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SNPs by SPR

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William Wells

Email: wells@biotext.com

Approximately 1.6 million [single nucleotide polymorphisms](#) (SNPs) have been identified and deposited in [public databases](#), but more are always needed for studies of other species and identification of mutations in candidate disease genes. In the January [Nature Biotechnology](#), Nakatani *et al.* outline a new method for SNP identification using capture by a mismatch-specific ligand followed by surface plasmon resonance (SPR; *Nat Biotechnol* 2001, **19**:51-55). The ligand, a dimeric naphthyridine, intercalates into and base-pairs with a G-G mismatch, discriminating against other mismatches. Mismatch-containing DNA is trapped by the immobilized ligand, and the DNA then changes the reflective index of polarized light hitting the SPR chip. There are disadvantages: ligands for other mismatches do not yet exist, and SPR does not identify the location of the mutation within the probed DNA fragment. But SPR can be [automated](#), and the re-usable system requires no labeling of DNA or other probes.

References

1. Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome.
2. A database of single nucleotide polymorphisms, [<http://www.ncbi.nlm.nih.gov/SNP/>]
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4. BIAcore for macromolecular interaction.