ダイナビーズストレプトアビジンの使用文献リスト

Automated protocols:

1. Meng Q. et al. (2001). Automated multiplex assay system for simultaneous detection of hepatitis B virus DNA, hepatitis C virus RNA and human immunodeficiency virus type 1 RNA. J.Clin.Microbiol. 39(8):2937-2945. full text
2. Pollock GS. et al. (2001). Effects of early visual experience and diurnal rhythms on BDNF mRNA and protein levels in the visual system, hippocampus and cerebellum. J. Neurosci. 21(11):3923-3931. full text
3. Miyashiro I. et al. (2001). Molecular strategy for detecting metastatic cancers with use of multiple tumor-specific MAGE-A genes. Clin. Chem. 47(3):505-512. full text
4. Stevens SJC. et al. (1999). Monitoring of Epstein-Barr virus DNA load in peripheral blood by quantitative competitive PCR. J.Clin. Microbiol. 37:2852-2857. full text

Single-stranded DNA templates:

5. von Wintzingerode F. et al. (2002). Basespecific fragmentation of amplified 16S rRNA genes analyzed by mass-spectrometry: A tool for rapid bacterial identification. PNAS. 99(10):7039-7044. full text
6. Pourmand N. et al. (2002). Multiplex pyrosequencing. Nucleic Acids Res. 30(7):e31. full text
7. Lindblad-Toh K. et al. (2000). Large-scale discovery and genotyping of singlenucleotide polymorphisms in the mouse. Nature Genetics. 24:381-386. full text
8. Dziembowski A. et al. (2001). Analysis of 3' and 5' ends of RNA by solid-phase S1 nuclease mapping. Anal. Biochem. 294:87-89.

Genome analysis:

9. Fletcher TM. et al. (2002). Structure and dynamic properties of a glucocorticoid receptor-induced chromatin transition. Mol. Cel. Biol. 20(17): 6466-6475. full text
10. Hansen-Hagge TE. et al. (2001). Identification of sample-specific sequences in mammalian cDNA and genomic DNA by the novel ligationmediated subtraction (Limes). Nucl. Acids Res. 29(4):e20. full text
11. Pradel N. et al. (2002). Genomic subtraction to identify and characterize sequences of Shiga toxin-producing Escherishia coli O91:H21. Appl. Env. Microbiol. 68(5):2316-2325. full text
12. Heald R. et al. (1996) Self-organization of microtubules into bipolar spindles around artificial chromosomes in Xenopus egg extracts. Nature 382:420-425.

13. Beulieu M. et al. (2001). PCR candidate region mismatch scanning:adaption to quantitative, high-throughput genotyping. Nucleic Acids Res. 29(5): 114-1124. full text

Sequence clean-up:

14. Fangan BM. et al. (1999) Automated system for purification of dye terminator sequencing products eliminates up-stream purification of templates. BioTechniques 26:980-983.
15. Bhalerao R. et al. (2003) Gene expression in autumn leaves. Plant Physiol. 131:1-13. full text

Sequence-specific capture:

16. Mangiapan G. et al. (1996). Sequence capture- PCR improves detection of mycobacterial DNA in clinical specimens. J. Clin. Microbiol. 34(5): 1209-1215. full text
17. Dong SM. et al. (2001). Detection of colorectal cancer in stool with the use of multiple genetic targets. J Natl Cancer Inst. 93(11): 858-865. full text
18. Refseth UH. et al. (1997). Hybridization capture of microsatellites directly from genomic DNA. Electrophoresis. 18(9):1519-1523.
19. Shuber AP. et al. (2002). Accurate, noninvasive detection of Helicobacter pylori DNA from stool samples: Potential usefulness for monitoring treatment. J. Clin. Microbiol. 40(1):262-264. full text

Gene expression analysis:

20. Kornmann B. et al. (2001). Analysis of circadian liver gene expression by ADDER, a highly sensitive method for the display of differentially expressed mRNAs. Nucleic Acids Res. 29(11). e51 full text
21. Laveder P. et al. (2002). A two-step strategy for constructing specifically self-subtracted cDNA libraries. Nucleic Acids Res. 30(9): e38 full text
22. Schramm G. et al. (2000).A simple and reliable 5'-RACE approach. Nucl. Acids Res. 28(22):e96 full text
23. Velculescu VE. et al. (1995). Serial analysis of gene expression. Science. 270(5235): 484-487.
24. Brenner S. et al. (2000). In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs. PNAS. 97(4): 1665-1670. full text

25. Sutcliffe JG. et al. (2000). TOGA: An automated parsing technology for analyzing expression of nearly all genes. PNAS. 97(5): 1976-1981. full text
26. Wang A. et al. (1999). Rapid analysis of gene expression (RAGE) facilitates universal expression profiling. Nucleic Acids Res. 27(23): 4609-4618. full text

Nucleic acid binding proteins:

27. Mehta A et al. (1998). A sequence-specific RNA binding protein complements Apobec-1 to edit apolipo protein B mRNA. Mol. Cel. Biol. 18(8): 4426-4432. full text
28. Nordhoff E. et al. (1999). Rapid identification of DNA-binding proteins by mass spectrometry. Nat. Biotechnol. 17: 884-888.
29. Brodsky AS. and Silver A. (2002). A microbeadbased system for identifying and characterizing RNA-protein interactions by flow cytometry. Mol. Cel. Proteomics 1(12):922-929. full text

Protein purification:

30. Girault S. et al. (1996). Coupling of MALDI-TOF mass analysis to the separation of biotinylated peptides by magnetic streptavidin beads. Anal. Chem. 68:2122-2126.
31. O'Reilly FM. et al. (2002). FKBP12 modulation of the binding of the skeletal ryanodine receptor onto the II-III loop of the dihydropyridine receptor. Biophys. J 82:145-155. full text
32. Chao S-H. and Price DH. (2001). Flavopiridol inactivates P-TEFb and blocks most RNA polymerase II transcription in vivo. J. Biol. Chem. 276(34):31793-31799. full text
33. deBaar MP. et al. (1999). Detection of human immunodeficiency virus type I nucleocapsid protein p7 in vitro and in vivo. J Clin. Microbiol. 37(1):63-67. full text

Specific cell isolation:

34. Konishi Y. et al. (2002). Isolation of living neurons from human elderly brains using immunomagnetic sorting DNA-liker system. Am. J. Pathol. 161(5):1567-1576. full text
35. Fahrer AM. et al. (2001). Attributes of gd intrepithelial lymphocytes as suggested by their transcription profile. PNAS 98(18):10261- 10266. full text
36. Johansen M. et al. (2002). An investigation of methods for enriching trophoblasts from maternal blood. Prenatal Diagnosis 15:921- 931.
37. Sun W. et al. (2001). Food-borne pathogens. Use of bioluminescent Salmonella for assessing the efficiency of constructed phagebased biosorbent. J Ind. Microbiol. Biotech. 27:126-128.

Biopanning:

38. Nord K. et al. (2001). Recombinant human factor VIII-specific affinity ligands selected from phage-displayed combinatorial libraries of protein A. Eur. J. Biochem. 268:4269-4277. full text
39. Biroccio A. et al. (2002). Selection of RNA aptamers that are specific and high-affinity ligands of the hepatitis C virus RNA-dependent RNA polymerase. J. Virol. 76(8):3688-3696. full text
40. Legendre D. et al. (1999). Engineering a regulatable enzyme for homogenous immunoassays. Nature Biotech. 17:67-72.
41. Lev A. et al. (2002). Isolation and characterization of human recombinant antibodies endowed with the antigen-specific, major histocompatibility complex-restricted specificity of T-cells directed toward the widely expressed tumor T-cell epitopes of the telomerase catalytic subunit. Cancer Res. 62(11):3184-3194. full text
42. Cumbers SJ. et al. (2002). Generation and iterative affinity maturation of antibodies in vitro using hypermutationg B-cell lines. Nat. Biotech. 20(11):1129-1134. full text
43. Demartis S. et al. (1999). A strategy for the isolation of catalytic activities from repertoires of enzymes displayed on phage. J. Mol. Biol. 286:617-633.
44. Pini A. et al. (1998). Design and use of a phage display library. J. Biol. Chem. 273(34):21769- 21776. full text
45. Cox JC. et al. (2002). Automated selection of aptamers against protein targets translated in vitro: from gene to aptamer. Nucleic Acids Res. 30(20):e108. full text