

VOLUME 4, SUBJECT INDEX

ACE. *See* Angiotensin-converting enzyme

Acute lymphoblastic leukemia (ALL), Ph+ PCR of *bcr-abl* in fusion transcripts, 283–287

Acute myelogenous leukemia, detection of allele loss, 6–12

Adenocarcinoma, assessment and semi-quantification of gene amplification from archival material, 178–184

AGLCR. *See* Asymmetric gap ligase chain reaction

ALL. *See* Acute lymphoblastic leukemia

Alleles

- detection of loss in a model hematopoietic neoplasm, 6–12
- determination of frequencies in pooled DNA samples, 13–18
- microsatellite, separation by PhastSystem, 380–381
- specific oligonucleotide probes (ASOs), in diagnostic test for Gaucher disease, 1–5

Alu repeat sequences, internal direct and inverted *Alu*, effect on PCR, 109–116

Amplification

- of DNA fingerprint profiles, comparison of gel matrices, 50–51
- of DNA segments using vectorette PCR, 71–75
- of DNA with arbitrary primers, and buffer components, 59–61
- efficiencies in competitive PCR for determination of mRNA, 219–226
- of gene fragments with very high G/C content, 124–125
- of immunoglobulin genes from mouse hybridoma cells, by PCR, 256–264
- inhibited by reverse transcriptase, 62–65
- of long sequences, genomic DNA, 294–298
- of MLO DNA from plant host species, 56–58
- from paraffin wax-embedded archival material, 178–184
- and rapid isolation of cDNA clones, 126–128
- refractory mutation system–PCR (ARMS–PCR), low-density lipoprotein receptor gene screening, 352–356
- total coding sequence, *NF1* gene, peripheral blood lymphocyte RNA, 311–313

Angiotensin-converting enzyme mRNA, quantitation in smooth muscle cells by PCR, 167–171

Apo ferritin H multigene family, PCR analysis, 85–88

Arbitrary primers, buffer components tailor DNA amplification with, 59–61

Archival samples

- heart tissue, mitochondrial DNA analysis, 309–310
- material, semiquantification of gene amplification, 178–184
- PCR reagents, 191–194

ARMS–PCR. *See* Amplification refractory mutation system–PCR

Artifact formation

- correcting for, and computation of genetic similarity coefficients, 38–43
- effects of, and computation of genetic similarity coefficients, 31–37
- PCR, 109–116

ASOs. *See* Allele-specific oligonucleotides

Asymmetric gap ligase chain reaction (AGLCR), 80–84

Background-minimized cassette mutagenesis–PCR (BMCM–PCR), using cassette-specific selection markers, 212–218

Bacteria. *See also* Mycoplasma

- contamination of cell cultures, PCR-based detection of, 199–208
- lysates, DNA fingerprinting using, 265–268

BAGS. *See* Batched analysis of genotypes

Batched analysis of genotypes (BAGS), 331–336

Bead, magnetic M-280–streptavidin, purification of single-stranded DNA, 227–233

Bending locus, of DNA molecules, 44–45

BMCM–PCR. *See* Background-minimized cassette mutagenesis–PCR

Buffer components, for DNA amplification with arbitrary primers, 59–61

CAL. *See* Coupled amplification and oligonucleotide ligation

Cancer. *See also* specific types

- assessment and semiquantification of gene amplification from archival material, 178–184
- tissues, detection of p53 gene mutation, by nonradioactive direct sequencing, 76–79

Capillary electrophoresis (CE), hybridization analysis of PCR products by, 303–304

Cassette ligation, and end trimming with PCR to clone exon–intron boundaries, 19–25

Catch-linker+PCR labeling, method to generate hapten-labeled DNA fragments from YAC, 209–211

cDNA clones, isolation by aliquot testing + PCR, 126–128

cDNA libraries, PCR screening, 126–128

CE. *See* Capillary electrophoresis

Cell culture contamination, PCR-based detection of, 199–208

Chemiluminescence

- detection, in diagnostic test for Gaucher disease, 1–5
- detection system, in nonisotopic SSCP protocol, 52–55
- technique for the detection of p53 gene mutation in cancer tissues, 76–79

Chromosome 5q–, method for detection of allele loss in, 6–12

Cloning exon–intron boundaries, PCR with end trimming and cassette ligation, 19–25

Coefficients, genetic similarity, computation for use with RAPD data, 31–37, 38–43

Colinearity, between large cloned DNA fragments and genomic DNA, 129–132

Colorimetric technique, for the detection of p53 gene mutation in cancer tissues, 76–79

Competitive PCR

- deletion mutant quantitative PCR assay for angiotensin-converting enzyme mRNA, 167–171
- evaluation of competitor type and size for use in the determination of mRNA, 219–226
- transcription-based system, 363–367

Contamination

- cell cultures, detected by PCR, 199–208
- PCR, 117–123

Coupled amplification and oligonucleotide ligation (CAL), for multiplex genetic typing, 337–345

Curvature, DNA, 44–45

Cytochrome *b* gene, species identification of highly processed meats, 241–243

ddF. *See* Dideoxy fingerprinting

Decontamination systems, reliability in PCR, 117–123

Degenerate oligonucleotide-primed PCR (DOP–PCR), to generate probes from yeast artificial chromosomes, 209–211

Degenerate RAPD primers (D-RAPD), in DNA fingerprinting of bacterial lysates, 265–268

Deletion mutants, quantitative PCR assay for angiotensin-converting enzyme mRNA, 167–171

Deoxyinosine, use of primers containing, with DNA polymerases and proofreading activity, 239–240

Detection

- allele loss in hematopoietic neoplasms, 6–12
- allele loss in myeloid disorders, 6–12
- chemiluminescence in diagnostic test for Gaucher disease, 1–5
- contamination in cell cultures by PCR, 199–208
- electrochemiluminescence, in competitive PCR assay, 327–330
- genetic polymorphisms in eukaryotic taxa, by PCR, 249–255
- HCV RNA by the asymmetric gap ligase chain reaction, 80–84
- mollicutes, contamination of cell cultures, 199–208
- mycoplasmas by PCR-based method, 199–208
- nonradioactive
 - competitive PCR assay, 327–330
 - direct sequencing, detection of p53 gene mutation in cancer tissues, 76–79
 - multiplex PCR screening, 352–356
 - single-strand conformation polymorphism protocol, for genetic screening, 52–55
- p53 gene mutation in cancer tissues, 76–79
- polymorphisms, 227–233
- quantitation of revertants of oral poliovirus vaccine, 62–65
- reverse transcriptase–PCR products, 234–238
- single-base substitutions in PCR-amplified DNA, 188–190
- Diabetes-associated gene, p69(ICA1), 154–159
- Diagnostic test, Gaucher disease, 1–5
- Dideoxy fingerprinting (ddF) and SSCP, 97–108
- Direct blotting electrophoresis, for genetic screening, 52–55
- Disease, genetic, diagnosis, 188–190
- DNA
 - allele frequencies in pooled samples, 13–18
 - amplification with arbitrary primers, and buffer components, 59–61
 - based markers in genome regions by two-primer RAPD reactions, 346–351
 - bending locus, PCR mapping, 44–45
 - buffer components for amplification with arbitrary primers, 59–61
 - curvature, 44–45
 - extraction method for PCR of MLO DNA from plant host species, 56–58

extraction procedure, 368–370

fingerprint profiles, gel matrices for resolving PCR-amplified, 50–51

fingerprinting, crude bacterial lysates using degenerate RAPD primers, 265–268

flanking genomic, method of amplifying, 19–25

fragments and genomic DNA, assessment of colinearity, 129–132

genomic, quantitation of methylation differences, 26–30

library screening, 46–49

mitochondrial, sequences used to identify the species origin of highly processed meats, 241–243

nonspecific synthesis during *in situ* PCR and solution-phase PCR, 89–96

PCR-amplified, detection of single-base substitutions, 188–190

PCR-based method to map the bending locus of, 44–45

polymerase UTMa, PCR with deoxyinosine-containing primers using, 239–240

polymerases with proofreading activity, used with deoxyinosine-containing primers, 239–240

pooling, and determination of microsatellite allele frequencies, 13–18

segments isolated using vectorette and subvectorette PCR, 71–75

sequences, repeated, effect on PCR, 109–116

single-stranded

- conformational polymorphism analysis results in enhanced polymorphism detection, 227–233
- conformation polymorphism and dideoxy fingerprinting, 97–108
- conformation polymorphism protocol, nonisotopic protocol, 52–55
- purified by magnetic M-280–streptavidin beads, 227–233
- tails, length requirement, for ligation-independent cloning of PCR products, 172–177

stain, SYBR Green I, 234–238

synthesis, nonspecific, during *in situ* PCR and solution-phase PCR, 89–96

DOP–PCR. *See* Degenerate oligonucleotide-primed PCR

D-RAPD. *See* Degenerate RAPD primers

Dyes, fluorescent, in quenched probe system, 357–362

ECL. *See* Electrochemiluminescence

Electrochemiluminescence (ECL) detection in competitive PCR assay, 327–330

Electrophoresis, direct blotting in nonisotopic SSCP protocol, 52–55

End trimming, and cassette ligation with PCR to clone exon–intron boundaries, 19–25

Enzyme, multisubstrate, structure–function relationships, 212–218

Errata, 65

ETCL–PCR. *See* PCR with end trimming and cassette ligation

Evaluation, competitor type and size for, in competitive PCR, 219–226

Exon–intron boundaries, cloning, and PCR with end trimming and cassette ligation, 19–25

Familial hypercholesterolemia (FH), screening, 352–356

Ferritin multigene family, analyzed by PCR, 85–88

FH. *See* Familial hypercholesterolemia

FISH. *See* Fluorescence *in situ* hybridization

Fluorescence

- based PCR–SSCP analysis, 275–282
- in situ* hybridization (FISH) probes, method for generating, from yeast artificial chromosomes, 209–211
- RT–PCR, analysis of gene expression in tissues, 154–159

Fluorescent dyes, oligonucleotides in quenched probe system, 357–362

G/C-rich sequences and PCR amplification, 124–125

Gap ligase chain reaction (gLCR), 80–84

GAS. *See* Group A streptococci

Gaucher disease (GD), diagnostic test, 1–5

GD. *See* Gaucher disease

Gel matrices, resolving PCR-amplified DNA fingerprint profiles, 50–51

Gene

- amplification from archival material, method for semiquantification, 178–184
- cytochrome *b*, for species identification of highly processed meats, 241–243
- expression in tissues analyzed by RT–PCR and laser-induced fluorescence, 154–159
- fragments with very high G/C content and amplification, 124–125
- mutation in cancer tissues, p53 detection by nonradioactive direct sequencing, 76–79
- mutation, screening, low-density lipoprotein receptor, 352–356

NF1 total coding sequence amplification, 311–313

quantitation by PCR reveals differential accumulation of ectopic enzyme in cell lines, 145–153

quantitation of methylation status, by solid-phase primer extension, 26–30

synthesis by Klenow assembly/extension—*Pfu* polymerase amplification (KAPPA), 299–302

Genetic screening

- for disorders, 1–5, 6–12, 52–55
- and single-strand conformation polymorphism, 52–55

Genetic similarity coefficients computed from RAPD data

- correcting for PCR artifacts, 38–43
- effects of PCR artifacts, 31–37

Genetic typing, 331–336, 337–345

Genomic DNA

- amplification of long sequences, 294–298
- and DNA fragments, assessment of colinearity, 129–132

Genomic fingerprinting, microsatellite-primed PCR, 249–255

Genomic regions, quantitation of methylation of, 26–30

Genotypes, batched analysis, 331–336

GLCR. *See* Gap ligase chain reaction

Group A streptococci (GAS), typing, by PCR method, 288–293

H ferritin multigene family, analyzed by PCR, 85–88

Hairpin ribozyme, alteration of specificity using PCR, 139–144

Hapten-labeled DNA fragments, generated from a trace amount of YAC, 209–211

HCV. *See* Hepatitis C virus

Heart tissue, archival, mitochondrial DNA analysis, 309–310

Hematologic malignancy, quantitation of gene methylation alterations for diagnosis or prognosis, 26–30

Hematopoietic neoplasm, detection of allele loss, 6–12

Hepatitis C virus (HCV) RNA, detection by the asymmetric gap ligase chain reaction, 80–84

Heteroduplex detection, of single-base substitutions in PCR-amplified DNA, 188–190

*Hpa*II-digested template, quantitation of, to monitor methylation alterations in hematologic malignancies, 26–30

Hybridization analysis, of PCR products by capillary electrophoresis, 303–304

Hybridoma cells, mouse, immunoglobu-

lin genes from, amplified by PCR, 256–264

Immunoglobulin genes, mouse hybridoma, amplified by PCR, 256–264

Inhibition, of PCR, and stimulation of primer–dimer formation by reverse transcriptase, 62–65

In situ PCR analysis, of nonspecific DNA synthesis, 89–96

Jumping reaction, in PCR, 109–116

KAPPA. *See* Klenow assembly/extension—*Pfu* polymerase amplification

Klenow assembly/extension—*Pfu* polymerase amplification (KAPPA), 299–302

Laser-induced fluorescence (LIF), and RT–PCR, analysis of gene expression in tissues, 154–159

LCR. *See* Ligase chain reaction

LDLR gene mutations. *See* Low-density lipoprotein receptor gene mutations

Length, requirement for single-stranded tails for ligation-independent cloning of PCR products, 172–177

Libraries, cDNA screening, by PCR, 46–49, 126–128

LIC. *See* Ligation-independent cloning

LIF. *See* Laser-induced fluorescence

Ligase chain reaction (LCR), 80–84

Ligation-independent cloning (LIC) of PCR products, length requirement of single-stranded tails, 172–177

Lipoprotein receptor gene mutations, screening, 352–356

Low-density lipoprotein receptor (LDLR) gene mutations, screening, 352–356

Lymphocytes, RNA extraction for RT–PCR, comparison of methods, 185–187

Magnetic M-280–streptavidin beads, purification of single-stranded DNA, 227–233

Manual Supplement, contents, 69, 137, 197, 248, 316, 382

Mapping, bending locus of DNA molecules, 44–45

MAPREC. *See* Mutant analysis by PCR and restriction enzyme cleavage

Meat products, highly processed, identified by mitochondrial DNA sequences, 241–243

Metastable single-strand DNA conformational polymorphism (mSSCP) analysis enhanced polymorphism detection, 227–233

Methylation, quantitation of, in specific genomic regions, 26–30

MF–PCR–SSCP. *See* Multiple fluorescence-based PCR single-strand conformation polymorphism

Microsatellite

- allele separation, with PhastSystem, 380–381
- determining allele frequencies in pooled DNA samples, 13–18
- markers, 331–336
- primed PCR, genomic fingerprinting, 249–255

Minisatellite variant repeat PCR (MVR–PCR), 71–75

Mitochondrial DNA

- analysis, archival heart tissue, 309–310
- sequences used to identify the species origin of highly processed meats, 241–243

MLOs. *See* Mycoplasma-like organisms

Mollicutes, contamination of cell cultures, PCR-based detection, 199–208

Mouse hybridoma cells, immunoglobulin genes from, amplified by PCR, 256–264

mRNA

- angiotensin-converting enzyme, quantitation by PCR, 167–171
- determination by competitive PCR, 219–226
- polyadenylation states, PCR analysis, 317–321
- species quantitation, by RT–PCR, on total mRNA population, 160–166

mSSCP. *See* Metastable single-strand DNA conformational polymorphism

Multigene family, H ferritin, PCR analysis, 85–88

Multiple fluorescence-based PCR single-strand conformation polymorphism (MF–PCR–SSCP), 275–282

Multiplex PCR

- approach, in nonisotopic SSCP protocol, 52–55
- bcr–abl* in fusion transcripts in Philadelphia-positive acute lymphoblastic leukemia, 283–287
- genetic typing, 337–345
- screening, nonradioactive, 352–356

Multisubstrate enzyme, structure–function relationships, 212–218

Mutagenesis, background-minimized cassette, PCR, 212–218

Mutant analysis by PCR and restriction enzyme cleavage (MAPREC), 62–65

Mutations, detection, 188–190

MVR–PCR. *See* Minisatellite variant repeat PCR

Mycoplasma

- contamination of cell cultures, PCR-based detection of, 199–208
- like organisms (MLOs), plant pathogenic, DNA extraction method, 56–58

Myelodysplasia, preleukemic, detection of allele loss, 6–12

Myeloid disorders, detection of allele loss, 6–12

Neoplasm, hematopoietic, detection of allele loss, 6–12

Neurofibromatosis type 1 gene. *See NF1 gene*

NF1 gene, total coding sequence amplification, 311–313

Nonradioactive detection

- competitive PCR assay, 327–330
- direct sequencing, detection of p53 gene mutation in cancer tissues, 76–79
- multiplex PCR screening, 352–356
- single-strand conformation polymorphism protocol, for genetic screening, 52–55

OLA. *See Oligonucleotide ligation assay*

Oligonucleotide ligation assay (OLA), amplification for multiplex genetic typing, 337–345

Oligonucleotides, and fluorescent dyes in quenched probe system, 357–362

p53 gene, detection of mutation in cancer tissues using nonradioactive direct sequencing, 76–79

Paraffin wax-embedded samples

- archival heart tissue, mitochondrial DNA analysis, 309–310
- archival material and a method for semiquantification of gene amplification, 178–184
- and PCR reagents, 191–194

Parameters affecting the sensitivities of dideoxy fingerprinting and SSCP, 97–108

PCR

- amplification of immunoglobulin genes from mouse hybridoma cells, 256–264
- amplification of gene fragments with very high G/C content, 124–125
- amplification of genomic DNA, 294–298
- amplification refractory mutation system, low-density lipoprotein receptor gene screening, 352–356
- amplified DNA fingerprint profiles, resolving by comparison of gel matrices, 50–51

analysis of the H ferritin multigene family, 85–88

artifacts

- formation, 109–116
- correcting for, and computation of genetic similarity coefficients, 38–43
- effects of, and computation of genetic similarity coefficients, 31–37

background-minimized cassette mutagenesis, using cassette-specific selection markers, 212–218

of *bcr-abl* in fusion transcripts in Ph+ ALL, 283–287

competitive

- evaluation of competitor type and size for use in the determination of mRNA, 219–226
- transcription-based system, 363–367

decontamination systems, reliability, 117–123

degenerate oligonucleotide-primed, to generate probes from yeast artificial chromosomes, 209–211

detection of mycoplasmas, 199–208

effect of internal direct and inverted *Alu* repeat sequences, 109–116

electrochemiluminescence detection

- in competitive assay, 327–330

group A streptococci typing, 288–293

in direct gene quantitation, 145–153

in situ and solution-phase analysis, of nonspecific DNA, 89–96

inhibition and primer–dimer stimulation by reverse transcriptase, 62–65

jumping reaction in, 109–116

mapping the bending locus of DNA molecules, 44–45

microsatellite-primed, genomic fingerprinting, 249–255

minisatellite variant repeat, 71–75

mRNA polyadenylation states, 317–321

nested, with room-temperature-stable reagents, 376–379

products

- analyzed by capillary hybridization, 303–304
- detected by quenched probe system, 357–362
- ligation-independent cloning of, length requirement of singled-stranded tails, 172–177

rapid isolation of cDNA clones, 126–128

rapid quantitative, in tissue specimens, 305–308

reactants on magnetic M-280–streptavidin beads, purification of single-stranded DNA, 227–233

reagents, wax-embedded, 191–194

reverse transcriptase

- generation of standard molecules for, 371–375
- and laser-induced fluorescence, analysis of gene expression, 154–159
- products detected by means of a novel, sensitive DNA stain, 234–238
- quantitation of mRNA species, 160–166

screening

- of cDNA libraries, 46–49
- nonradioactive, 352–356

semiquantitation of gene amplification

- from archival material, 178–184

single-strand DNA conformational polymorphism (PCR-SSCP) analysis enhances polymorphism detection, 227–233

single-tube nested, 376–379

site-directed mutagenesis, 269–274

SSCP analysis, fluorescence based, 275–282

used to alter hairpin ribozyme specificity, 139–144

used to identify the species origin of highly processed meats, 241–243

vectorette and subvectorette, used to isolate transgene flanking DNA, 71–75

with deoxyinosine-containing primers using DNA polymerases with proofreading activity, 239–240

with end trimming and cassette ligation (ETCL–PCR), to clone exon–intron boundaries, 19–25

PCR–SSCP. *See PCR–single-strand DNA conformational polymorphism*

PhastSystem, separation of microsatellite alleles, 380–381

Philadelphia-positive acute lymphoblastic leukemia, PCR of *bcr-abl* in fusion transcripts in, 283–287

Plants, DNA extraction and PCR amplification of MLO DNA from, 56–58

Poliovirus vaccine, oral, detection and quantitation of revertants, 62–65

Polyadenylation analysis by PCR, 317–321

Polymorphic microsatellite markers, 331–336

Polymorphisms, detection enhanced by using metastable single-strand DNA conformational polymorphism, 227–233

Polyphenolics, and DNA extraction, 56–58

Primer–dimer formation, stimulation by reverse transcriptase, 62–65

Primer extension, solid-phase, to quanti-

tate methylation of specific genome regions, 26–30

Primers, arbitrary, buffer components tailor DNA amplification with, 59–61

Product news, 133–134, 244–245

Proofreading activity, polymerases with and PCR with deoxyinosine-containing primers, 239–240

Proteinase K and SDS, DNA extraction procedure, 368–370

Pseudogenes, revealed by PCR analysis of the H ferritin multigene family, 85–88

QPCR system 5000. *See* Quantitative PCR system 5000

Quantitation

- and detection of revertants of oral poliovirus vaccine, 62–65
- gene, by PCR, 145–153
- of methylation of specific genomic regions, 26–30
- of mRNA species by RT–PCR on total mRNA population, 160–166
- of RNA extracted from lymphocytes, by RT–PCR, 185–187

Quantitative analysis

- gene expression in tissues by RT–PCR and laser-induced fluorescence, 154–159
- PCR determination in tissue specimens, 305–308
- RT–PCR products by means of a novel, sensitive DNA stain, 234–238

Quantitative PCR (QPCR) system 5000, and competitive PCR, transcription-based system, 363–367

Quenched probe system, for detecting PCR product, 357–362

Random amplified polymorphic DNA (RAPD) markers

- genetic polymorphism screening, 346–351
- genetic similarity coefficients, 31–37, 38–43

RAPD. *See* Random amplified polymorphic DNA

Rat-1 cells, *v-fos* transformants, and revertants, and PCR direct gene quantitation, 145–153

Reagents

- room-temperature stable, PCR, 376–379
- wax-embedded, 191–194

Reliability, of PCR decontamination systems, 117–123

Reverse transcriptase–PCR

- comparison of methods for RNA extraction from lymphocytes, 185–187

competitive, electrochemiluminescence detection in, 327–330

generation of standard molecules for, 371–375

primer–dimer formation, 62–65

products, novel and sensitive DNA stain, 234–238

quantitation

- of angiotensin-converting enzyme mRNA, 167–171
- of mRNA species, 160–166

quantitative analysis of gene expression, 154–159

YACs, identification of terminal exons, 322–326

Revertants, oral poliovirus vaccine, detection and quantitation of, 62–65

Ribozymes, specificity alteration, using PCR, 139–144

RNA, extraction from lymphocytes for RT–PCR, comparison of methods, 185–187

Room-temperature-stable reagents, nested PCR, 376–379

RT–PCR. *See* Reverse transcriptase–PCR

Sanger dideoxy sequencing, 97–108

Screening

- cDNA libraries, 46–49, 126–128
- Gaucher disease, 1–5
- genetic disorders, 1–5, 6–12, 52–55

SDS and proteinase K, DNA extraction procedure, 368–370

Semiquantification, of gene amplification from archival material, 178–184

Similarity coefficients, genetic, computed from RAPD data, 31–37, 38–43

Single-base substitutions, in PCR-amplified DNA, 188–190

Single-stranded DNA (ssDNA)

- conformational polymorphism analysis results in enhanced polymorphism detection, 227–233
- conformation polymorphism and dideoxy fingerprinting, 97–108
- conformation polymorphism protocol, nonisotopic protocol, 52–55
- purified by magnetic M-280–streptavidin beads, 227–233

tails, length requirement, for ligation-independent cloning of PCR products, 172–177

Site-directed mutagenesis, PCR method for high fidelity, 269–274

Solution-phase PCR, analysis of nonspecific DNA synthesis, 89–96

Species, of highly processed meat products identified by mitochondrial DNA sequences, 241–243

SSCP. *See* Single-strand conformation polymorphism

ssDNA. *See* Single-stranded DNA

Stain, DNA, SYBR Green I, 234–238

Streptococci, group A, typing, by PCR method, 288–293

Structure–function relationships of multisubstrate enzyme, 212–218

Subvectorette and vectorette PCR, to isolate transgene flanking DNA, 71–75

SYBR Green I DNA stain, 234–238

Template integrity, for PCR amplification of genomic DNA, 294–298

Template-calibrated RT–PCR, and laser-induced fluorescence, analysis of gene expression, 154–159

Tissue specimens, rapid quantitative PCR in, 305–308

Transcription-based competitive PCR system, 363–367

Transgene flanking DNA, isolated using vectorette and subvectorette PCR, 71–75

trans hairpin ribozyme, alteration of specificity using PCR, 139–144

Transfection assays, transient, 145–153

Tumors, assessment and semiquantification of gene amplification from archival material, 178–184

UITma DNA polymerase, with proofreading activity, PCR with deoxyinosine-containing primers using, 239–240

Vaccine, oral poliovirus, detection and quantitation of revertants, 62–65

Vectorette and subvectorette PCR, to isolate transgene flanking DNA, use of, 71–75

Vir typing, group A streptococci, 288–293

Wax-embedded samples

- archival heart tissue, mitochondrial DNA analysis, 309–310
- archival material and a method for semiquantification of gene amplification, 178–184

PCR reagents, 191–194

YACs. *See* Yeast artificial chromosomes

Yeast artificial chromosomes (YACs)

- identification of terminal exons, 322–326
- simple method to generate hapten-labeled DNA fragments from, 209–211

Yeast Genome Sequencing Programme of the European Community, 129–132

VOLUME 4, AUTHOR INDEX

Adzuma, K., 275
Alfandari, D., 46
Allen, M.J., 71
Altschuler, M., 139
Altwegg, M., 368
Aslanidis, C., 172
Atkinson, R.G., 249
Bahramian, M.B., 145
Barranger, J.A., 1
Bartlett, J.M.S., 178
Bassam, B.J., 59
Battistini, L., 185
Bautista, D., 76
Benedetto, J.-P., 160
Benhattar, J., 76
Berdoz, J., 256
Bertонcini, J., 76
Bevilacqua, M.A., 85
Beyermann, B., 241
Bhatnagar, R.K., 212
Blair, P., 191
Bobba, A., 309
Bonnet, J., 160
Borneman, J., 139
Brandt, P., 241
Brookes, A.J., 209
Brosnan, C.F., 185
Burdick, B.A., 191
Buzás, Z., 380
Caetano-Anollés, G., 59
Callis, M., 352
Camaschella, C., 309
Candrian, U., 117
Cerney, M.B., 80
Chaubert, P., 76
Cheifetz, S., 363
Chen, Y., 294
Chen, L., 269
Cheng, J., 227
Cheng, S., 294
Choong, C.S., 219
Chumakov, K.M., 62
Cimino, F., 85
Claxton, D., 6
Collick, A., 71
Cooke, T.G., 178
Cooper, D.L., 1, 265
Costanzo, F., 85
Currie, B., 288
D'Agostino, P., 85
Danenber, K.D., 305
Danenber, P.V., 305
Darribére, T., 46
Darvasi, A., 13
de Jong, P.J., 172
Deetz, K., 357
DeGrandis, P., 139
DeGrandis, S.A., 363
Deisseroth, A.B., 6
DeSilva, U., 322
Devon, R.S., 209
Di Bacco, A., 126
Dosch, H.-M., 154
Dussurget, O., 199
Edmands, S., 283
Eggerding, F.A., 337
Eggersdorfer, I., 52
Ehrlich, M., 109
Fairman, J., 6
Fanburg, B.L., 167
Faniello, M.C., 85
Fattah, F.A., 212
Flood, S.J.A., 357
Forssmann, W.-G., 124
Frattini, A., 126
Fujiwara, H., 239
Fujiwara, K., 239
Fulco, A.J., 269
Gaedigk, R., 154
Galasinski, S., 139
Gallery, F., 89
Gardiner, R.C., 249
Gardner, D., 288
Garret, M., 160
Giannattasio, S., 309
Gibb, K., 56
Giusti, W., 357
Goldenberger, D., 368
Gosden, J.R., 209
Green, E.D., 322
Gresshoff, P.M., 59
Hamoui, S., 160
Hampel, A., 139
Harper, P.S., 311
Hartas, J., 288
Hashimoto, K., 239
He, G., 50
Heiskanen, M., 26
Heroux, J.A., 327
Hiesel, R., 241
Higuchi, R., 294
Hill, C., 305
Höflein, C., 117
Hofmann, T.A., 322
Holowachuk, E.W., 299
Hörnschemeyer, D., 376
Hu, J., 346
Hurley, D.M., 219
Itakura, M., 19, 275
Iwahana, H., 19, 275
Jarret, R.L., 50
Jeffreys, A.J., 71
Ji, W., 109
Karges, W.J.P., 154
Kasuga, T., 227
Katashima, R., 19, 275
Keller, C., 52
Kemp, D.J., 288
Khatib, H., 13
Kirk, J., 283
Kleesiek, K., 376
Kleinz, R., 371
Knoblauch, H., 52
Kong, X.-J., 167
Kopp, D.W., 1
Kotze, M.J., 188, 352
Krahenbuhl, J.-P., 256
Kratochvil, J.D., 80
Krizman, D.B., 322
Kury, F., 234
Laffler, T.G., 80
Laine, S., 26
Lamboy, W.F., 31, 38
Langenhoven, E., 352
Lanning, R.W., 265
Lanzillo, J.J., 167
LeDuc, C., 331
Lee, A., 283
Leichman, L.L., 305
Lenz, H.-J., 305
Liang, Q., 269
Lichter, J., 331
Liedtke, W., 185
Lippolis, R., 309
Liu, Q., 97
Livak, K.J., 357
Lüthy, J., 117
MacConnell, P., 89
Majumder, K., 212
Marmaro, J., 357
Marra, E., 309
Marshall, R.L., 80
Mathews, J.D., 288
Maule, J.C., 209
McCulloch, R.K., 219
Meltzer, P.S., 322
Miller, P., 331
Mitchelson, K.R., 227
Monath, T.P., 256
Monforte, J.A., 294
Morgan, R.L., 80
Nagarajan, L., 6
Niederhauser, C., 117
Nuovo, G.J., 89
Oto, M., 303
Padovan, A., 56
Palotie, A., 26
Parry, P., 331
Peeters, A.V., 188, 352
Perschil, I., 368
Plotski, Y., 13
Porcellini, A., 85
Porteous, D.J., 209
Prakash, C.S., 50
Priest, D.G., 305
Qiu, J., 50
Qu, G.A., 109
Quaresima, B., 85
Quiros, C.F., 346
Radich, J., 283
Raine, C.S., 185

Ramanujam, R., 191
Rawadi, G., 199
Reske-Kunz, A.G., 371
Ritzler, M., 368
Ross, R., 371
Ruhoff, M.S., 299
Sakallah, S.A., 1
Sakallah, S.A., 265
Salles, F., 317
Sansieri, C., 1
Schmitz, G., 172
Schneeberger, C., 234
Schuster, H., 52
Selvapandian, A., 212
Shen, M.H., 311
Shibasaki, Y., 209
Siitari, H., 26
Siwkowski, A., 139
Slorach, E.M., 209
Soller, M., 13
Sommer, S.S., 97
Speiser, P., 234
Sripakash, K.S., 288
Strickland, S., 317
Strina, D., 126
Suehiro, T., 303
Susani, L., 126
Sustachek, J.C., 80
Svänen, A-C., 26
Szczepanik, A.M., 327
Takahashi, Y., 275
Theart, L., 352
Thiart, R., 352
Tiano, M.T., 85
Trent, J.M., 322
Tsujisawa, T., 19
Tuzun, S., 50
Underwood, M.A., 178
Unseld, M., 241
Upadhyaya, M., 311
Valle, F., 44
van Eysden, J., 346
Van Houten, B., 294
Varga, L., 380
Verhasselt, P., 129
Vezzoni, P., 126
Villa, A., 126
Volckaert, G., 129
Warshamana, G.S., 109
Wegmüller, B., 117
Weising, K., 249
Weiss, J., 124
Weiss, N., 52
Wilkinson, E.T., 363
Willman, C.L., 6
Wolff, C., 376
Wolff, D., 376
Yoshimoto, K., 19
Yoshimoto, K., 275
Yuasa, Y., 303
Zarbl, H., 145

SEARCH THE CONTENTS OF GENES & DEVELOPMENT....ON-LINE!

The contents page of each 1995 issue of *Genes & Development* is made available on-line as soon as the issue is published.

Now you can preview the latest issue **before** you get it! And you can do keyword searches on the titles of all the year's issues months before the index or the abstracts are published elsewhere.

You can do all this at your computer! All you need is access to the World Wide Web.

Here's a sample of what you would see when you call up the Table of Contents of a recent issue of *Genes & Development*.

The screenshot shows a window titled "NCSA Mosaic: Document View". The menu bar includes "File", "Options", "Navigate", "Annotate", and "Help". The "Navigate" menu is underlined. The "Title" field contains "Genes and Development December 1, 1994 (Volume 8, Issue 23)". The "URL" field contains "http://www.cshl.org/journals/gnd/8/23.html". To the right of the URL field is a small graphic of a globe with a line and a dot. The main content area displays the following table of contents:

Genes and Development December 1, 1994	
<i>Volume 8, issue 23</i>	
Research papers	
Intercellular C-signaling and the traveling waves of <i>Myxococcus</i> Brian Sager and Dale Kaiser 2793	
cAMP regulates morphogenesis in the fungal pathogen <i>Ustilago maydis</i> Scott Gold, Gillian Duncan, Katherine Barrett, and James Kronstad 2805	
Myc-mediated apoptosis requires wild-type p53 in a manner independent of cell-cycle arrest and the ability of p53 to induce p21 ^{WAF1/CIP1} Andrew J. Wagner, John M. Kokontis, and Nissim Hay 2817	
Lymphohematopoietic progenitors immortalized by a retroviral vector harboring a dominant-negative retinoic acid receptor can recapitulate lymphoid, myeloid, and erythroid development Schickmann Tsai, Stephen Bartelmez, Ewa Sitnicka, and Steven Collins 2831	
Influence of a steroid receptor DNA-binding domain on transcriptional regulatory functions Jeffrey A. Lefstin, Jay R. Thomas, and Keith R. Yamamoto 2842	
The WD repeats of Tup1 interact with the homeo domain protein Alpha2 Kelly Komachi, Michael J. Redd, and Alexander D. Johnson 2857	
TFIIF--TAF--RNA polymerase II connection N. Lynn Henry, Allyson M. Campbell, William J. Feaver, David Poon, P.	

At the bottom of the window is a toolbar with buttons for "Back", "Forward", "Home", "Reload", "Open...", "Save As...", "Clone", "New Window", and "Close Window".

The contents pages of *Genes & Development* are available at your fingertips. Just log into World Wide Web site -- <http://www.cshl.org/journals/>



Subscribe Today!

Cold Spring Harbor Laboratory Press, 10 Skyline Drive, Plainview, N.Y. 11803-2500
Phone: 1-800-843-4388 or 516-349-1930 FAX: 516-349-1946
E-mail: cshpress@cshl.org at World Wide Web Site <http://www.cshl.org/>



Introducing the first agarose that can challenge polyacrylamide.

MetaPhor agarose

Polyacrylamide

Until now, when you wanted the finest resolution of PCR* products and small DNA fragments (less than 800 bp), you probably made a polyacrylamide gel. Preparing that gel, however, was tedious and time-consuming.



But now there's something better. It's a new kind of agarose that not only offers speed and convenience, but also has twice the resolution capabilities of any other agarose. It's new MetaPhor™ agarose from FMC.

In fact, as you can see from the above results, MetaPhor agarose gives you resolution so fine (down to a 4 bp difference) that it rivals polyacrylamide. And we think that makes it a clear winner.

Just dissolve MetaPhor agarose in 1X TBE buffer, cast and chill the gel in your submarine chamber, load your samples, and go. It's as easy as that.

So take the MetaPhor challenge, and see how our new MetaPhor agarose performs. When you do, you'll understand why scientists who want the best go straight to the source. To learn more, or to place your order, call us today at **800-341-1574**.



Go straight to the source.

For Research Use Only. Not for use in diagnostic procedures.

FMC and MetaPhor are trademarks of FMC Corporation. U.S. Patent No. 5,143,646; applications in other countries. ©1993 FMC Corporation.
FMC BioProducts, 191 Thomaston Street, Rockland, ME 04841. Customer Service: 800-341-1574 Technical Service: 800-521-0390 FAX: (207) 594-3491
FMC BioProducts Europe, Risingevej 1, DK-2665 Vallenbaek Strand, Denmark. Tel.: 45-42-73-11-22 FAX: 45-42-73-56-92