

## Claims

What is claimed is :

1. A probe nucleic acid (PNA) comprising:

(a) a single-stranded sequence, 1/2 TBR, which is capable of forming, under hybridising conditions, a hybrid, TBR, with a 1/2 TBR present in a target nucleic acid (TNA);

(b) an OSA, which is 1) no attached support or indicator, or 2) an attached support or indicator or both selected from the group consisting of attachment to bead, polymers, and surfaces, and/or indicators;

wherein said TBR is capable of binding with high affinity to a TBA, said TBA being a substance capable of discriminating between a paired TBR and a TBR having unpaired nucleotides.

2. The PNA of claim 1 wherein the TBR is comprised of one or more recognition sites for a nucleic acid binding protein, a DNA binding protein, a DNA-RNA hybrid binding protein or an RNA binding protein.

3. The PNA of claim 1 wherein the TBR is a nucleic acid binding protein recognition site present in the genome of a pathogen or is a binding site associated with a pathogenic condition in a vertebrate genome or is a nucleic acid binding protein recognition site present in the genome of an organism which contaminates a fermentation process.

4. The PNA of claim 2 wherein the TBR is the HIV-LTR or a portion thereof.

5. A method of using the TBA of claim 1 to bind a particular nucleic acid sequence in a target nucleic acid sample which comprises:

(a) fragmenting the nucleic acid in the target nucleic acid sample;

(b) contacting, under hybridising conditions, the fragmented nucleic acid with a probe nucleic acid complementary to the particular nucleic acid sequence of interest, wherein said probe nucleic acid, upon hybridisation with said particular nucleic acid sequence of interest forms a target binding region to which said TBA specifically binds.

6. The method of claim 5 further comprising the step of:

(c) monitoring the shift in mobility of nucleic acids in the target nucleic acid sample as a function of the size such that binding of the TBA to a particular fragment in the sample modifies the mobility of the fragment.

7. A method of differentially binding a nucleic acid binding protein to a nucleic acid sequence correlated with a pathogenic condition which comprises:

(a) selecting a particular configuration of nucleic acid binding protein sequences present in the nucleic acid sequence correlated with a pathogenic condition as a target sequence for designing a probe nucleic acid which will hybridise to that particular configuration of nucleic acid sequences if present in a test sample, and further, ensuring that a binding site for an available nucleic acid binding protein is formed upon hybridisation of said probe nucleic acid and said particular configuration of nucleic acid sequences chosen as a target;

(b) selecting a nucleic acid binding protein which specifically binds to the selected particular configuration of nucleic acid binding protein sequences correlated with a pathogenic condition, but which does not bind to sequences not correlated with said pathogenic condition;

(c) hybridizing said probe nucleic acid with a test sample suspected of containing said particular configuration of nucleic acid binding protein sequences present in nucleic acid sequences correlated with a pathogenic condition;

(d) contacting said nucleic acid binding protein with any hybrids formed in step (b); and

(e) detecting any binding of said nucleic acid binding protein with said hybrids.

8. The method of claim 7 wherein said particular configuration of nucleic acid binding protein sequences is chosen from a necessary step or control point in the development of a pathogenic condition.

9. The method of claim 5 or 7 wherein said method is carried out in an automated fashion.

10. The method of claim 9 wherein the method is carried out in the Abbott Laboratories IMx machine.

11. The method of claim 9 carried out in a microtiter plate.

12. A method for identifying specific nucleic acid sequences in a sample comprising:

a. Fragmenting the nucleic acids in said sample to expose the nucleic acids and reduce the size complexity of the nucleic acids;

b. Contacting a TBA with the sample, said TBA comprising two or more nucleic acid binding components each of which has a relatively weak binding for its nucleic acid recognition unit within the TBR but which in combination provides strong binding for the complete TBR; and

c. Eliminating any "cross-talk" produced by binding of the TBA to cousin nucleic acids that contain individual recognition units, which comprises contacting the sample with excess nucleic acid binding components with relatively strong binding affinity for cousin nucleic acids that contain the

individual recognition units but relatively weak binding relative to the TBA's affinity for binding to the complete TBR having said two or more nucleic acid binding components.

13. A method for nucleic acid detection comprising

(a) obtaining a sample containing a hybrid to be detected or containing a target nucleic acid and a probe nucleic acid which hybridise to form a probe-target hybrid; and

(b) contacting the hybrid of step (a) with a nucleic acid binding molecule or assembly, TBA, wherein the TBA is capable of binding to and stabilizing the probe-target hybrid in a sequence specific manner, and further wherein the TBA is capable of discriminating between a hybrid formed by the probe and the target nucleic acid, and a hybrid having one or more mismatches formed by the probe and a closely related or unrelated sequence.

14. The method of claim 13 which further comprises contacting the hybrid of step (a) or (b) with a label that binds specifically to the nucleic acid bound by the TBA.

15. The method according to claims 13, wherein said label further comprises an indicator that is protein a selected from the group consisting of enzymes capable of catalysing reactions leading to production of colored reaction products; a radionuclide; or colored beads.

16. The method according to claims 13-15, further comprising

(a) fragmenting the nucleic acid in the target nucleic acid sample;

(b) contacting, under hybridising conditions, the fragmented nucleic acid with a probe nucleic acid complementary to the particular nucleic acid sequence of interest, wherein said probe nucleic acid, upon hybridisation with

said particular nucleic acid sequence of interest forms a target binding region to which said TBA specifically binds.

17. The method according to claims 13-16 further comprising the step of:  
monitoring the shift in mobility of nucleic acids in the target nucleic acid sample as a function of the size such that binding of the TBA to a particular fragment in the sample modifies the mobility of the fragment.