Reviewers, Volume 6 (1996)

The editors would like to thank the Editorial Board members and the following referees who were kind enough to review papers and provide advice during 1996.

Adams, Mark
Archibald, Alan
Arnheim, Norman
Asai, David
Ashburner, Michael
Barsh, Greg
Bates, Gilliam
Batzer, Mark
Beattie, Craig
Beavis, William
Behringer, Richard
Beier, Dave
Bellen, Hugo
Belmont, John
Bertranpetit, Jaume
Bhattachara, Shomi
Blaisdell, Edwin
Bork, Peer
Bradley, Allan
Brodeur, Garrett
Brody, Lawrence
Brown, Carol
Brown, Patrick
Bucan, Maja
Buchwald, Manuel
Buckler, Alan
Budarf, Marcia
Buetow, Kenneth
Burmeister, Margit
Camper, Sally
Carrano, Anthony
Casey, Graham
Chaplin, David
Chasin, Larry
Chee, Mark
Churchill, Gary
Clemens, Paula
Compton, John
Coulson, Alan
Craigen, William
Crawford, Michael
Cross, Sally
Curran, Thomas
Cutting, Gary
D'Eustachio, Peter
Daiger, Steven
Davidson, Daniel
Deininger, Prescott
Dietrich, Fred
Dietrich, William
Dietz, Hal
diRienzo, Anna
Dove, Bill
Dracopoli, Nicholas
Drayna, Dennis
Dryja, Ted
Dunham, Ian
Duyk, Geoffrey
Eichler, Evan
Elgar, Greg
Ensign, Jerry
Epstein, Henry
Ericson, Leif
Evans, Glen
Ewens, Warren
Fan, Jian-Bing
Fearon, Eric
Federspiel, Nancy
Ferre, Francois
Fodor, Steve
Freimer, Nelson
Garcia, Pablo
Gardiner, Kathleen
George, Al
Georges, Michel
Gerhard, Daniella
Gesteland, Raymond
Ghosh, Soumitra
Gilliam, Conrad
Gnirke, Andi
Goffinet, Andre
Goodfellow, Peter
Goodman, Howard
Grompe, Marcus
Grosschedl, Rudi
Gyapay, Gabor
Heinkoff Steve
Heintz, Nathaniel
Herman, Gail
Hoffman, Eric
Horsthekme, Bernard
Hudson, Thomas
Hughes, Austin
Hughes, Mark
Jessell, Thomas
Jones, David
Kaiser, Chris
Kaiser, Dale
Kazazian, Haig
Keating, Mark
Kellems, Rod
Kemp, David
Kere, Juha
King, Robert
Kingsley, David
Kinzler, Ken
Korneluk, Robert
Krogstad, Don
Kruglyak, Leonid
Kucherlapati, Raju
Kunkel, Thomas
Kuroda, Mitzi
Lalande, Marc
Landsman, David
Lawrence, Jeannie
LeBeau, Michelle
Ledbetter, David
Lennon, Greg
Ley, Tim
Lipman, David
Litt, Michael
Little, Peter
Loomis, William
Lopez, Javier
Lupski, James
MacGregor, Grant
Mandel, Jean-Louis
Maraia, Richard
Martienssen, Robert
Matera, Greg
Matise, Tara Cox
McClelland, Michael
McPherson, John
Meisler, Miriam
Meltzer, Paul
Merriwether, Andy
Messing, Joachim
Milbrandt, Jeffrey
Mitchelmore, Richard
Monaco, Anthony

6:1233–1234 ©1996 by Cold Spring Harbor Laboratory Press ISSN 1054-9803/96 $5.00

Moore, Graham
Morgan, Kenneth
Motulsky, Arno
Moyzis, Robert
Mulligan, John
Murray, Jeffrey
Nadeau, Joseph
Nathans, Jeremy
Nicholls, Robert
Nicols, Roger
Noller, Harry
Nussbaum, Robert
O'Connell, Peter
Olson, Jane
Orr, Harry
Ostell, James
Ostrander, Elaine
Ott, Jurgen
Page, David
Palazzolo, Michael
Patel, Pragna
Patterson, Andrew
Pavan, William
Perlin, Mark
Perlman, Alan
Pevzner, Pavel
Ponder, Bruce
Popovitch, Brad
Poustka, Annemarie
Quackenbush, John
Reid, Thomas
Reitman, Harold
Rice, John
Roach, Jared
Rommens, Joanna
Rosenthal, Andre
Rubin, Edward
Sankoff, David
Sapienza, Carmen
Schafer, Alex
Schlessinger, David
Schmidt, Renate
Shaw, Sarah
Sheffield, Val
Sherman, Stephanie
Shork, Nicholas
Shuler, Gregory
Sikela, James
Silverman, Gary
Siracusa, Linda
Smith, Douglas
Smith, Hamilton
Sogin, Mitch
Speed, Terry
Spencer, Forest
Stefansson, Kari
Stein, Jeffrey
Stoneking, Mark
Strauss, Arnold
Tabin, Cliff
Tagle, Daniel
Thomas, Jeffrey
Thomas, Karen
Thomas, Winston
Tilghman, Shirley
Timms, Kristin
Touchman, Jeffrey
Trent, Jeffrey
Trowsdale, John
Tsai, Ming
Vollrath, Douglas
Warren, Steve
Waterman, Mike
Waterson, Robert
Weber, James
Weir, Bruce
Wijsman, Ellen
Witman, George
Wold, Barbara
Wolfe, Allan
Wolfe, Roger
Wootton, John
Woychik, Richard
Wynshaw-Boris, Tony
Yanagisawa, Masashi
Zogbi, Huda

Advertisers, Volume 6 (1996)

Bios Laboratories, Inc.

Cambridge Healthtech Institute

Clontech Laboratories

Cold Spring Harbor Laboratory Meetings

Cold Spring Harbor Laboratory Press

Fresenius AG-Diagnostik

Genset

Integrated Separation Systems

Leica, Inc.

Life Technologies

MJ Research

Molecular Bio-Products, Inc.

New England BioLabs

Oligos Etc., Inc. & Oligos Therapeutics

Olympus Microscopes

Perkin-Elmer Corporation

Qiagen, Inc.

Quantum Biotechnologies

Research Genetics, Inc.

Robbins Scientific Corp.

Rockland, Inc.

Schleicher & Schuell

Stratagene

Takara Shuzo Co., Ltd.

Time Logic, Inc.

6:1235 ©1996 by Cold Spring Harbor Laboratory Press ISSN 1054-9803/96 $5.00

Author Index, Volume 6 (1996)

Aaronson, J.S., 829
Abbott, C.M., 715
Adams, L.G., 956
Adamson, A.W., 1084
Aerssens, J., 404
Agochiya, M., 235
Ai, Y., 980
Alarcón-Riquelme, M.E., 1170
Alexander, L.J., 371
Alibert, O., 492
Altschmied, J., 102
Alward, W.L.M., 862
Amaldi, F., 1226
Andersson, L., 907
Anoia, E., 980
Ansari-Lari, M.A., 314
Antonarakis, S.E., 747
Anttinen, A., 965
Arcot, S.S., 1084
Ashikawa, I., 935
Assum, G., 267
Auffray, C., 492
Aurias, A., 43
Avraham, K.B., 361
Ayyagari, R., 504
Bader, I., 1056
Baens, M., 404
Balciuniene, J., 1170
Bale, A., 633
Ballabio, A., 880
Bardenheuer, W., 176
Barker, D.L., 893
Barrantes, R., 142, 1177
Baskaran, N., 633
Bassi, M.T., 880
Batus, S., 132
Batzer, M.A., 1084
Baudler, M., 102
Beattie, C.W., 371
Becker, M., 807
Beeghly, A., 290
Bell, C.J., 1149
Bell, J., 155
Belmonte, S., 19
Benavides, E., 724
Benke, J., 414
Benomar, A., 965
Bentley, D.R., 943
Berger, R., 361
Bergsma, D.J., 980
Berno, A.J., 80
Berzi, P., 580
Bhargava, A.K., 633
Bhattacharya, S.S.,92, 1093
Bianchi, N.O., 601
Bird, A.C., 92
Blangero, J., 724
Blevins, R.A., 829
Boguski, M.S., 846
Bois, F., 492
Bonaldo, M.F., 791, 807
Borén, J., 1123
Borkowski, J.A., 829
Borowsky, R.L., 280
Bouchez, D., 19
Bouffard, G.G., 255
Bowe, A.E., 515
Braden, V.V., 255
Breidenbach, H.H., 58
Brenner, S., 1185, 1207, 1226
Brice, A., 965
Brinkmann, U., 187
Bröcker, F., 176
Brok-Simoni, F., 361
Broughton, W.J., 590
Brouwers, B., 580
Brown, P.O., 639
Buchberg, A.M., 300
Budarf, M.L., 1149
Bunker, C.H., 142
Burgess, R.R., 886
Burghes, A.H.M., 1200
Burke, D.T., 336
Burn, T.C., 525
Butler, R.J., 620
Buys, C., 176
Caldara, F., 35
Callow, M.J., 1123
Camilleri, C., 19
Capuano, V., 448
Carrano, A.V., 1084
Carson, E., 124
Cawthon, R., 58
Cecconi, F., 1226
Cesareni, G., 1226
Chakraborty, R., 142, 1177
Chambers, D.M., 715
Chandrasekharappa, S., 504
Charlier, C., 580
Chatterjee, A., 465
Chen, H., 747
Chiang, P.-W., 1013
Chiapelli, B., 807
Chinault, C., 504
Chissoe, S., 807
Chong, S.S., 735
Chrast, R., 747
Chrétien, N., 1216
Christian, S.L., 742
Christner, P.J., 300
Chua, M., 431, 1192
Chung, W.K., 431, 1192
Ciuffetti, L.M., 1160
Clark, M., 290
Coffey, A.J., 943
Connors, T.D., 515, 525
Conti, C.J., 1070
Conway, D., 235
Cooke, I.E., 620
Cooper, M.L., 1110
Copeland, N.G., 361
Cox, D.R., 218
Crawford, A.M., 667, 876
Crkvenjakov, R., 132
Crollius, H.R., 943
Crosio, C., 1226
Cuthbertson, R.P., 876
Dackowski, W.R., 515, 525
Daiger, S.P., 255
Darby, K., 858
David, G., 965
Davison, C., 92
Davison, D.B., 454
Day, I.N.M., 558
de Jong, P., 235
de la Chapelle, A., 202, 218, 249, 351
de Luna, R.I.O., 1050
Debry, R.W., 702
Deininger, P.L., 1084
Deka, R., 142, 1177
Demczuk, S., 43
DeVault, J.D., 571
Dewdnewy, J., 19
Dietrich, N., 807
Digre, K., 965
Dixon, J., 26
Dixon, M.J., 26
Dlouhy, S.R., 678
Dodds, K.G., 667
Doggett, N.A., 515
Dolan, M., 19
Dow, J.A.T., 972
Drinkwater, C., 124
DuBuque, T., 807
Duggirala, R., 724
Dyanov, H., 132
Easty, D.J.. 880
Eckman, B., 829
Edwards, Y.H., 226
Ehrlich, S.D., 448
Ehrsson, H., 965
Elliston, K.O., 829
Emanuel, B.S., 1149
Enad, S., 893
Evans, K., 92
Fan, J.-B., 218
Farnir, F., 580
Fattorini, P., 235
Favello, A., 807
Feng, J., 956
Feng, Y., 678
Ferrell, R.E., 142, 1177
Ferretti, V., 1
Fink, T., 267
Flejter, W.L., 1133
Fogel, E.J., 1013
Förnzler, D., 102
Forsius, H., 249
Fortina, P., 893
Fox, M., 226
Francomano, C.A., 1050
Freiberg, C., 590
Freimer, N.B., 211
Frey, M.R., 688, 702
Galleron, N., 448
Gallo, M., 187
Galloway, S.M., 667
Ganesan, T.S., 620
Garza, J.C., 211
Georges, M., 580, 907
Ghetti, B., 678
Gibbs, R.A., 314

6:1236–1239 ©1996 by Cold Spring Harbor Laboratory Press ISSN 1054-9803/96 $5.00

Gibson, U.E.M., 995
Gillan, A., 972
Gilliam, T.C., 351
Giovannoni, S.J., 1160
Gish, W., 807
Glynn, M.W., 633
Godfrey, M., 392
Gokkel, E., 361
Goldstein, L.S., 1070
Goodman, H.M., 19
Gorin, M.B., 538
Gotley, D., 124
Graeser, D., 943
Green, E.D., 202, 255
Greenwood A.D., 336
Gregory, C.Y., 92
Gregory, S.G., 943
Grigoriev, A., 943
Grimm, L., 1056
Grimmond, S., 124
Gros, P., 956
Grujic, D., 132
Guichard, V., 492
Guo, C., 404
Guo, S.-W., 1133
Guo, Y., 972
Gyllensten, U.B., 1170
Haila, S., 202
Hall, J.M., 781
Hampson, R.M., 1093
Hanrahan, V., 667
Hardcastle, A.J., 1093
Hardin, S.H., 545
Harris, D., 893
Hashad, M., 956
Hawkins, M., 807
Hayashi, K., 551
Hayward, N., 124
Heid, C.A., 986, 995
Heine, D., 195
Heiss, N.S., 478, 922
Hejtmancik, J.F., 504
Hellebrand, H., 1056
Herman, G.E., 465
Herzog, H., 858
Hill, D.F., 668
Hillier, L., 807, 1110
Hirvasniemi, A., 351
Hoang, L., 1207
Hodes, M.E., 678
Hodgetts, R., 155
Höglund, P., 202
Holloway, E., 943
Holmberg, C., 202
Holmberg, M., 965
Holmgren, G., 965
Homayouni, R., 545
Hood, L., 1029
Hopkinson, D.A., 226
Hori, T., 439
Hornigold, N., 235
Hort, Y.J., 858
Houlgatte, R., 492
Housman, D., 290, 515
How, G.-F., 1185
Hu, A., 218
Hu, Z., 371
Huang, L., 19
Hudson, T.J., 1149
Hughes, K.J., 571
Hultman, M., 807
Humphray, S.J., 943
Humphries, P., 255
Humphries, S.E., 558
Hundrieser, J., 142
Hunter, K.W., 290
Imai, T., 439
Imran, S., 829
Inazuka, M., 551
Incerti, B., 880
Innerarity, T.L., 1123
Innis, J.W., 327
Isosomppi, J., 1002
Ito, H., 439
Jay, M.R., 92
Jenkins, N.A., 361
Jerome, N., 1029
Jimenez, S.A., 300
Jin, L., 1177
Johnson, M.R., 1050
Johnson, O.A., 571
Johnston, P.G., 114
Jones, H.B., 761
Jones, L.B., 545
Jordan, S.A., 255
Jülicher, K., 176
Kaiser, K., 972
Kanagy, B., 1084
Kandpal, R.P., 633
Kapsetaki, M., 1077
Karttunen, L., 392
Katso, R.M., 620
Kazianis, S., 280
Keele, J.W., 371
Kere, J., 202
Khambata, S., 195
Kim, U.-J., 612
Kimmerly, W., 414
King, M.-C., 1029
Kioschis, P., 478, 922
Kiss, I., 972
Klinger, K.W., 515, 525
Klockars, T., 1002
Knights, C.J., 943
Kolb, R., 102
Koprivnikar, K., 26
Korenberg, J.R., 1013
Korn, B., 478, 922
Korneluk, R.G., 1216
Krasikov, T., 688
Kucaba, T., 807
Kumlien, J., 943
Kurata, N., 661, 935
Kurnit, D.M., 1013
Laan, M., 1002
Labella, T., 943
LaCava, M., 1070
Lacy, M., 807
Lafrenière, R.G., 1216
Lagercrantz, J., 124
Lai, E., 612
Lalioti, M.D., 747
Lam, V., 943
Lamerdin, J.E., 1084
Lamour, V., 43
Lamy, B., 492
Landes, G.M., 515, 525
Lanfranchi, G., 35
Lanoil, B.D., 1160
Lapidus, A., 448
Lashkari, D., 1013
Le, M., 807
Le, N., 807
Leal, S.M., 351
Ledbetter, D.H., 735, 742
LeDuc, C.A., 781
Lee, C.C., 465
Lee, I., 1123
Lee, M.K., 1029
Lee, P., 290
Lee, R., 1192
Lehesjoki, A.-E., 218, 351
Lehrach, H., 290, 943
Leibel, R.L., 431, 1192
Lekoape, K.M., 226
Lennon, G., 791, 807
Leopold, R.A., 571
Leroy, E., 492
Lesser, J., 742
Levin, M.L., 465
Lewis, K., 414
Lewis, S., 414
Li, K., 943
Li, Y., 504
Li, Y., 956
Lichter, J., 1216
Lilley, C.E., 314
Lindblad, K., 965
Lindholm, E., 1170
Lindqvist, A.-K.B., 1170
Lipes, B., 612
Lipinski, M., 43
Little, P.F.R., 235
Livak, K.J., 986
Locke, J., 155
Lodhi, M.A., 10
Loebel, D.A.F., 114
Loftus, S.K., 26
Lönnqvist, L., 392
Lönnqvist, T., 870
Lorain, S., 43
Lu, F., 314
Lu, J., 314
Lustre, V., 414
Lux, A., 176
Ma, Q., 300
Maffitt, D.R., 1110
Magnusson, P.K.E., 1170
Majumder, P.P., 142
Makalowski, W., 846
Maldergem, L.V., 1093
Malley, T., 314
Manne, J., 300
Mansfield, E.S., 893
Mardis, E., 807
Mardis, E.R., 1118
Margolskee, R.F., 1077
Mariage-Samson, R., 492
Mariottini, P., 1226
Marra, M., 807, 1118
Marsh, S., 943
Martin, C., 414
Martinez, J.M., 58
Maruya, E., 51
Marynen, P., 404
Marzluff, W.F., 688, 702
Matera, A.G., 688, 702
Matsuda, Y., 439
McCollum, J.C., 545
McCombie, W.R., 10
McDermid, H., 155
McDermid, H.E., 1149
McEntire, B.B., 280
McEuen, M., 1029

McGarvey, S.T., 142
McGrath, R., 300
McGuire, R.E., 255
McKinnon, P.J., 1077
McTaggart, K.E., 1149
Meindl, A., 1056
Meitinger, T., 1056
Michaelis, S., 176
Miki, T., 142
Millholland, J.M., 525
Milosavljevic, A., 132
Minobe, Y., 935
Misfud, J., 943
Mitchell, B.D., 724
Mody, J., 195
Modzelewski, A., 195
Monaco, A.P., 943
Monani, U., 1200
Moore, B., 807
Morizot, D.C., 280
Morris, M., 807
Morris, M.A., 747
Mortlock, D.P., 327
Moskow, J.J., 300
Mott, R., 943
Muraro, T., 35
Muzny, D.M., 314
Myers, R.M., 218, 1103
Myerson, J., 829
Nagase, T., 439
Nairn, R.S., 280
Nanda, I., 102
Narang, S.K., 571
Nash, D., 155
Nayudu, M., 1093
Nelson, M.R., 327
Nesburn, K., 980
Nestorowicz, A., 504
Neville, C.E., 1216
Nichols, B.E., 862
Nikali, K., 870
Nikoskelainen, E., 965
Ning, Y., 742
Nomura, N., 439
Nordenskjöld, M., 124
Novak, E.K., 538
Nystuen, A., 862
O'Brien, E.P., 538
O'Connell, P., 724
O'Dell, S.D., 558
Opalka, B., 176
Pacchioni, B., 35
Palazzolo, M., 414
Pallavicini, A., 35
Palotie, A., 1002
Pandolfo, D., 35
Parsons, J., 807
Parsons, J.D., 1110
Passmore, H.C., 195
Pastan, I., 187
Paunesku, T., 132
Peeters, P., 404
Peltonen, L., 392, 870, 1002
Pena, S.D.J., 601
Pennacchio, L.A., 218, 1103
Permutt, M.A., 504
Perret, X., 590
Piétu, G., 492
Pilgrim, D., 155
Pinto, L.H., 538
Plasterk, R.H.A., 169
Playford, M., 943
Playford, M.P., 620
Pollock, P., 124
Polymeropoulos, M.H., 187, 1050
Potts, M.D., 667
Poustka, A., 478, 922, 943
Power-Kehoe, L., 431, 1192
Pragliola, A., 465
Prange, C., 807
Prochazka, M., 646
Ptacek, L.J., 965
Pujic, P., 448
Putt, W., 226
Rairdan, G., 155
Rak, K.H., 943
Rakar, S., 124
Ramu, E., 290
Ranta, S., 351
Rappaport, E., 893
Rappold, G., 943
Rechavi, G., 361
Reinhart, L.J., 724
Resenchuk, S., 290
Riazi, M.A., 1149
Riba, L., 290
Rifkin, L., 807
Rochefort, D.L., 1216
Rodriguez, L.V., 1070
Roe, B.A., 43
Rogner, U.C., 478, 922
Rohlfing, T., 807
Rohrer, G.A., 371
Rokhlina, T.R., 862
Romero, R., 414
Roschke, A., 742
Roschke, A.V., 735
Rosenthal, A., 590
Ross, B., 351
Ross, M., 1056
Ross, M.T., 943
Rossier, C., 747
Roter, A.H., 781
Rouleau, G.A., 1216
Roy, K., 155
Rubin, E.M., 1123
Rubin, G.M., 71
Rusiniak, M.E., 538
Saha, B.K., 1093
Saha, N., 1177
Saito, T., 439
Saji, H., 51
Sakallah, S., 142
Salbego, D., 132
Salo, P., 249
Sankoff, D., 1
Santos, F.R., 601
Sarwal, M.M., 1207
Sasaki, T., 661
Sasaki, T., 935
Savontaus, M.-L., 965
Scarso, S., 35
Schalkwyk, L., 290
Schalling, M., 965
Schartl, M., 102
Schellenberg, K., 807
Scherer, S.W., 202
Schindelhauer, D., 1056
Schmid, M., 102
Schurr, E., 956
Schütte, J., 176
See, C.G., 943
Seki, N., 439
Seymour, A.B., 538
Shalon, D., 639
Sheffield, V.C., 862
Shine, J., 858
Shipman, P.A., 724
Shirley, G., 414
Shivakumar, S., 724
Shizuya, H., 612
Shoham, J., 361
Shouse, S., 612
Shriver, M.D., 142, 1177
Siebert, R., 176
Silins, G., 124
Simon, A.J., 361
Siracusa, L.D., 300
Skach, W.R., 980
Smith, D.I., 176
Smith, R.F., 454, 465, 653
Smith, R.J.H., 504
Smith, S.J., 639
Smith, T.M., 1029
Smith, T.P.L., 371
Soares, M.B., 132, 791, 807
Song, W.-J., 1013
Sontag, J.-M., 1207
Sorokin, A., 448
Soularue, P., 492
Sowden, J., 226
Spanos, S., 314
Stambolian, D., 980
Stanton, V., Jr., 515
States, D.J., 1110
Stern, M.P., 724
Stevanin, G., 965
Stevens, J., 986
Stivers, D.N., 142
Stone, E.M., 862
Stone, N.E., 218
Stott, D., 226
Strezoska, Z., 132
Stultz, K., 414
Su, J., 290
Sugawara, T., 439
Sun, D., 414
Sunden, S.L.F., 862
Suomalainen, A., 870
Sutcliffe, J.S., 742
Sviderskaya, E.V., 880
Swank, R.T., 538
Syvänen, A.-C., 392
Szabo, C.I., 1029
Tahira, T., 551
Tahvanainen, E., 249
Tan, F., 807
Tanigami, A., 735
Tanoue, H., 935
Taylor, K., 235
Taylor, M., 1029
Templeton, J.W., 956
Theodor, L., 361
Thierrey-Meg, J., 807
Thiselton, D.L., 1093
Tilghman, S., 773
Tinkov, F., 290
Tisovec, R., 702
Todd, K., 943

Toppo, S., 35
Török, T., 972
Toth, S., 43
Townson, S., 124
Trevaskis, E., 807
Trevisan, S., 35
Trottier, Y., 965
Tsui, L.-C., 202
Ulinowski, Z., 235
Umehara, Y., 935
Underwood, K., 807
Uresandi, O.C., 724
Vainer, M., 893
Valle, G., 35
van der Hout, A.H., 176
Van Horn, S., 980
Van Keuren, M.L., 1013
Van Raay, T.J., 525
van Tuinen, P., 504
Vanmanshoven, P., 580
Varilo, T., 870
Vatcheva, R., 943
Venkatesh, B., 1185
Vieten, L., 176
Villanueva, A.S., 249
Vos, H.L., 1050
Vromans, H., 580
Wadelius, C., 1170
Wang, J., 688
Wang, M., 612
Wang, M.L., 19
Wang, X.C., 620
Wang, Y., 678
Wang, Z., 1070
Wang, Z.-F., 688, 702
Ward, L., 124
Warrington, J.A., 218, 628
Wasmuth, J.J., 26, 628
Waterston, R., 807
Watson, A.R., 781
Weber, B.H.F., 92
Weber, G., 124
Wehnert, M., 465, 1056
Wei, J., 678
Wei, Y., 1216
Weinstock, L.A., 1118
Weissenbach, J., 202, 351
Weissman, S.M., 633
Wiemann, S., 922
Wiese, B.A., 454
Wijesuriya, S.D., 92
Wilkie, T.M., 1207
Willers, C., 176
Williams, D., 235
Williams, P.M., 986, 995
Willour, V., 218
Wilson, R., 807
Wohldman, P., 807
Wöhr, G., 267
Wojzynski, M.K., 454
Wolf, M.L., 1093
Wolfe, J., 235
Wooddell, C.L., 886
Worley, K.C., 454, 465
Wu, K.-Y., 1013
Yamamoto, K., 661
Yamauchi, M., 439
Yanak, B.L., 538
Yano, M., 661
Yin, S.-J., 142
Yokoyama, S., 51
Yu, L.M., 142, 1177
Zachgo, E.A., 19
Zander, C., 965
Zehetner, G., 943
Zenklusen, J.C., 1070
Zeremski, M., 132
Zhang, J., 846
Zhong, X., 142
Zhuchenko, O., 465
Zuo, L., 1216

Subject Index, Volume 6 (1996)

A

ADCA. *See* Autosomal dominant cerebellar ataxias
adRP. *See* Retinitis pigmentosa
Algorithm, base-calling, for DNA sequencing data analysis (Berno), 80–91
Allele
  size, homoplasy at microsatellite loci (Garza and Freimer), 211–217
  typing, of HLA class II antigens by PCR–LIS–SSCP (Maruya et al.), 51–57
Allelic transcript
  discrimination, sNuPE (Greenwood and Burke), 336–348
  levels, quantitation of (Kartunnen et al.), 392–403
α_2 subunit gene of glycine receptor, human, structure of (Monani and Burghes), 1214–1220
Alphoid heteroduplex (αh), PCR-based polymorphism, Y chromosome (Santos et al.), 600–611
Alu fossil relics, distribution and insertion polymorphism (Arcot et al.), 1084–1092
Alu repeats, human *BRCA1* gene (Smith et al.), 1029–1049
Amplification, uniform, of DNA mixture with variable GC content (Baskaran et al.), 633–638
Amplisome, human extrachromosomal structure, BAC cloning and mapping of (Wang et al.), 612–619
Ancestral mutation, tracing the Finnish IOSCA mutation (Varilo et al.), 870–875
Animal genomics (Georges and Anderson), 907–921
AP-PCR/RAPD mapping, in *Xiphophorus* genetic hybrids (Kazianis et al.), 280–289
APECED. *See* autoimmune polyglandular disease type 1
Apoptosis, *CAS* gene (Brinkmann et al.), 187–194
Arabidopsis thaliana, chromosome 2 physical map (Zachgo et al.), 19–25
Arbitrarily primed polymerase chain reaction. *See* AP-PCR/RAPD
Arylsulfatase (*As-1*) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
As-1 gene. *See* Arylsulfatase gene
Asymmetric PCR, to generate long primers and single-stranded DNA (Wooddell and Burgess), 886–892
AT. *See* Ataxia telangiectasia
Ataxia telangiectasia (AT), identification of new gene designated NPAT physically linked to the ATM gene (Imai et al.), 439–447
Autoimmune polyglandular disease type 1 (APECED), putative isolation of gene (Stone et al.), 218–225
Automated DNA sequencing, hexamer string primers (Lodhi et al.), 10–18
Automated genotyping, microsatellite panels for (Lindqvist et al.), 1170–1176
Autosomal dominant cerebellar ataxias (ADCA), CAG repeat expansion in SCA7 (Lindblad et al.), 965–971
Autosomal dominant disorder, TCOF1, transcriptional map of candidate gene region (Loftus et al.), 26–34
Autosomal dominant retinal dystrophy, SFD (Wijesuriya et al.), 92–101
Autosomal optic neuropathy, fine mapping of GLC1A (Sunden et al.), 862–869
Autosomal recessive disorders
  Ataxia telangiectasis (Imai et al.), 439–447
  EPMR, genetic and physical mapping of locus (Ranta et al.), 351–360

B

b(Hexb). *See* Hexosaminidase gene
BAC. *See* Bacterial artificial chromosome
Bacillus subtillis, novel YAC sequencing (Sorokin et al.), 448–453
Bacterial artificial chromosome (BAC)
  cloning system, cloning and mapping of human extrachromosomal structure (Wang et al.), 612–619
  marriage, combining two smaller overlapping BACs (Borén et al.), 1123–1130
Bacterial chromosome mapping and sequencing, new approach using MLA PCR (multiplex long accurate PCR) and YACs (Sorokin et al.), 448–453

6:1240–1254 ©1996 by Cold Spring Harbor Laboratory Press ISSN 1054-9803/96 $5.00

Bacterial clone contig, of human EPM1 region of 21q22.3 (Stone et al.), 218–225
Bacterial clones (large-insert), RARE cleavage techniques (Borén et al.), 1123–1130
Bacterium, marine, genome structure of *Pseudoalteromonas haloplanktis* (Lanoil et al.), 1160–1169
Base-calling algorithm, for DNA sequencing data analysis (Berno), 80–91
Bayesian statistical methods, for analysis of FISH mapping data (Guo and Fletjer), 1133–1148
Bcg/Ity/Lsh locus, bovine *NRAMP1* is homolog of murine *Nramp1* (Feng et al.), 956–964
BCM Search Launcher, WWW interface (Smith et al.), 454–462
BDGP, *Drosophila* genome database (Rubin), 71–79
Bloch-Sulzberger syndrome. *See* Incontinentia pigmenti
Bone remodeling disorders, pycnodysostosis and osteoporosis (Johnson et al.), 1050–1055
Bovine *NRAMP1,* maps to BTA 2, comparative genetics of (Feng et al.), 956–964
Bovine *syndactyly* locus, IBD mapping of (Charlier et al.), 580–589
Bpa, murine bare patches, conserved gene order with loci in human Xq28 (Levin et al.), 465–477
Brachyury mutant mice, human *T* gene is homologous to murine *T(Brachyury)* gene (Edwards et al.), 226–233
BRCA1 human gene, complete genomic sequence of (Smith et al.), 1029–1049
Breast cancer cells, BT474, amplication of *CAS* gene (Brinkmann et al.), 187–194
Breast–ovarian cancer susceptibility gene *BRCA1,* complete genomic sequence of (Smith et al.), 1029–1049
BT474 breast cancer cells, amplification of *CAS* gene (Brinkmann et al.), 187–194

C

CAE. *See* Capillary array electrophoresis
Caenorhabditis elegans, consequences of future research (Plasterk), 169–175
CAG repeat expansions, analysis of SCA7 families for presence of (Lindblad et al.), 965–971
Cancers, genomic copy number syndromes, quantitation of sequences using fluorescent-PCR (Chiang et al.), 1013–1026
Candidate genes
  congenital chloride diarrhea (Höglund et al.), 202–210
  EPM1 (Stone et al.), 218–225
  GLC1A (Sunden et al.), 862–869
Capillary array electrophoresis (CAE), for short tandem repeat genotyping, (Mansfield et al.), 893–903
Cat eye syndrome (CES), critical region mapping and YAC contig construction (McDermid et al.), 1149–1159
Catch22 disorders, human chromosome 22 (Lorain et al.), 43–50
Cathepsin K gene, nonsense mutation and pycnodysostosis (Johnson et al.), 1050–1055
CD4 gene, and *TPI* gene, gene-rich cluster between the two (Ansari-Lari et al.), 314–326
cDNA libraries
  designed for EST sequencing (Lanfranchi et al.), 35–42
  human ESTs generated from (Hillier et al.) 807–828
  human infant brain, discovering distinct genes by SBH (Milosavljevic et al.), 132–141
  normalization and subtraction approaches to facilitate gene discovery (Bonaldo et al.), 791–806
CDPX2, human X-linked dominant chondrodysplasia punctata, Xq28 (Levin et al.), 465–477
Cell proliferation, *CAS* gene (Brinkmann et al.), 187–194
Cellular apoptosis susceptility (*CAS*) human gene, amplification in BT474 breast cancer cells and mapping on chromosome 20q13 (Brinkmann et al.), 187–194
Cereal genetics, ordered YAC library of rice chromosome 6 (Umehara et al.), 935–942
Cerebellar cDNA library, mouse chromosome 16 (Wei et al.), 678–677
CES. *See* Cat eye syndrome
Cf2r gene. *See Thrombin receptor* gene
CFTR. *See* Cystic fibrosis trans-

membrane transductance regulator
chAB4 primate-specific multisequence family, structure and chromosomal surroundings of (Wöhr et al.), 267–279
Chloride diarrhea gene (CLD), physical mapping of in human chromosome 7q31 (Höglund et al.), 202–210
Chromosome 1p
human, mapping of OBR in nonconserved region from mouse chromosome 4 and rat chromosome 5 (Chung et al.), 431–438
human OBR gene (Chung et al.), 1192–1199
Chromosome 1q21, human, cathepsin K mutation (Johnson et al.), 1050–1055
Chromosome 3, mouse, histone gene cluster (Wang et al.), 702–714
Chromosome 4, mouse, gene order compared to rat chromosome 5 and human 1p (Chung et al.), 431–438
Chromosome 5
homologs of pearl locus on mouse chromosome 13 (Seymour et al.), 538–544
human, radiation hybrid map of (Warrington and Wasmuth), 628–632
mouse, *Sc1* genomic structure is similar to *Sparc* (McKinnon et al.), 1077–1083
Chromosome 6
human, plasma glucose linked to (Stern et al.), 724–734
mouse
high incidence of LOH (Zenklusen et al.), 1070–1076
susceptibility locus for hepatomas (Zenklusen et al.), 1070–1076
rice, ordered YAC library of (Umehara et al.), 935–942
Chromosome 6q27, human *T* gene maps to (Edwards et al.), 226–233
Chromosome 7, physical mapping in the CLD gene region (Höglund et al.), 202–210
Chromosome 7q, human, mappping the RP10 locus for autosomal dominant retinitis pigmentosa (McGuire et al.), 255–266
Chromosome 8p, mapping of *EPMR* locus to (Ranta et al.), 351–360
Chromosome 10, mouse, mouse cystatin B gene (Pennacchio and Myers), 1103–1109
Chromosome 11, human, plasma glucose linked to (Stern et al.), 724–734
Chromosome 11p14–15.1, YAC contig spanning the USH1C and HI loci (Ayyagari et al.), 504–516
Chromosome 11q
cloning of novel human VEGF-related gene (Gimmond et al.), 124–131
identification of new gene (NPAT) in major AT locus (Imai et al.), 439–447
Chromosome 12, human, dominant (CNA1) and recessive (CNA2) map to same region of (Tahvanainen et al.), 249–254
Chromosome 12p13, *CD4–TPI* gene cluster (Ansari-Lari et al.), 314–326
Chromosome 13
genetic map of the pearl locus (Seymour et al.), 538–544
mouse, histone gene cluster (Wang et al.), 688–701
Chromosome 13q14.12–13q14.2, human RB gene (Herzog et al.), 858–861
Chromosome 13q22, human, utilization of FISH in positional cloning (Laan et al.), 1002–1012
Chromosome 15
bovine *syndactyly* locus (Charlier et al.), 580–589
human, *fibrillin 1* (*FBN1*) gene (Siracusa et al.), 300–313
Chromosome 16, mouse, C3-C4 region, isolation of novel clones and partial transcription map of (Wei et al.), 678–677
Chromosome 16p13.3
and *PKD1* gene (Dackowski et al.), 515–524
PKD1 and *TSC2* genes (Burn et al.), 525–537
Chromosome 17, human, complete genomic sequence of *BRCA1* gene (Smith et al.), 1029–1049
Chromosome 17p13.3, human, *LIS1* and *14-3-3ε* (Chang et al.), 735–741
Chromosome 20q13, *CAS* gene maps on (Brinkmann et al.), 187–194
Chromosome 21, human
EPM1 region of 21q22.3 (Stone et al.), 218–225
exon trapping (Chen et al.), 747–760
Chromosome 21q22.3, human
cystatin B gene (Pennacchio and Myers), 1103–1109
PWP2 as candidate gene for

diseases mapping to this region (Lafrenière et al.), 1216–1226
Chromosome 22, human, ordering of cosmid clones using cross-screening method (Locke et al.), 155–165
Chromosome 22q11.2, human, long-range map and YAC contig for CES (McDermid et al.), 1149–1159
Chromosome X
human
integrated YAC map of (Roest Crollius et al.), 943–955
long range map of 3.5-Mb region in Xp11.23–22 (Schindelhauer et al.), 1056–1069
inactivation, marsupials, methylation analysis (Loebel and Johnston), 114–123
ruminant, linkage map (Galloway et al.), 667–677
Chromosome Xq28, human, novel transcripts in candidate region for IP2 (Rogner et al.), 922–934
Chromosome Y
evolution, based on microsatellite loci analysis (Deka et al.), 1177–1184
haplotypes, human, evolutionary study (Santos et al.), 600–611
human, cosmid map (Taylor et al.), 235–248
Chromosomes
lengths, reciprocal translocation (Sankoff and Ferretti), 1–9
structure, palindromes (Wöhr et al.), 267–279
walking, carried to the extreme by new cross-screening method (Locke et al.), 155–165
CLN5 disease. *See* Neuronal ceroid lipofuscinosis disease
CNA1, cornea plana congenita, maps to chromosome 12 (Tahvanainen et al.), 249–254
CNA2, cornea plana congenita, maps to chromosome 12 (Tahvanainen et al.), 249–254
Collagen receptor a2-subunit (Itga2) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
Colon cancer cell lines, aberrant chromosome 20q with *CAS* gene (Brinkmann et al.), 187–194
Congenital chloride diarrhea, physical mapping in the CLD gene region (Höglund et al.), 202–210
Connective tissue diseases, MFS (Kartunnen et al.), 392–403
Conservation of genes, human OA1 and murine Oa1 (Bassi et al.), 880–886
Contig assembly, using new cross-screening method (Locke et al.), 155–165
Corn earworm (*Helicoverpa zea*), *D. melanogaster hobo* transposable element is functional in (DeVault et al.), 571–579
Cornea plana congenita, CNA1 and CNA2 map to same region of chromosome 12 (Tahvanainen et al.), 249–254
Cosmid map, of human Y chromosome (Taylor et al.), 235–248
CpG
islands, methylation analysis in marsupial X-linked (Loebel and Johnston), 114–123
mutation sites, universal assay for (O'Dell et al.), 558–568
Craniofacial development, TCOF1, transcriptional map of candidate gene region (Loftus et al.), 26–34
Cross-screening, new method for rapid contig assembly (Locke et al.), 155–165
CSF1R. *See* Macrophage colony-stimulating factor receptor gene
Cspg2 gene. *See* Versican gene
CTG repeats, evolution and distribution of at the human DM locus (Deka et al.), 142–154
Cystatins, isolation and characterization of mouse cystatin B gene (Pennacchio and Myers), 1103–1109
Cystic fibrosis transmembrane transductance regulator (CFTR) target mRNA, quantitative sequence analysis using RT-PCR (Gibson et al.), 995–1001

D

D locus gene cluster, *Xiphophorus* fish, evolution of *Xmrk* oncogene (Förnzler et al.), 102–113
Data analysis, DNA sequencing, graph theoretic approach to (Berno), 80–91
Data Base for Expressed Sequence Tags (dbEST), 319,311 submitted (Hillier et al.), 807–828
dbEST. *See* Data Base for Expressed Sequence Tags
DDR. *See* Discoidin domain receptor
DGS. *See* DiGeorge syndrome

Dhfr gene. *See* Dihydrofolate reductase gene
Diabetes
non-insulin dependent (NIDDM) (Prochazka), 646–649
type II, plasma glucose linked to chromosomes 6 and 11 (Stern et al.), 724–734
DiGeorge Syndrome (DGS) critical region, human chromosome 22, HIRA gene identification (Lorain et al.), 43–50
Dihydrofolate reductase (*Dhfr*) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
Discoidin domain receptor (DDR), new class of receptor tyrosine kinases (RTKs), genomic structure of (Playford et al.), 620–627
DM. *See* Myotonic dystrophy
DNA
microarrays, analysis of complex DNA samples (Shalon et al.), 639–645
sequencing
automated, hexamer string primers (Lodhi et al.), 10–18
data analysis, graph theoretic approach to (Berno), 80–91
end sequencing of large insert clones (Marra et al.), 1118–1122
high-throughput, lane tracking software for (Cooper et al.), 1110–1117
Drosophila
genome, euchromatic portion, P1-based physical map of (Kimmerly et al.), 414–430
Genome Project review (Rubin), 71–79
hobo transposable element functional in *H. zea* (DeVault et al.), 571–579
plasmid rescue of second chromosome (Guo et al.), 972–979
DXS52 locus, human Xq28, transcript map of (Heiss et al.), 478–491
Dye terminatiors, used with thermostable "sequence" to sequence symbiotic replicon of *replicon* (Freiberg et al.), 590–600
DYS19 microsatellite locus, PCR-based polymorphism, Y chromosome (Santos et al.), 600-611

E

Ea recombinational hot spot, mouse MHC (Khambata et al.), 195–201
Electrophoresis
capillary array (Mansfield et al.), 893–903
DNA sequencing, lane tracking software (Cooper et al.), 1110–1117
Emphysema, *Tsk* mice as model for (Siracusa et al.), 300–313
End sequence determination, of large insert clones (Marra et al.), 1118–1122
Energy transfer fluorescent primers, for end sequence determination from large insert clones (Marra et al.), 1118–1122
Epilepsy
EPMR, genetic and physical mapping of locus (Ranta et al.), 351–360
progressive myoclonus epilepsy of the Unverricht-Lundborg type (EPM1), cystatins (Pennacchio and Myers), 1103–1109
EPM1. *See* Progressive myoclonus epilepsy
See also Epilepsy
EPMR. *See* Progressive epilepsy with mental retardation
Escherichia coli, large insert libraries hosted in (Dackowski et al.), 515–524
ESTs. *See also* Expressed sequence tags
ETS-variant gene *6,* genomic structure and polymorphic markers within (Baens et al.), 404–413
ETV6. See ETS-variant gene *6*
Euchromatic genome, *Drosophila,* P1-based physical map of (Kimmerly et al.), 414–430
Evolution
Alu fossil relics (Arcot et al.), 1084–1092
dynamics, of CTG repeats at human DM locus (Deka et al.), 142–154
history, human Y chromosome haplotypes (Deka et al.), 1177–1184
microsatellite evolution (Crawford and Cuthbertson), 876–879
studies
chAB4 primate-specific multisequence family (Wöhr et al.), 267–279
histone genes (Wang et al.), 688–701
molecular, comparative analysis of mouse and human orthologs (Makalowski et al.), 846–857
Y-chromosome haplotypes (Santos et al.), 600–611
Exon trapping
human chromosome 21 (Chen et al.), 747–760
to identify transcribed sequences in chromosome 16p13.3 (Burn et al.), 525–537

Expressed Gene Anatomy Database (EGAD) (Hillier et al.), 807–828
Expressed sequence tags (ESTs)
high-throughput, assessment of data (Aaronson et al.), 829–845
human skeletal muscle, catalog of transcripts (Lanfranchi et al.), 35–42
280,000 human, generation and analysis of (Hillier et al.), 807–828
Extrachromosomal structure, human, BAC cloning and mapping of (Wang et al.), 612–619

F

FBN1, gene encoding fibrillin-1 (Kartunnen et al.), 392–403
FBN1 gene, tandem duplication within gene associated with mouse *Tight skin (Tsk)* mutation (Siracusa et al.), 300–313
Fibrillin 1 gene. *See FBN1* gene
Fibrillin mRNA levels, using solid-phase minisequencing (Karttunen et al.), 392–403
Finnish disease heritage, tracing the ancestral IOSCA mutation (Varilo et al.), 870–875
FISH. *See* Fluorescence in situ hybridization
Fluorescence in situ hybridization (FISH)
localization of mouse *Sc1* to chromosome 5 (McKinnon et al.), 1077–1083
techniques
gene map construction by (Guo and Fletjer), 1133–1148
utilization of in positional cloning (Laan et al.), 1002–1012
Fluorescence-based four-color electrophoretic gel images, lane tracking software for (Cooper et al.), 1110–1117
Fluorescent postlabeling, one-tube post-PCR method (Inazuka et al.), 551–557
Fluorescent probe
hybridization, DNA microarray system for analyzing complex DNA samples (Shalon et al.), 639–645
Taqman system for detecting PCR products (Heid et al.), 986–994; (Gibson et al.), 995–1001
Fluorescent-PCR assay, quantitative analysis assays, genomic sequence copy number, and transcriptional abundance (Chiang et al.), 1013–1026
Fluorescent sequencing, hexamer string primers (Lodhi et al.), 10–18
FlyBase, *Drosophila* genome database (Rubin), 71–79
Forensics, microsatellite panels for automated genotyping (Lindqvist et al.), 1170–1176
Founder effect, in SFD (Wijesuriya et al.), 92–101
*14-3-3*ε gene, human, no homology to *LIS1* but also maps to chromosome 17p13.3 (Chong et al.), 735–741
Fugu rubripes Japanese pufferfish
PCR-based isolation of Gα genes (Sarwal et al.), 1207–1215
PDGFR and CSF1R genes, conserved linkage with human genes (How et al.), 1185–1191
U15 snoRNA coding sequences in ribosomal protein S3 (*rpS3*) gene (Crosio et al.), 1227–1231
Fused mouse mutation (Tilghman), 773–780
Fusion of large DNA, using RARE-cleavage protocol (Borén et al.), 1123–1130

G

G protein α subunit multigene family, PCR-based isolation of genes in *Fugu* fish (Sarwal et al.), 1207–1215
G6PHD gene. *See* Glucose-6-phosphate dehydrogenase gene
Gα genes. *See* G protein α subunit multigene family
Galactokinase (*GALK1*) gene, human, fine structure of (Bergsma et al.), 980–985
GALK1. See Galactokinase gene
GC-rich cosmids, sequencing using dye terminators and thermostable "sequenase" (Freiberg et al.), 590–560
GC-rich templates, uniform amplification of DNA mixture with variable GC content (Baskaran et al.), 633–638
GenBank, impact of growth on sequence data base searching (Smith), 653–660
Gene Index, human genome, development of (Aaronson et al.), 829–845
Gene map construction, by FISH technique, statistical methods (Guo

and Fletjer), 1133–1148
Gene therapy project, cystic fibrosis transmembrane receptor (CFTR) mRNA (Gibson et al), 995–1001
Gene transcripts, novel, in human muscles (Piétu et al.), 492–503
Genodermatosis. *See* Incontinentia pigmenti
Genome
instability, detected using fluorescent-PCR (Chiang et al.), 1013–1026
scanning, utility of microsattelite markers (Lindqvist et al.), 1170–1176
sequencing. *See* DNA sequencing.
Genomic distances, reciprocal translocation (Sankoff and Ferretti), 1–9
Genomic sequencing, impact of large-scale genomic sequencing on sequence data base searching (Smith), 653–660
Genotyping, human, high-throughput (Hall et al.), 781–790
Glaucoma, fine mapping of GLC1A (Sunden et al.), 862–869
GLC1A. *See* Juvenile Open Angle Glaucoma
Glucose-6-phosphate dehydrogenase (*G6PHD*) gene, marsupial, methylation analysis (Loebel and Johnston), 114–123
Glycine receptor, structure of human α_2 subunit gene (Monani and Burghes), 1200–1206
Goeminne syndrome (TKC), human Xq28 (Rogner et al.), 922–934
GTPase activating protein (*Rasa*) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544

H

Haploinsufficiency diseases, human chromosome 22 (Lorain et al.), 43–50
Haplotypes
analysis, *TIMP3* localization (Wijesuriya et al.), 92–101
evolution of human Y chromosome (Deka et al.), 1177–1184
Helicoverpa zea. *See* Corn earworm
Helix-loop-helix (HLH) motif, protein encoded by *ETV6* (Baens et al.), 404–413
Hematologic malignancies, genomic organization of *ETV6* (Baens et al.), 404–413
Hepatomas, human TSG is conserved in mice and involved in development of (Zenklusen et al.), 1070–1076
Hexamer string primers, automated DNA sequencing (Lodhi et al.), 10–18
Hexosaminidase b(Hexb) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
HI. *See* Hyperinsulinism locus
High-throughput DNA sequencing, lane tracking software for (Cooper et al.), 1110–1117
High-throughput EST sequence data, assessment of (Aaronson et al.), 829–845
High-throughput genotyping human (Hall et al.), 781–790
using CAE (Mansfield et al.), 893–903
HIRA human gene, in DGS critical region of chromosome 22 (Lorain et al.), 43–50
Histone gene cluster
mouse chromosome 3 (Wang et al.), 702–714
mouse chromosome 13 (Wang et al.), 688–701
HLA class II antigens, high resolution allele typing by PCR–LIS–SSCP (Maruya et al.), 51–57
Hmgcr gene. *See* 3-Hydroxyy-3-methylglutaryl coenzyme A reductase gene
Homologous alleles, differential expression of (Greenwood and Burke), 336–348
Homoplasy, at microsatellite loci (Garza and Freimer), 211–217
Hprt. *See* X-linked genes
Htr1a gene. *See* 5-Hydroxytryptamine 1a receptor human gene
Human *BRCA1* gene, complete genomic sequence of (Smith et al.), 1029–1049
Human *CAS* gene. *See Cellular apoptosis susceptibility* human gene
Human chromosome region (HCR) 3p14.1, construction of YAC contig for (Bardenheuer et al.), 176–186
Human genes, comparative analysis of mouse and human orthologs (Makalowski et al.), 846–857
Human Genome Project, reflective overview (Tilghman), 773–780
3-Hydroxy-3-methylglutaryl coenzyme A reductase (*Hmgcr*) gene, pearl re-

gion of mouse chromosome 13 (Seymour et al.), 538–544
5-Hydroxytryptamine 1a receptor (*Htr1a*) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
Hyperinsulinism (HI) locus, chromosome 11p14–15.1, physical mapping of (Ayyagari et al.), 504–514
Hypopigmentation mutation, mouse pearl mutation (Seymour et al.), 538–544

I

IBD mapping. *See* Identity-by-descent mapping
Identity-by-descent (IBD) mapping, of bovine *syndactyly* locus (Charlier et al.), 580–589
IMAGE Consortium (Aaronson et al.), 829–845; (Bonaldo et al.), 791–806
Immunoglobulin supergene family, *CD4* (Ansari-Lari et al.), 314–326
Incontinentia pigmenti (IP2), chromosome Xq28, transcriptional analysis of candidate region (Rogner et al.), 922–934
Infant brain (1NIB) library (Bonaldo et al.), 791–806
Infant liver/spleen (1NFLS) library, (Bonaldo et al.), 791–806
Infantile Onset Spinocerebellar Ataxia Locus (IOSCA), genealogical and haplotype analysis of Finnish mutation (Varilo et al.), 870–875
Interspersed repetitive sequence PCR. *See* IRS-PCR genomics
Intronic microsatellites. *See* Microsatellites
Introns, novel T-cell specific G protein-coupled receptor gene encoded within intron 17 of human RB gene (Herzog et al.), 858–861
IOSCA. *See* Infantile Onset Spinocerebellar Ataxia Locus
IP2. *See* Incontinentia pigmenti
IRS–PCR genomics, physical mapping of the mouse genome (Hunter et al.), 290–299
Itga2 gene. *See* Collagen receptor a2-subunit gene

J

Japanese pufferfish. *See Fugu rubripes*
Japanese rice genome. *See* Rice genome
Juvenile Open Angle Glaucoma (GLC1A), fine mapping of (Sunden et al.), 862–869

K

Karyotype distributions, reciprocal translocation (Sankoff and Ferretti), 1–9

L

Lamina-associated polypeptide 2 (LAP2), sequence homology to Tmpos (Berger et al.), 361–370
Lane tracking software, for four-color fluorescence-based electrophoretic gel images (Cooper et al.), 1110–1117
Large insert clones, end sequencing for (Marra et al.), 1118–1122
Large-insert bacterial clones, genome methods for (Borén et al.), 1123–1130
Lepidoptera species, genetic transformation system for (DeVault et al.), 571–579
Leukemia *ETV6* gene
  genomic organization and polymorphic markers (Baens et al.), 404–413
  involvement in translocations and deletions (Baens et al.), 404–413
Linkage map, ovine X chromosome (Galloway et al.), 667–677
Linkage studies, type II diabetes, plasma glucose linked to chromosomes 6 and 11 (Stern et al.), 724–734
LIS1 gene, Miller–Dieker syndrome (Chong et al.), 735–741
Liver adenomas. *See* Hepatomas
Livestock
  diseases, bovine *NRAMP1* gene (Feng et al.), 956–964
  genomics (Georges and Anderson), 907–921
  species, comprehensive map of porcine genome (Rohrer et al), 371–391
LOH. *See* Loss of heterozygosity
Loss of heterozygosity (LOH)
  on chromosome 6 in mouse liver adenomas (Zenklusen et al.), 1070–1076
  studies, utility of microsatellite markers (Lindqvist et al.), 1170–1176
Low ionic strength single-stranded conformation polymorphism (LIS-SSCP), high resolution

allele typing of HLA antigens (Maruya et al.), 51–57

M

Macrophage colony-stimulating factor receptor (CSF1R) gene, conserved linkage between *Fugu* pufferfish and human genome (How et al.), 1185–1197
Major histocompatibility complex, mouse, *Ea* recombinational hot spot (Khambata et al.), 195–201
Marfan syndrome (MFS), fibrillin transcripts in (Karttunen et al.), 392–403
Marine bacterium, *Pseudoalteromonas haloplanktis* genome structure (Lanoil et al.), 1160–1169
Marsupials, methylation analysis of a X-linked CpG island (Loebel and Johnston), 114–123
MAS (marker-assisted selection schemes), in animal breeding (Georges and Anderson), 907–921
MDS. *See* Miller–Dieker syndrome
Melanomas
  Xiphophorus fish as animal model (Kazianis et al.), 280–289
  in *Xiphophorus* fish hybrids (Förnzler et al.), 102–113
Mental retardation
  human chromosome Xp11.23–22 region (Schindelhauer et al.), 1056–1069
  syndromes, Prader–Willi Syndrome (Ning et al.), 742–746
Merck Gene Index. *See* Gene Index
Methylation analysis, of marsupial X-linked CpG island (Loebel and Johnston), 114–123
MFS. *See* Marfan syndrome
MHC. *See* Major histocompatibility complex
Microarrays. *See* DNA microarrays
Microdissected DNA, mouse chromosome 16, direct cDNA selection (Wei et al.), 678–677
Microfibrillar components, *FBN1* and *FBN2* (Kartunnen et al.), 392–403
Microsatellites
  hybrid capture technique, simultaneous isolation of various STR markers (Prochazka), 646–649
  intronic, in human OBR gene (Chung et al.), 1192–1199
  loci
    analysis of in human Y chromosome haplotypes (Deka et al.), 1177–1184
    homoplasy for size at (Garza and Freimer), 211–217
  markers, utility of in genome scanning, LOH, and forensic analysis (Lindqvist et al.), 1170–1176
  sheep, mutations in (Crawford and Cuthbertson), 876–879
Microtubule-associated protein 5/lb (*Mtap5*) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
Miller–Dieker syndrome (MDS), *14-3-3ε* has no homology to *LIS1* (Chong et al.), 735–741
MLA PCR (multiplex long accurate PCR), used in new approach for bacterial chromosome mapping and sequencing (Sorokin et al.), 448–453
Model systems, *Fugu* fish for vertebrate genome research (Sarwal et al.), 1207-1215; (How et al.), 1185–1191
Mottled (Mo). See X-linked genes
Mouse, trinucleotide repeat-containing gene (Chambers and Abbott), 715–723
Mouse genes, comparative analysis of mouse and human orthologs (Makalowski et al.), 846–857
Mouse genome, IRS–PCR physical mapping (Hunter et al.), 290–299
Mouse thymopoietin gene, molecular characterization of (Berger et al.), 361–370
Mtap5. *See* Microtubule-associated protein 5/1b gene
Multigene family
  α subunit of glycine receptor, structure of human α_2 gene (Monani and Burghes), 1200–1206
  G protein α subunit, PCR-based isolation of genes in *Fugu* fish (Sarwal et al.), 1207–1215
Multisequence family, primate-specific chAB4 (Wöhr et al.), 267–279
Muscles, human, expression profile of novel genes (Piétu et al.), 492–503
Mutation rates, sheep microsatellites (Crawford and Cuthbertson), 876–879
Myocardial hypertrophy, *Tsk* mice as model for (Siracusa et al.), 300–313

Myotonic dystrophy (DM)
-associated CTG repeat, evolutionary dynamics of in diverse human populations (Deka et al.), 142–154
evolutionary dynamics of CTG repeats in diverse human populations (Deka et al.), 142–154

N

Natural resistance associated macrophage protein 1, bovine *NRAMP1* is homolog of murine *Nramp1* gene (Feng et al.), 956–964
Neurobiological (molecular) studies, selected mouse cerebellar cDNA library (Wei et al), 678–677
Neurofibromatosis 1 (NF1), long RT–PCR of locus (Martinez et al.), 58–66
Neuromuscular genetic disorders, myotonic dystrophy (DM) (Deka et al.), 142–154
Neuronal ceroid lipofuscinosis (vLINCL, CLN5) disease, human chromosomal region 13q22, FISH in positional cloning (Laan et al.), 1002–1012
NIDDM. *See* Non-insulin dependent diabetes mellitus
Non-insulin dependent diabetes mellitus, genetics of (Prochazka), 646–649
Normalized libraries, 1NIB and 1NFLS (Bonaldo et al.), 791–806
NPAT, new gene in AT locus physically linked to the ATM gene (Imai et al.), 439–447
Nramp1. See Natural resistance associated macrophage protein 1
Nuclear proteins, thymopoietins (Tmpos) (Berger et al.), 361–370
Nucleic acid sequence analysis, quantitative PCR and RT–PCR (Gibson et al.), 995–1001; (Heid et al.), 986–994

O

OA1 human gene. *See* Ocular albinism type I
Oa1 mouse gene, cloning of murine homolog of human OA1 gene (Bassi et al.), 880–885
Obesity, human, genomic structure of human OB receptor (Chung et al.), 1192–1199
Obesity receptor (OBR) gene, human,
genomic structure and identification of intronic microsatellites (Chung et al.), 1192–1199
mapping to 1p in a region of nonconserved gene order from mouse and rat (Chung et al.), 431–438
Obesity, human, mapping of the OBR to chromosome 1p (Chung et al.), 431–438
OBR. *See* Obesity receptor gene
Octamer sequencing, novel method of primer walking using octamer oligonucleotides to prime DNA sequencing reactions (Hardin et al.), 545–550
Ocular albinism type I (OA1) human gene, cloning murine homolog of (Bassi et al.), 880–885
Ohno's rule, confirmation of (Galloway et al.), 667–677
Oligonucleotide sequence signatures (OSSs) (Milosavljevic et al.), 132–141
Oncogene promoter, *Xmrk* from *Xiphophorus* fish genome (Förnzler et al.), 102–113
1NFLS. *See* Infant liver/spleen library
1NIB. *See* Infant brain library
Orthologous sequences, mouse and human, comparative analysis of (Makalowski et al.), 846–857
OSSs. *See* Oligonucleotide sequence signatures
Osteoporosis, bone remodeling disorders (Johnson et al.), 1050–1055
Otc. See X-linked genes
Ovarian cancer. *See* Breast–ovarian cancer susceptibility gene
Ovine X chromosome, linkage map of (Galloway et al.), 667–677

P

P1 cloning vector, *Drosophila* genomic library generated in (Kimmerly et al.), 414–4303
P1/cosmid contig, as compared to cosmid/lambda phage contig (Dackowski et al.), 515–524
Palindromic structures, chAB4 multisequence family (Wöhr et al.), 267–279
PAR-SN, novel paternal expressed transcription PWS critical region (Ning et al.), 742–746
Paternally expressed transcript, novel, Prader–Willi Syndrome (PWS)

critical region (Ning et al.), 742–746
PCR
amplification, of *NF1* (Martinez et al.), 58–66
asymmetric, to generate long primers and single-stranded DNA (Wooddell and Burgess), 886–892
-based Y-linked polymorphisms (Santos et al.), 600–611
map construction, MLA PCR used in new approach for bacterial chromosome mapping and sequencing (Sorokin et al.), 448–453
novel "real time" quantitative method (Heid et al.), 986–994
products, one-tube fluorescent postlabeling of (Inazuka et al.), 551–557
quantitative fluorescent-based technique assays genomic sequence copy number and transcriptional abundance (Chiang et al.), 1013–1026
PCR–LIS–SSCP. *See* Low ionic strength single-stranded conformation polymorphism
PDGFR. *See* Platelet-derived growth factor receptor gene
Pearl locus, mouse chromosome 13, genetic map of (Seymour et al.), 538–544
Periodic tryptophan protein 2 gene, yeast, isolation and genomic structure of human homolog (Lafrenière et al.), 1216–1226
Periventricular heterotopia, human Xq28 (Rogner et al.), 922–934
Pest control management, and manipulation of insect genomes (DeVault et al.), 571–579
Physical mapping, use of radiation hybrids (Jones), 761–769
PKD1 gene. *See* Polycystic kidney disease gene
Plasmid rescue, of the *Drosophila* second chromosome (Guo et al.), 972–979
Platelet-derived growth factor receptor (PDGFR) gene, conserved linkage between *Fugu* pufferfish and human genome (How et al.), 1185–1191
pNGR234*a* symbiotic genes, *Rhizobium,* identification of (Freiberg et al.), 590–600
Polycystic kidney disease (*PKD1*) gene
physical map of 700-kb segment on chromosome 16p13.3 (Dackowki et al.), 515–526
transcriptional map of 700-kb segment on chromosome 16p13.3 (Burn et al.), 525–537
Polygenes, QTL mapping (Georges and Anderson), 907–921
Polymorphisms, human Y chromsome (Santos et al.), 600–611
Porcine genome, comprehensive map of (Rohrer et al.), 371–391
Positional cloning
isolation of defective gene in XLRP (Thiselton et al.), 1093–1102
utilization of FISH techniques using 13q22 as an example (Laan et al.), 1002–1012
Prader–Willi Syndrome (PWS), critical region, novel parternally expressed transcript (Ning et al.), 742–746
Primer walking, novel method using octamer-primed cycle sequencing (Hardin et al.), 545–550
Progressive epilepsy with mental retardation (EPMR), genetic and physical mapping of locus on chromosome 8p (Ranta et al.), 351–360
Progressive myoclonus epilepsy, Unverricht–Lundborg type (EPM1), human chromosome 21 (Stone et al.), 218–225
Promoter capture, method that uses transcription factors to extract promoters from large genomic clones (Mortlock et al.), 327–335
Promoters, efficient isolation method from large genomic clones (Mortlock et al.), 327–335
Pseudoalteromonas haloplanktis, complex genome structure composed of two separate genetic units (Lanoil et al.), 1160–1169
Pufferfish. *See Fugu rubripes*
PWP2. *See* Periodic tryptophan protein 2 gene
PWS. *See* Prader–Willi Syndrome
Pycnodysostosis, nonsense mutation in cathepsin K gene of human chromosome 1q21 (Johnson et al.), 1050–1055

Q

QC RT–PCR. *See* Real time quantitative reverse transcriptase (RT)–PCR

QTL, multifactorial traits or polygenes, mapping of in livestock (Georges and Anderson), 907–921
Quantitative DNA sequence analysis, "real time" quantitative PCR (Heid et al.), 986–994
Quantitative fluorescent-PCR, assays genomic sequence copy number and transcriptional abundance (Chiang et al.), 1013–1026
Quantitative mRNA sequence analysis, "real time" quantitative RT–PCR (Gibson et al.), 995–1001

R

Radiation hybrid map, of human chromosome 5 (Warrington and Wasmuth), 628–632
Radiation hybrids, selected subsets of (Jones), 761–769
Random amplification of polymorphic DNA (RAPD). *See* AP-PCR/RAPD
RARE cleavage techniques (Borén et al.), 1123–1130
Rasa gene. *See* GTPase activating protein gene
Rat chromosome 5, gene order compared to mouse chromosome 4 and human 1p (Chung et al.), 431–438
RB gene. *See* Retinoblastoma susceptibility gene
Real time quantitative PCR (Heid et al.), 986–994
Real time quantitative reverse transcriptase (RT)–PCR (Gibson et al.), 995–1001
of *NF1* (Martinez et al.), 58–66
RecA-assisted restriction endonuclease (RARE) cleavage techniques (Borén et al.), 1123–1130
Receptor tyrosine kinases (RTKs), discoidin domain receptor (DDR), is new class of (Playford et al.), 620–627
Reciprocal translocation, karyotype distributions (Sankoff and Ferretti), 1–9
Recombinational hot spot, *Ea,* mouse MHC (Khambata et al.), 195–201
Repetitive DNA
families, chAB4 primate-specific (Wöhr et al.), 267–279
sequences, Alu fossil relics (Arcot et al.), 1084–1092
Retinal degeneration, human chromosome Xp11.23–22 region (Schindelhauer et al.), 1056–1069
Retinitis pigmentosa (RP)
autosomal dominant (adRP), refined mapping of RP10 locus on chromosome 7q (McGuire et al.), 255–266
mapping the *RP2* locus in XLRP (Thiselton et al.), 1093–1102
Retinoblastoma susceptibility gene, human, intron 17 encodes a novel T-cell specific G protein-coupled receptor (Herzog et al.), 858–861
RH map. *See* Radiation hybrid map
Rhizobium, sequencing the symbiotic replicon (Freiberg et al.), 590–600
Ribosomal protein S3 (*rpS3*) gene, *Fugu,* comparison with *Xenopus* and human counterparts (Crosio et al.), 1227–1231
Rice chromosome 6, ordered YAC library of (Umehara et al.), 935–942
Rice genome, Japanese, gene isolation and sequencing (Sasaki et al.), 661–666
RNA analysis, sNuPE, quantitative (Greenwood and Burke), 336–348
RP. *See* Retinitis pigmentosa
RP2 locus for XLRP, genetic and physical mapping of (Thiselton et al.), 1093–1102
rpS3 gene. *See* Ribosomal protein S3 gene
RT–PCR. *See* Real time quantitative reverse transcriptase (RT)–PCR

S

SBH. *See* Sequencing by hybridization
Sc1 mouse gene, similar genomic structure to *Sparc* mouse gene (McKinnon et al.), 1077–1083
SCA7. *See* Spinocerebellar ataxia type 7
Scleroderma, *Tsk* mice as model for (Siracusa et al.), 300–313
Sequence data base searching, impact of large-scale genomic sequencing on (Smith), 653–660
Sequence-tagged site content mapping. *See* STS content mapping
Sequencing
by hybridization (SBH), distinct gene discovery from infant brain cDNA libraries (Milosavljevic et al.), 132–141

octamer, novel method of primer walking (Hardin et al.), 545–550
SFD. *See* Sorsby's fundus dystrophy
Sheep, mutations in microsatellites (Crawford and Cuthbertson), 876–879
Short interspersed elements (SINEs), Alu repeats (Arcot et al.), 1084–1092
SINEs. *See* Short interspersed elements
Single nucleotide primer extension (sNuPE), quantitative range, variability and multiplex analysis (Greenwood and Burke), 336–348
Site-directed deletions, in large insert clones, using RARE-cleavage protocol (Borén et al.), 1123–1130
Site-directed mutagenesis, in large-insert bacterial clones, using RARE-cleavage protocol (Borén et al.), 1123–1130
Site-selected transposon mutagenesis (SSM), plasmid rescue of the *Drosophila* second chromosome (Guo et al.), 972–979
Skeletal dysplasia, pycnodysostosis, cathepsin K mutation (Johnson et al.), 1050–1055
Skeletal muscle, human, catalog of expressed sequence tags (ESTs) (Lanfranchi et al.), 35–42
snoRNAs, U15 snoRNA coding sequences in *Fugu rpS3* gene (Crosio et al.), 1227–1231
sNuPE. *See* Single nucleotide primer extension
Solid-phase minisequencing, fibrillin mRNA levels (Karttunen et al.), 392–403
Sorsby's fundus dystrophy (SFD), founder effect in (Wijesuriya et al.), 92–101
Sp1 transcription factor. *See* Transcription factor Sp1
Sparc mouse gene, similar genomic structure to *Sc1* mouse gene (McKinnon et al.), 1077–1083
Spinocerebellar ataxia type 7 (SCA7), identification of expanded CAG repeats using repeat expansion detection (RED) method (Lindblad et al.), 965–971
Splice variants, of DDR (Playford et al.), 620–627
SSM. *See* Site-selected transposon mutagenesis
Stem–loop sequence, histone mRNAs (Wang et al.), 688–701
Stop codons, premature (Karttunen et al.), 392–403
STR markers, isolation of using microsatellite hybrid capture technique (Prochazka), 646–649
Str, murine striated, conserved gene order with loci in human Xq28 (Levin et al.), 465–477
STS content mapping, of *Drosophila* genome (Kimmerly et al.), 414–430
Subtractive hybridization, an approach to facilitate gene discovery (Bonaldo et al.), 791–806
Sus scrofa, comprehensive map of genome (Rohrer et al.), 371–391
Symbiotic genes. *See* pNGR234*a* symbiotic genes
Syndactyly locus, bovine, IBD mapping (Charlier et al.), 580–589

T

T-cell specific receptor, chicken, G protein-coupled receptor encoded within intron 17 of RB gene is human homolog of (Herzog et al.), 858–861
*Taq*I restriction site, forced site in universal assay for CpG mutation sites (O'Dell et al.), 558–568
Taqman system, for detecting PCR products (Heid et al.), 986–994; (Gibson et al.), 995–1001
T(Brachyury) gene, mouse, human homolog *T* (Edwards et al.), 226–233
TCOF1. *See* Treacher Collins syndrome
Thrombin receptor gene (Cf2r) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
Thymopoietin (*Tmpo*) gene, mouse, molecular characterization of (Berger et al.), 361–370
Tight skin (Tsk) mutation, mice, model for human connective tissue diseases (Siracusa et al.), 300–313
TIMP3 human gene. *See* Tissue inhibitor of metalloproteinases-3 gene
Tissue inhibitor of metalloproteinases-3 (*TIMP3*) gene, involvement in SFD and genetic localization of (Wijesuriya et al.), 92–101
TKC. *See* Goeminne syndrome
Tmpo. See Thymopoietin gene
TMPO, human (Berger et al.), 361–370
TPI. See Triosephosphate isomerase gene
Transcription factors
Sp1, used to extract promoters from large ge-

nomic clones (Mortlock et al.), 327–335
T (human), gene structure, cDNA sequence and assignment to chromosome 6q27 (Edwards et al.), 226–233
Transcription map, comparative, of murine *Bpa/Str* region and human Xq28 (Levin et al.), 465–477
Transcriptional abundance, assayed by fluorescent-PCR-based technique (Chiang et al.), 1013–1026
Transgenics, second phase of genome research in livestock (Georges and Anderson), 907–921
Translocation, reciprocal. *See* Reciprocal translocation
Translocations, and *ETV6* gene (Baens et al.), 404–413
Transposable element, *D. melanogaster hobo* functional in *H. zea* (DeVault et al.), 571–579
Treacher Collins syndrome (TCOF1), transcriptional map of candidate gene region (Loftus et al.), 26–34
Trinucleotide repeats (TRs), mouse brain cDNA clones containing TRs (Chambers and Abbott), 715–723
Triosephosphate isomerase (*TPI*) gene, and *CD4* gene, gene rich cluster between the two (Ansari-Lari et al.), 314–326
TRs. *See* Trinucleotide repeats
TSG. *See* Tumor suppressor gene
Tsk mutation. *See Tight skin* mutation
Tuberous Sclerosis Type 2 (*TSC2*) gene, transcriptional map of 700-kb segment on chromosome 16p13.3 (Burn et al.), 525–537
Tumor suppressor gene
candidate, *14-3-3ϵ* (Chong et al.), 735–741
evidence that putative human TSG is conserved in mice (Zenklusen et al.), 1070–1076
family, human retinoblastoma susceptibility gene, intron 17 encodes a novel G protein-coupled receptor (Herzog et al.), 858–861
putative HCR 3p14.1, YAC contig of (Bardenheuer et al.), 176–186
Type II diabetes. *See* Diabetes
Tyrosine kinase receptors, PDGFR and CSF1R (How et al.), 1185–1197

U

USH1C. *See* Usher syndrome type 1C
Usher syndrome type 1C (USH1C) locus, chromosome 11p14–15.1, physical mapping of (Ayyagari et al.), 504–514

V

Vascular endothelial growth factor (VEGF)
gene family, human, cloning of novel VEGF-related-factor (VRF) (Grimmond et al.), 124–131
-related-factor (VRF), human, novel member of VEGF gene family (Gimmond et al.), 124–131
Vascular permeability factor (VPF). *See* Vascular endothelial growth factor
VEGF gene family. *See* Vascular endothelial growth factor
Versican (*Cspg2*) gene, pearl region of mouse chromosome 13 (Seymour et al.), 538–544
vLINCL disease. *See* Neuronal ceroid lipofuscinosis disease
VRF. *See* Vascular endothelial growth factor-related-factor

W

Waismann syndrome, human Xq28 (Rogner et al.), 922–934
Wallaroo marsupial, methylation analysis of X-linded CpG island (Loebel and Johnston), 114–123
World Wide Web (WWW), BCM Search Launcher (Smith et al.), 454–462
WWW. *See* World Wide Web

X

X chromosome. *See* Chromosome X
X-linked diseases
long-range map of 3.5-Mb region in Xp11.23–22 (Schindelhauer et al.), 1056–1069
X-linked retinitis pigmentosa (XLRP), genetic localization for *RP2* locus (Thiselton et al.), 1093–1102
X-linked genes, *Hprt, Mottled* (*Mo*), and *Otc*, and sNuPE assay (Greenwood and Burke), 336–348

X-linked mutations, murine male lethal bare patches (*Bpa*) and striated (*Str*), homology to respective human disorders (CDPX2 and IP2) (Levin et al.), 465–477
X-linked retinitis pigmentosa (XLRP), genetic and physical mapping of *RP2* locus (Thiselton et al.), 1093–1102
Xiphophorus fish
  AP-PCR/RAPD mapping in genetic hybrids (Kazianis et al.), 280–289
  genome, *Xmrk* oncogene promoter (Förnzler et al.), 102–113
XLRP. *See* X-linked retinitis pigmentosa
Xmrk oncogene promoter, *Xiphophorus* fish, unusual organization of gene cluster (Förnzler et al.), 102–113
Xp11.23-22 region, genomic map using restriction-site based techniques (Schindelhauer et al.), 1056–1069
Xq28 human chromosomal band
  comparative transcription map of murine *Bpa* and *Str* critical regions (Levin et al.), 465–477
  transcript map of DXS52 region (Heiss et al.), 478–491

Y

Y chromosome. *See* Chromosome Y
YAC. *See* Yeast artificial chromosome
YAC-deficient chromosomal intervals, clone recovery from (Dackowski et al.), 515–524
YAP (polymorphic *Alu* insertion), PCR-based polymorphism, Y chromosome (Santos et al.), 600–611
Yeast
  PWP2 gene, isolation and genomic structure of human homolog (Lafrenière et al.), 1216–1226
  segregation gene *CSE1*, human *CSE1* gene is homolog of (Brinkmann et al.), 187–194
Yeast artificial chromosome (YAC)
  contig for human chromosome region (HCR) 3p14.1 (Bardenheuer et al.), 176–186
  in CLD gene region (Höglund et al.), 202–210
  library, of rice chromosome 6 (Umehara et al.), 935–942
  map, integrated, of human X chromosome (Roest Crollius et al.), 943–955
  physical map of *A. thaliana* chromosome 2 (Zachgo et al.), 19–25
  sequencing, new approach using MLA PCR in *Bacillus subtillis* (Sorokin et al.), 448–453

GENOME RESEARCH

... the new genetics

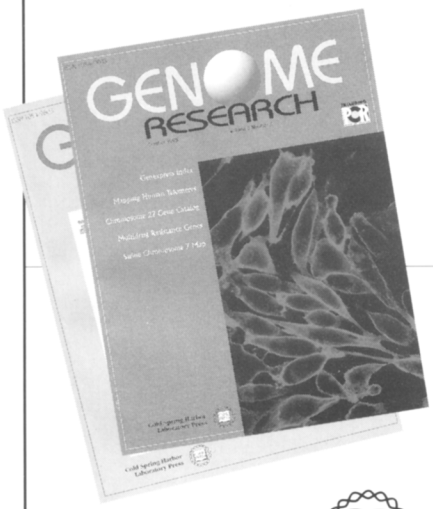
Here's why:

1. Genome Research publishes the best and most creative research on physical and genetic mapping, DNA sequencing, gene discovery, informatics, statistical and mathematical methods, technology development, and gene function.

A Novel In Vivo Method to Detect DNA Sequence Variation
Malek Faham and David R. Cox

The Genexpress Index: A Resource for Gene Discovery and the Genic Map of the Human Genome
Rémi Houlgatte, Régine Mariage-Samson, Simone Duprat, Anne Tessier, Simone Bentolila, Bernard Lamy, and Charles Auffray

A Biometrical Genome Search in Rats Reveals the Multigenic Basis of Blood Pressure Variation
Nichola J. Schork, Josä E. Krieger, Maria R. Trolliet, Klebber G. Franchini, George Koike, Eduardo M. Krieger, Eric S. Lander, Victor J. Dzau, and Howard J. Jacob



Karyotype Distributions in a Stochastic Model of Reciprocal Translocation
David Sankoff and Vincent Ferretti

A Physical Map of Chromosome 2 of Arabidopsis thaliana
Eve Ann Zachgo, Ming Li Wang, Julia Dewdney, David Bouchez, Christine Camilleri, Stephen Belmonte, Lu Huang, Maureen Dolan, and Howard M. Goodman

2. Genome Research supplements and enhances editorial content with electronic presentations on the World Wide Web.

Check out the example at http://www.cshl.org/journals/gr/supplement/ and on-line abstracts for 1996 issues.

3. Genome Research publishes review articles that put current research accomplishments into perspective.

Hyper-recombination and Bloom's Syndrome: Microbes Again Provide Clues About Cancer
Rodney Rothstein and Serge Gangloff

Around the Genomes: The Drosophila Genome Project
Gerald M. Rubin

4. Genome Research is expanding the "PCR Methods and Applications" section to incorporate more methods germane to genome research — henceforth, the "Genome Methods" section.

Cross-screening: A New Method to Assemble Clones Rapidly and Unambiguously into Contigs
John Locke, Greg Rairdan, Heather McDermid, David Nash, David Pilgrim, John Bell, Kenneth Roy, and Ross Hodgetts

5. Genome Research has also begun publishing letters — concise reports describing the structure, sequence, expression, and/or other biologically relevant features of a gene, with supplementary data made available electronically.

Don't get left behind. Subscribe today!

COLD SPRING HARBOR LABORATORY PRESS
10 Skyline Drive Plainview, NY 11803-2500
Phone 1-800-843-4388 or 516-349-1930 • Fax 516-349-1946
E-mail: cshpress@cshl.org or World Wide Web Site http://www.cshl.org/

Manuscripts may be submitted to:
GENOME RESEARCH
Cold Spring Harbor Laboratory Press
1 Bungtown Road, Cold Spring Harbor, NY 11724

Immunological Services

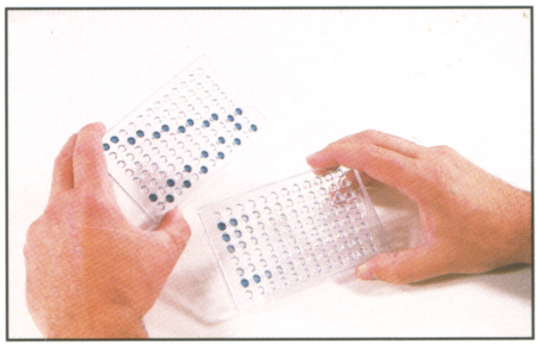
Antigen Production and Purification

- Peptide Antigens
- Soluble Protein Antigens
- Cell Tissue Extracts
- Large-Scale Mammalian and Insect Cell Culture

Bioreactor used for large scale production of Eukaryotic cells and cell products. (Fibroblasts, Monoclonals, Chinese hamster ovary, Baculovirus expression, etc.)

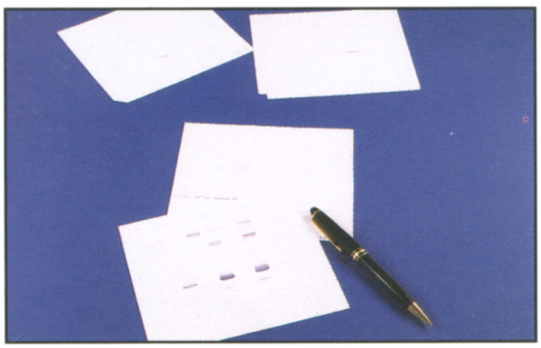
Assay and Kit Formatting

- ELISA
- Radioimmunoassay
- Immunofluorescence
- Flow Cytometry
- Immunohistochemistry



Antibody Testing and Characterization

- Immunoprecipitation
- Western Blotting
- ELISA
- Cell and Tissue Staining
- Peptide Mapping



Antibody Production and Purification

- Monoclonal and Polyclonal Development
- Large and Small Scale Monoclonal Production
- Affinity Purification
- Antibody Fragmentation
- Enzyme and Fluorescein Labeling
- Immobilization

Research Genetics, Inc.

2130 Memorial Pkwy, SW • Huntsville, AL • 35801
U.S. or Canada 800-533-4363 • U.K. 0-800-89-1393 • FAX 205-536-9016
Homepage http://www.resgen.com