0049], in my opinion I understand them to mean that the force from the applied voltage neither slows the processivity of the enzyme nor allows the nucleic acid to move in the direction of transport faster than the enzyme can process it at the active site; rather, the processivity rate is the controlling factor. Controlling the translation rate in this manner, by the applied voltage, such that it is equivalent to the processivity rate of the enzyme should, in my view, result in the constant number of bases between the active site and the nanopore.

29 As I understand it, it is therefore the combination of the fixed distance between the active site of the enzyme and the nanopore together with the rate of translation controlled by the applied voltage that allows determination of both the base identity and its position within the nucleic acid template. As Mr Kiddle put it at the hearing, *"..because you know the number of bases or can control or set up the number of bases between the pore and the enzyme this enables you to assign the presence of the modified base to your sequence…*".

30 The teaching in the description is therefore for an enzyme that is fixed by some means at a known distance from the nanopore and having a controlled processivity rate. What I consider the specification does not tell the skilled addressee however is how to do either of these things.

31 I can find nothing in the application as filed that teaches someone working the invention how to suitably attach an enzyme to a nanopore. As I see it there are three considerations. First, the enzyme needs to be fixed in such a manner that it is stable enough to prevent movement in order that the number of bases between the active site and the nanopore remains consistent; second, the enzyme needs to be in the correct orientation so that the active site is accessible to the template strand and can process it through the pore and third, there needs to be a means to determine how many bases there are between the active site and the nanopore.

32 I can accept that the skilled person would be aware of general methods for the attachment of one protein to another but in this instance attachment must be made so that the enzyme functions in the desired manner; this to my mind amounts to more than just an *ad hoc* sticking together of two molecules but is a much more detailed procedure that would require planning and identification of orientation of the molecules and knowledge that they are functioning together. At the hearing Mr Kiddle did not expand on the attachment process but thought that both alternatives (*i.e.* physical attachment or use of an electric field) were known for nanopore sequencing techniques. I note that the issue of enzyme attachment was raised in paragraph 18 of the examiner's report dated 23 May 2018, but a response in the applicant's skeleton argument was not provided (markedly, comments on paragraphs 17 and 19 of the same report (23 May 2018) were given).

33 I am prepared to acknowledge that the skilled person would be aware of the use of processive enzymes in conjunction with nanopores but not that this amounts to common general knowledge of attachment of the enzymes in the manner required in the present case. Mr Kiddle did not refer to any of the cited documents to supplement his thoughts although I note that D3 (Akeson *et al.*) does disclose a number of proposed embodiments to immobilize enzymes adjacent a nanopore aperture, although there is no requirement that the enzyme and the pore are at a

fixed distance and that there is a known number of bases between the two. In addition, the examples in D3 do not teach immobilization of an enzyme at all.

34 The alternative suggestion of the use of an electric field provided by the voltage applied across the nanopore to hold the enzyme in place is, to my mind, not precise enough to provide all of the stable operating conditions required for the system. Furthermore, this suggestion does not seem to take into account that the same voltage would have to be managed in order that the processivity of the enzyme might be kept constant. I am not convinced that the same voltage can reliably carry out both processes and keep either one under the strict control that would be required such that there is a controlled number of bases between the active site and the nanopore. The specification provides no help in this regard, merely indicating at paragraph [00119] that:

"…voltage is applied such that the enzyme is drawn toward the pore, and is held in place sterically. The voltage provides a constant force, pulling the nucleotide into the pore, and the enzyme either pays out the nucleic acid through the pore in the direction of the force, or pulls the nucleic acid into the pore against the field as described herein"

35 The example provided in paragraphs [00170]-[00172] of the specification does not provide any helpful detail either, merely stating that a helicase in solution is added on top of a substrate having an array of MspA nanopores, and that a voltage is applied. There are no details of how a helicase might be attached other than the fact that a voltage is applied. In my opinion there would be no guarantee here that the enzyme is in the correct position to function correctly and is stable enough to provide a fixed number of bases between the active site and the nanopore.

36 The specification also provides me no help with how to determine or control the rate of translation of the nucleic acid through the pore using an applied voltage such that the rate is substantially equivalent to the rate of processing by the enzyme. It is not clear to me how the applied voltage can be thus used to keep the number of bases between the active site and the nanopore constant. I consider that the common general knowlege of nanopore sequencing is such that it is known that an applied voltage can be used to control the rate of translation of nucleic acids through a nanopore but I do not think that it is a simple matter to take this knowledge and use it to balance the translation rate with the processivity rate of an enzyme. The skilled person would not know the rate at which an enzyme might process a nucleic acid template; something that I think would also likely be dependent upon the local reaction conditions. One can't simply turn to a handbook of enzyme processivity rates and then manage this with a voltage to acquire the necessary rate of transport through the pore such that the number of bases is consistent.

37 Again, the example at paragraphs [00170]-[00172] does not provide any help in this regard. Other than a statement that a voltage is applied across the nanopore there is no further detail relating how the voltage is used to control the rate of translation of the nucleic acid in relation to the processivity of the helicase.

38 When I asked Mr Kiddle if the applicants have carried out nanopore squencing as described in the application he said that he didn't know and continued that the example tells someone how to create a template for sequencing, how to use a

helicase with a nanopore and the number of times it would be useful to repeat the procedure to get a useful result. This is indeed true, but what I don't see in the example is sufficient detail for the skilled person to work the claimed invention.

39 The final phrase of claim 1, *"...determining the presence of modified bases in the template nucleic acid by correlating changes in the rate of translation of the nucleic acid through the nanopore to changes in the kinetics of the processive enzyme from the interaction of the modified base with the processive enzyme."* is describing a part of the method that can only feasibly be carried out once the enzyme and nanopore are in a fixed position with a known number of bases between them such that changes resulting from a modified base in the active site of the enzyme can be linked to measurements taken in the nanopore and thereby allow determination of the identity and position of a modified base in a nucleic acid template strand.

40 It is my opinion that the level of direction given by the description, including the example at paragraphs [00170]-[00172], is not enough to enable an unimaginative skilled person to attach an enzyme at a desired location and control the processivity rate in such a way as to enable the method to be carried out as claimed. Such a method may be theoretically conceivable but would most certainly place an undue burden on the skilled person and, in my view, would not be possible without exercising a considerable degree of research. As well as ensuring that the choice of enzyme is one that would function under the required conditions and performing the necesary experimentation to affix the enzyme to the pore in the correct orientation, the skilled person would need to be sure of the stability of the attachment and to determine that the number of bases between the active site and the pore remains constant. Any movement of the enzyme would change the position of the active site with respect to the pore and thereby alter the distance and number of bases between these two parts.

41 I can see no teaching in the specification as to how to overcome any of these issues. The skeleton arguments are silent on these points and at the hearing there was no explanation of how the enzyme is attached in order that the distance between the active site and nanopore remains constant. Whilst the application suggests that the enzyme should be fixed in space to ensure that the distance between the base modification event at the enzyme and the bases in the nanopore remain constant it is not possible for the applicant to now add technical features to describe how this might be done and thereby overcome these issues without contravening Section 76.

42 Towards the end of the hearing, with reference to paragraphs [00170]-[00172], Mr Kiddle explained that Example 1 is merely a protocol for carrying out the invention and, because it is clearly written in the present tense, denotes that it is for a proposed piece of work rather than work which has been done. This would be in contrast to the text describing the figures which, because it is written in the past tense, is work which has in fact been carried out. I asked Mr Kiddle if he thought that the example represented a hypothetical way in which one could carry out the invention; he agreed and proceeded to attempt to convince me that the invention is at a level of conception that is above relying on a specific example; that the explanation and discussion of the figures provide the level of generality to support the concept underlying the invention.

43 I must admit I have more than a little difficulty accepting this argument and in my view it does not assist the applicant's contention that the specification is sufficient. There is of course no requirement that all details of an invention are present in the application as filed (M.O.P.P. 14.85 states: "*The specification does not need to disclose all the details of the operation to be carried out in order to perform the invention since an enabling disclosure is to be interpreted by the skilled person, in light of the common general knowledge, who is reasonably expected to carry out tests"*) but in order to be sufficient there must be at a minimum something amounting to one embodiment or example that can be put into effect. It is established practice that if anything new has to be found out by a person of reasonably competent skill following the directions in the specification in order to succeed in working the invention then the disclosure is not complete enough. In my opinion it is evident that the skilled person would have to ascertain a number of pieces of information relating to enzyme attachment and operation in order to successfully work the present invention.

44 At the hearing, and in his skeleton arguments, Mr Kiddle maintained that the claim is acceptable since *"...the invention is a concept fit for generalization..."* and cited *Regeneron Pharmaceuticals v Genentech* [2012] EWHC 657 (Pat) in support.

45 I don't think that this case law helps the applicant overcome the sufficiency issue from which the application suffers. The principle of general application that *Regeneron* is concerned with relates to when limited examples may be used to enable the general terms used in the claims and is typically associated with insufficiency by excessive claim breadth. Since there are no sufficiently disclosed examples in the present application I do not consider that this case law is relevant and I need not consider it further.

46 In summary, I consider the specification of GB1500009.4 to be classically insufficient insofar as it does not disclose the invention in a manner which is clear enough and complete enough for the invention to be performed by a person skilled in the art.

47 Since I have found the specification to be classically insufficient, I do not need to consider sufficiency on the grounds of excessive claim breadth.

48 As per paragraphs 3 and 11 above, the specification of applications GB1803482.7 and GB1807346.0 are also classically insufficient for the same reasons as GB1500009.4.

Conclusion

49 Having carefully considered all the information available to me I find that the specification of GB1500009.4, GB1803482.7 and GB1807346.0 does not disclose the invention in a manner which is clear enough and complete enough for the invention to be performed by a person skilled in the art as required by section 14(3) of the Act. GB1500009.4, GB1803482.7 and GB1807346.0 are classically insufficient. It is not readily apparent that this failure can be addressed by amendment without contravening Section 76. I therefore refuse all 3 applications.

Appeal

50 Any appeal must be lodged within 28 days after the date of this decision.

C L Davies

Deputy Director acting for the Comptroller