Subject Index

A

17-AAG experimental compound, 378–380, 506–510

ABL tyrosine kinase inhibitors, 479–481.
See also Imatinib

ABT-737 experimental compound, 469, 474–475

Acute myeloid leukemia (AML), 193

Acute promyelocytic leukemia (APL), 85

Adenocarcinoma
colorectal, p53 and p73 regulation in, 121–127

of lung
cancer stem cells of, 247–248
EGFR gene mutations in, 3–5, 73–79
EGFR inhibitor treatment response in, 73–79, 419–425, 483–484
genomic profile of, 5–6, 11, 16–17, 20
pancreatic ductal, 17–21, 65–70
prostatic, mouse models of, 283, 287–289

Adenomatous polyposis coli (APC) gene.
See APC gene

Adult stem cells. *See* Stem cells, adult

Aflatoxin B1 ingestion, and hepatocellular carcinoma, 251

Aging
mitochondrial alterations and, 367–370
tumor suppressors and, 177–182

AKT1 gene and AKT1 protein, in radiation-induced cell death, 114–118

AML (acute myeloid leukemia), 193

Anaerobic glycolysis, in cancer cells, 363

Androgen dependence, in prostate cancer, 192–193

Aneuploid breast tumors, ROMA CGH and FISH analysis of, 51–62

Aneuploidy
of p53 knockout mouse cells in tissue culture, 490–491
telomere-related, 200

Angiogenesis
mechanisms and control of, 399–400
oncogene addiction and, 389–396
VEGF in, 411–413

Angiogenesis inhibitors
endogenous
overexpression of, and tumor growth suppression, 392–393
structural basis for functions of, 399–407
therapeutic use of. *See* Antiangiogenic therapy

Angiopoietins, as target for antiangiogenesis therapy, 415

Animal models. *See* Mouse models

Antiangiogenic therapy. *See also* Angiogenesis inhibitors
for breast cancer, 375–380
chemotherapeutic resistance in, 395, 526
targets for, 411, 414–415
VEGF Trap as, 411–415

Anti-p53 antibodies, staining of, 491–492

APC gene, and colorectal cancer, 192

APC gene mutations, IGF2 loss of imprinting and, 335, 338–339

APL (acute promyelocytic leukemia), 85

Aplastic anemia, telomere shortening and, 205–207

Apoptosis
Bcl-2 life/death switch and, 469–475, 526
Perp and AKT1 polymorphisms and, 111–118
pVHL and, in hereditary pheochromocytoma, 159, 161–162
regulation of, 357–361

Arf gene
activation of expression of, 130–132, 135
in stem cell self-renewal and cancer cell proliferation, 179–181

Arf tumor suppressor. *See also* p19Arf protein
p53-dependent and -independent functions of, 129–135

Arf/p53 tumor surveillance network, E2F transcription factor in regulation of, 309–315

Ascl-1 expression, in mouse model of SCLC, 225–231

Association studies, for polygenic inheritance investigations, 35–38

Astrocytoma
mouse models of, 283–287
in neurofibromatosis type 1, 173–175

ATM (ataxia telangiectasia mutated) protein
activation of, 99–102
in neoplastic proliferation and aging, 181
phosphorylation of substrates by, 102
SMC1 substrate of, 102–108

ATP production, in growing cells, 357, 361

Autophagy, and transient growth factor-independent survival of cells, 358–360

Avastin (bevacizumab), 377, 379, 411

B

B23. *See* NPM (nucleophosmin)

Bak regulation, in apoptosis, 471–472, 475

Basal-like breast cancer, inactive X-chromosome abnormalities in, 93–96

Base excision repair pathway, in treatment of breast cancer in BRCA1/2 carriers, 142

BAY43-9006 experimental compound.
See Sorafenib

Bcl-2 life/death switch, in tumorigenesis and therapy, 469–475

Bcl-2 proteins, in maintenance of cell survival, 357

Beckwith-Wiedemann syndrome, 335–337

Beta-cells, Myc activation in, 265–267

Bevacizumab (Avastin), 377, 379, 411

BH3 mimetics, therapeutic potential of, 469, 473–475

BH3-only proteins, of Bcl-2 family, and apoptosis, 469–471, 475

Biomarkers of cancer. *See also* Prognostic tools; Screens
in breast cancer, 317, 324
clinical proteomics and, 246, 517–523
loss of genetic imprinting as, 337–340
in lung cancer, 246
p53 status as, 491
predictive of EGFR inhibitor response in NSCLC, 483–486
serum proteins as, 481

Biopsies, patient, proteomic profiling of, 517–523

B-lymphocyte cell line, EBV-transformed, 111–118

Bmi-1 proto-oncogene and Bmi-1 protein, 177–182

BMS-354825 (dasatinib), 481

bobbed rDNA locus, dMyc association with, 302–304

Bone metastasis of breast cancer, site-specific metastasis genes and, 152–155

B-Raf inhibitors, 500–501

Brain tumors. *See* Astrocytoma; Glioma, malignant

BRCA1 mutant cancer
cancer therapy strategies for, 139–146, 526
Xi abnormalities in, 93–96

BRCA1/2 genes
contribution to breast cancer susceptibility, 35
epigenetic inactivation of, 330

BRCA1/2 proteins
deficiency of, and homologous recombination defect, 139–140
in recruitment of ATM, 106–108

Breakage-fusion-bridge cycles, in dicentric chromosome formation, 199, 201–202

Breast cancer. *See also* entries beginning with Mammary
aneuploid and diploid, ROMA CGH and FISH analysis of, 51–62
BRCA1 mutant and sporadic basal-like, Xi abnormalities in, 93–96

- Breast cancer (*Continued*)
 in *BRCA1/2* carriers
 carboplatin chemotherapy clinical trials, 141–142, 146
 therapeutic strategies for, 139–146, 526
 cellular microenvironment and, 343–352
 chemotherapeutic resistance in, and kinase screening in tissue culture, 455–456
 extracellular matrix in tumor induction and progression, 345, 349–352
 murine, complete regression in response to antiangiogenic stress, 375–380
 new mutator phenotype, 46
 pathways of tumor progression in, 283
 polygenic inherited predisposition to, 35–40
 primary tumorigenicity, and organ-specific metastasis genes, 155–156
 resequencing of protein kinase gene family in, 43–48
 site-specific genes in metastasis of, 149–158
 tumor progression pathways in, 289
 Breast cancer and ovarian cancer syndrome, 66
 Burkitt's lymphoma, 84
- C**
- Cancer. *See also specific cancer types, e.g., Adenocarcinoma, Breast cancer*
 biomarkers of. *See Biomarkers of cancer*
 epigenetic changes in, 329–332, 335–340, 427–431, 527
 initiation of. *See Tumorigenesis*
 metastasis of. *See Metastasis*
 progression of. *See Tumor progression*
 treatment of. *See Chemotherapeutic resistance; Therapeutic strategies for cancer; specific drugs and drug classes*
- Cancer cells
 invasiveness of, Tks5 and, 168–169
 metastasis of. *See Metastasis*
 microenvironment of, 343–352, 383–387, 526–527
 nutrient uptake and apoptosis suppression in, 357–361
 proliferation of
 vs. angiogenesis induction, 391–392
 proto-oncogene and tumor suppressor activation and, 177–182
 proteomic profiling of, and personalized therapy, 517–523
 RNAi in study of signaling networks in, 435–441
- Cancer drug development, progress and challenges in, 499–510
- Cancer genetics research, history of, 83–90
- Cancer kinome targets, and personalized molecular cancer therapeutics, 499–510
- Cancer risk assessment. *See Biomarkers of cancer*
- Cancer stem cells
 in lung cancer, 247–248
 telomerase activity in, 205–207
 in tumorigenesis, 193, 225
- Cancer stem cell theory, telomerase activity and, 205–207
- Cancer-signaling networks
 protein-signaling network models, clinical proteomic analysis of, 517–523
 RNAi studies of, 435–441
- Carboplatin chemotherapy, in *BRCA1/2* mutant breast cancer, 141–142, 146
- Carcinoma. *See also Adenocarcinoma*
 ductal carcinoma in situ, 317, 322–324
 hepatocellular carcinoma, 218–222, 251–260
 renal cell carcinoma, 159, 161, 465
 squamous cell carcinoma
 of esophagus, 332
 of lung, 11, 16–17, 20
- Carcinoma-associated fibroblasts, 383–387
- β -Catenin, 219–220, 222
- Cathepsin proteases, as lung cancer biomarker, 246
- CDH1* gene, epigenetic inactivation of, 330
- Cdk inhibitors, 234, 502–504
- Cdk2 kinase, 234, 237–238
- Cdk4 kinase, 235–237
- Cdk4R24C kinase, mutant, melanoma induction by, 235
- Cdk6 kinase, genetic analysis of in vivo role of, 236–237
- Cdks (cyclin-dependent kinases)
 in cell cycle regulation and cancer, 233–239
 genetic analysis of in vivo role of, 236–238
 phenotypic expression of mutations of, 234
- cDNA expression, screens using, in mammalian tissue culture cells, 449–458
- Cell cycle, cyclin-dependent kinases in, 233–239
- Cell type of origin, and metastatic proclivity, 293
- Cell-based screens, for novel p53 activators, 494
- Centromeres, dysfunction of, and genomic instability in human cancer, 321–322
- CGH. *See Comparative genomic hybridization*
- Chemotherapeutic drugs. *See specific drugs and drug classes, e.g., Erlotinib, Tyrosine kinase inhibitors*
- Chemotherapeutic resistance
 acquired, to kinase inhibitors, 3, 6, 73–79, 480–481, 525–526
 in antiangiogenic therapy, 395, 526
 and kinase screening in breast cancer and NSCLC cells, 455–457
 tissue polarity in regulation of, 349
 in vitro, to gefitinib, 423–424
- Chemotherapy. *See Therapeutic strategies for cancer; specific drugs and drug classes*
- Choroid plexus epithelial cells, pRb pathway inactivation in, 283–289
- Chromatin changes, promoter region methylation and, 329–330
- Chromosomal translocation in human cancer, mouse models mimicking, 275–281
- Chromosome formation, dicentric, breakage-fusion-bridge cycles in, 199
- Chronic myelogenous leukemia (CML)
 hematopoietic stem cells and, 193
 kinase inhibitor therapy for, 3, 194, 419, 479–481, 526
- Chronic myelomonocytic leukemia (CMML), 479–480
- Cip/Kip proteins, in cell cycle regulation, 234, 237–238
- CKI proteins, expression of, in cancer, 233
- Clear-cell renal carcinoma, 159, 161
- Clinical markers. *See Biomarkers of cancer; Prognostic tools*
- Clinical proteomics. *See Proteomics, clinical*
- Clinical trials
 carboplatin chemotherapy, in *BRCA1/2* mutant breast cancer, 141–142, 146
 of gefitinib in NSCLC, 419
 of VEGF Trap for cancer and vascular eye diseases, 414–415
- CML. *See Chronic myelogenous leukemia*
- CMML (chronic myelomonocytic leukemia), 479–480
- CNS lymphoma, epigenetic silencing in, 331
- Collagen, type 1, and cancer progression, 385
- Colony-forming assays for stem cells, 188
- Colorectal adenocarcinoma cell lines, p53 and p73 regulation in, 121–127
- Colorectal cancer
 adenomatous polyposis coli gene and, 192
 epigenetic gene silencing in, 428–429
 loss of genetic imprinting and, 337–338
 mouse model for, 338–340
- Combination therapy, network-targeted, 521–522
- Comparative genomic hybridization (CGH)
 analysis of aneuploid and diploid breast tumors, 51–62
 genetic study of human lung cancer subtypes, 11–22
- Competitive repopulation assay for stem cells, 188
- Costello syndrome, 462
- COX-2 (prostaglandin-endoperoxide synthase 2), association with p16^{Ink4a} hypermethylation, 322–324
- CpG dinucleotide, methylation of, 329–332
- Cre-expressing lentivirus vectors, T₁₂₁ induction by, 286–287, 289
- Cre-loxP recombination system, 275, 277–279
- CT (micro-computed tomography), in murine lung cancer modeling, 245

CXCL-12 (stromal-cell derived factor 1 α), 384
 CYC202 (seliciclib; *R*-roscovitine), 502–504
 Cyclin-dependent kinase (Cdk) inhibitors, 234, 502–504
 Cyclin-dependent kinases. *See* Cdk
 Cyclins, 233–234
 Cytotoxic therapy, apoptotic regulation in, 469, 473–475

D

Darwinian model of tumor progression and metastasis, 291–293
 Dasatinib (BMS-354825), 481
 DCIS. *See* Ductal carcinoma in situ
 Delta-like ligand 4, as target for antiangiogenesis therapy, 415
 Diagnostics. *See* Biomarkers of cancer; Personalized molecular cancer therapeutics/ diagnostics; Prognostic tools
 Dicentric chromosome formation, breakage-fusion-bridge cycles in, 199
 Diploid breast tumors, ROMA CGH and FISH analysis of, 51–62
 dMnt transcription factor, 299–305
 dMyc transcription factor, 299–305
 DNA alterations, lineage-restricted, in human tumors, 27–32
 DNA, complementary, expression screens using, 449–458
 DNA damage response/DNA repair
 ATM-dependent, 99–108
 in *BRCA* mutant cells, 139–146, 526
 telomere dysfunction and, 200–201
 DNA methylation, altered, 329–332, 335–340, 427–431
 DNA microarrays, for genotyping, 26–27
 DNA, mitochondrial, variations in disease and climatic adaptation, 365–367
 DNA repair defects. *See* DNA damage response/DNA repair
 DNA, ribosomal, *bobbed* locus, dMyc association with, 302–304
 DNA-bar coding strategy, 439–440
 DNA-based genomic studies, 26–27
Drosophila Myc and Mnt transcription factors (dMyc; dMnt), transcriptional regulation by, 299–305
 Drug development, progress and challenges in, 499–510
 Drug discovery, molecular profiling in, 445–448
 Drug resistance. *See* Chemotherapeutic resistance
 Ductal carcinoma in situ (DCIS), epithelial cell p16^{Ink4a} activity in, 317, 322–324
 Dyskeratosis congenita, autosomal dominant, 205–207

E

E2F transcription factors, in regulation of *Arf/p53* tumor surveillance network, 309–315
 E6 oncoprotein of human papillomaviruses, 209–213

E6/E6AP complex, 209–213
 EBV-transformed human B-lymphocyte cell line, 111–118
EGFR gene
 copy number of, and response to *EGFR* inhibitors, 484
 mouse model mutations, 242–243
 mutations of
 in lung adenocarcinoma, 3–5, 73–79
 in malignant glioma, 421
 in non-small-cell lung cancer, 3–5, 242–243, 419–425, 483–484
 and response to *EGFR* inhibitors, 73–79, 419–425, 483–484
 T790M, 423
 sequencing of, 502
EGFR inhibitors. *See* Epidermal growth factor receptor (*EGFR*) inhibitors
EGFR protein
 amplification of, in malignant glioma, 421
 expression of, and response to *EGFR* inhibitors, 484–485
 in non-small-cell lung cancer, 3–5, 242–243, 419–425
 EKB 569 experimental compound, 424–425
 Embryonic stem cells, mouse, homologous recombination techniques in, 275–281
 Endocrine signaling
 androgen dependence in prostate cancer, 192–193
 in small-cell lung cancer, 226
 Endostatin, structure and mechanism of action of, 400–402
 Endothelial cells, in angiogenesis, 400
 Epidermal growth factor receptor. *See* *EGFR* gene; *EGFR* protein
 Epidermal growth factor receptor (*EGFR*) inhibitors. *See also specific drugs*
 clinical response in NSCLC, predictive markers for, 483–486
 differential sensitivity to, in lung adenocarcinoma, 73–79
 irreversible, 424–425
 lung cancer response to, 3–4, 73–79, 419–425
 oncogene addiction and, 3–4, 26, 43–44, 422–423
 resistance to, 3, 419–425, 479–481, 525–526
 Epigenetic silencing
 in cancer and preneoplasia, 329–332
 in tumor progression, 427–431
 Epigenetics
 in cancer research, 527
 loss of genetic imprinting in cancer causality, 335–340
 Epithelial-to-mesenchymal transition and cancer cell invasion and metastasis, 294–295
 FSP1 and, 384
 metalloproteinases and, 350–351
 Erlotinib (Tarceva)
 clinical response in NSCLC
 predictive markers for, 483–486
 resistance to, 242–243, 419–421, 526
 oncogene addiction and, 3–4, 26, 43

relapse with, and differential sensitivity to, 75–77
ER^{TAM} switch, 265–267, 270–271
 Esophageal cancer, 332
 Estrogen receptor, modified, in reversible switch, 265–267, 270–271
Ews-Erg fusion, and neoplasia induction, 280
 Extracellular matrix, in tumor induction and progression, 343–352, 383–387, 526–527
 Extracellular signals, in maintenance of cell survival, 357–361

F

Familial atypical multiple mole and melanoma syndrome, 66
 Fibroblast secreted protein 1, and cancer progression, 384
 Fibroblasts
 in cancer progression, 383–387
 carcinoma-associated, 383–387
 mammary, compared to mammary epithelial cells, 318–320
 in tumor induction and progression, 344
 Firestorm pattern of genomic change, 57–59, 62
 Fish. *See* Tks5 protein
 Fluorescence in situ hybridization (FISH), 51–62
 Fluorescence molecular tomography, for lung cancer biomarker identification, 246
 FSP1, and epithelial-to-mesenchymal transition, 384

G

Gastrointestinal stromal tumors, 419, 479–480
 Gefitinib (Iressa)
 clinical response in NSCLC
 predictive markers for, 483–486
 resistance to, 242–243, 419–425, 526
 oncogene addiction and, 3–4, 26, 43–44, 422–423
 relapse with, and differential sensitivity to, 75–77
 Gene expression studies. *See* Epigenetics
 Gene inactivation/expression, in cancer and preneoplasia, 329–332
 Gene sequencing, of protein kinase gene family, in somatic mutations in human cancer, 43–48, 527
 Gene silencing
 aberrant, in tumor progression, 427–431
 in cancer and preneoplasia, 329–332
 by promoter region methylation, 329–330, 335
 Genetic modifier screens, for kinase identification, 455–457
 Genetic suppression, RNAi and cDNA screening of, 457
 Genome-wide scans, polygenic inherited predisposition to breast cancer, 38–40
 Genomic binding, by *Drosophila* Myc and Mnt transcription factors, 299–305

- Genomic instability
 metalloproteinases and, 350–351
 telomere dysfunction and, 197–203
- Genomic profiles of human lung cancer
 subtypes, 11–22
- Genomics
 in cancer research, 527–528
 and drug development, 499–510
 and lineage addition in human cancer, 25–32
 lung cancer analysis and, 245–246
- Genotype–phenotype relationships, in a mouse model for human small-cell lung cancer, 225–231
- Genotypes of cancer, 5–6
- Genotypic progression, in liver tumor genesis, 217–223
- Genotyping, DNA microarrays for, 26–27
 GFAP gene, and T_{121} expression, 284–285
 Gleevec (imatinib). *See* Imatinib
- Glial fibrillary acidic protein gene. *See* *GFAP* gene
- Glioma, malignant
 EGFR mutations and amplification in, 421
 kinase inhibitor therapy for, 480
- Glucose-dependent metabolism, in growing cells, 361
- Growth factors, in regulation of cell survival, 358–360
- H**
- H1299 colorectal adenocarcinoma cell line, p53 and p73 regulation in, 121–127
- Haplo-insufficiency, 490
- HCT116 colorectal adenocarcinoma cell line, p53 and p73 regulation in, 121–127
- Hemangioblastoma, pVHL tumor suppressor protein and, 159, 161
- Hematopoietic malignancies. *See also* Leukemia; Lymphoma
 leukemia/lymphoma genes, and solid tumor genesis, 83–90
 mouse model for, 277–279
 promoter region methylation in, 329–330
- Hematopoietic stem cells, and tumorigenesis, 187, 193, 205–207
- Hepatitis B and C viruses, and hepatocellular carcinoma, 217, 251
- Hepatocellular carcinoma
 genetically defined, generation and analysis of, 251–260
 mouse models of, 218–222
 her2/neu oncogene overexpression in breast cancers, 375–380
- Hereditary nonpolyposis colon cancer, 66
- Hexokinase II, expression and binding of, in cancer cells, 363–364
- HIC1* (hypermethylated-in-cancer 1) gene, 429–430
- HIF. *See* Hypoxia-inducible factor
- Histone code, promoter region methylation and, 330
- History of cancer genetics research, 83–90
- HKI 272 experimental compound, 424–425
- Homology-directed repair pathway, in telomere-related genome instability, 199–200
- Hormone-refractory prostate cancer, 192–193
- Hsp90 molecular chaperone inhibitors, 378–380, 505–510
- hTERT* gene and hTERT protein
 in autosomal dominant dyskeratosis congenita, 205–207
 in telomerase regulation by human papillomaviruses, 209–214
- hTR* gene and hTR protein, in autosomal dominant dyskeratosis congenita, 205–207
- Human cancer. *See also specific cancer types, e.g.,* Breast cancer
 lineage-restricted DNA alterations in, 27–32
 somatic mutations in, protein kinase gene family resequencing, 43–48
- Human papillomaviruses, telomerase regulation by, 209–214
- Hypereosinophilic syndrome, 479–480
- Hyper-/hypomethylation of DNA. *See* DNA methylation, altered
- Hypermethylated-in-cancer 1 (*HIC1*) gene, 429–430
- Hypoxia, in small Id-deficient breast tumors, 378
- Hypoxia-inducible factor (HIF)
 in mouse model of mammary tumors, 378
 von Hippel-Lindau tumor suppressor protein and, 159–162
- I**
- Id proteins, loss of, and central necrosis of murine breast tumors, 375–380
- IGF2* gene, loss of imprinting and, 335–340
- Imaging technology
 for lung cancer biomarker identification, 246
 for murine lung cancer modeling, 243–245
- Imatinib (Gleevec)
 for chronic myelogenous leukemia, 194
 as model for EGFR inhibitors, 419
 oncogene addition and, 26, 43–44
 resistance to, 3, 242, 479–481, 526
- Immortalization of cells, viral oncoproteins and, 209–214
- Imprinting, loss of. *See* Loss of imprinting
- Inactive X chromosome (Xi)
 abnormalities in BRCA1 mutant and sporadic basal-like breast cancer, 93–96
- Individualized therapy. *See* Personalized molecular cancer therapeutics/diagnostics
- Inflammation, chronic, and stromal promotion of cancer, 383
- INK4* genes and INK4 proteins, 129–135
- Ink4* genes and Ink4 proteins, 129–135, 234. *See also* p16^{Ink4a} protein
- Ink4a* gene, in stem cell self-renewal and cancer cell proliferation, 179–181
- Insulin-like growth factor II, 335. *See also* *IGF2* gene
- Intrabodies. *See* Intracellular antibodies
- Intracellular antibodies (intrabodies), mouse models for testing of, 275–276
- Intrahepatic seeding of genetically modified liver progenitor cells, 254–255
- Invadopodia, Tks5 and, 167–170
- Invasion-metastasis cascade, 149–150, 291–292
- Invertor chromosomal translocation model, 275, 279–281
- Iressa (gefitinib). *See* Gefitinib
- Irradiation
 -induced cell death, *AKT1* gene and AKT1 protein in, 114–118
 p53 response to, 491
 and stromal promotion of cancer, 383
- J**
- c-Jun, apoptosis regulation by, 159, 161–162
- K**
- Kidney tumors. *See* Renal cell carcinoma; Wilms' tumor
- Kinases. *See* Protein kinase family
- Knockin gene fusion, for development of translocation mimics, 275, 277, 280–281
- Knudson hypothesis, epigenetic modification of, 337
- K-ras murine models of lung cancer, 2–3, 241–242, 245–246
- K-ras protein. *See also* Ras effector pathways
 activation of, in tumor progression, 283, 285–286
 p53 cooperative effects, 243
- KRAS* mutations
 in NSCLC, and response to EGFR inhibitors, 485–486
 in pancreatic ductal cancer, 65–70
- L**
- Lentivirus vectors
 Cre-expressing, for T_{121} induction, 286–287, 289
 in RNAi and cDNA screening, 451–454
- Leukemia
 acute myeloid, 193
 acute promyelocytic, 85
 chronic myelogenous, 3, 193–194, 419, 479–481, 526
 chronic myelomonocytic, 479–480
- Leukemia cell lines, promoter region methylation in, 329–330
- Leukemia/lymphoma genes, and genesis of solid tumors, 83–90
- Lineage addition in human cancer, 25–32
- Lineage-restricted DNA alterations, in human tumors, 27–32
- Lipid synthesis in growing cells, 361
- LIT1* antisense transcript gene, loss of imprinting of, 335–337
- Liver tumors
 hepatocellular carcinoma, 218–222, 251–260

- intrahepatic seeding of genetically modified progenitor cells, 254–255
- mouse models of, 217–223
- in situ cancer generation, 255–256
- L-myc amplification, in mouse model of SCLC, 225–231
- Loss of imprinting and cancer risk, 337–339
- IGF2* gene and, 335–339
- mouse model of, 338–339
- Lucentis (ranibizumab), 411
- Lung cancer. *See also* Adenocarcinoma, of lung; Non-small-cell lung cancer
- acquired treatment resistance in, 3, 73–79, 410–425, 479–481, 525–526
- biomarkers of, 246
- cancer stem cells in, 247–248
- EGFR inhibitor response of, 3–4, 419–425
- genomic profiles of subtypes of, 11–22
- lineage-restricted DNA alterations in, 28–30
- murine models of
- non-small-cell lung cancer, 2–3, 5, 241–248
- small-cell lung cancer, 225–231
- Lung metastasis of breast cancer, site-specific metastasis genes and, 153–155
- Lymphocytes
- EBV-transformed human B-lymphocyte cell line, 111–118
- normal, promoter region methylation in, 329–330
- Lymphoma
- Burkitt's, 84
- leukemia/lymphoma genes, and genesis of solid tumors, 83–90
- primary CNS, epigenetic silencing in, 331
- M**
- Macromolecular drugs, mouse models for testing of, 275–276
- Macrophages, in tumor induction and progression, 344
- Macular degeneration, age-related, 411, 414–415
- Magnetic resonance imaging (MRI), in murine lung cancer modeling, 245
- Malignant glioma. *See* Glioma, malignant
- Malignant melanoma. *See* Melanoma, malignant
- Malignant peripheral nerve sheath tumors, 173, 175
- Mammalian tissue-culture cells. *See* Tissue-culture cells, mammalian
- Mammary cancer. *See* Breast cancer
- Mammary epithelial cells
- assays of, in 3-dimensional gels, 345–349
- genetic and epigenetic changes in a carcinogenic subpopulation, 317–326
- malignant transformation in, 343, 350–352
- pRb pathway inactivation in, 283, 289
- Mammary fibroblasts, compared to mammary epithelial cells, 318–320
- Mammary gland, extracellular matrix of, in tumor induction and progression, 345, 349–352
- Markers of cancer. *See* Biomarkers of cancer
- Mathematical modeling of information from protein microarray studies, 517, 520–521
- Matrix metalloproteinase-3 (MMP-3; stromelysin-1), 343, 350–351
- Matrix metalloproteinase-13 (MMP-13), 385
- Mcl-1 in Bak regulation, 471–472, 474–475
- Mdm2, blockage of p53 interaction with, 493
- Melanocytes, transformed, metastatic phenotype of, 295
- Melanoma, malignant
- induction by mutant Cdk4R24C kinase, 235
- lineage-dependent oncogene in, 25, 30–32
- metastatic mechanisms in, 295
- sorafenib for, 465–466
- MET* proto-oncogene, in liver tumor development, 217–223
- Metalloproteinase. *See* Matrix metalloproteinase
- Metastasis
- mechanisms of, 149–150, 291–295, 527
- site-specific genes for, in breast cancer, 149–158
- Tks5 protein in, 167–170
- Methyl-guanine methyl transferase, expression of, and promoter region methylation, 330
- MGMT* gene, epigenetic inactivation of, 330
- Micro-computed tomography (CT), in murine lung cancer modeling, 245
- Microenvironment, in tumor induction and progression, 343–352, 383–387, 526–527
- MITF* gene and *MITF* protein, 25, 30–32
- Mitochondria
- bioenergetics of, 365
- defects of associated with cancer, 363–365
- mtDNA variations in disease and climatic adaptation, 365–367
- in pathophysiology of aging and cancer, 367–372
- MLH1* gene, epigenetic inactivation of, 330
- Mil* and *MLL* genes, 277–278, 280–281
- MMP. *See* Matrix metalloproteinase
- Mnt transcription factor, in *Drosophila*, 299–305
- Molecular chaperone Hsp90, inhibitors of, 378–380, 505–510
- Molecular profiling, in oncology drug discovery, 445–448
- Mouse models
- of astrocytoma, 283–287
- of autosomal dominant dyskeratosis congenita, 206
- of breast tumors, and regression with antiangiogenic stress, 375–380
- in cancer research, overview, 526
- in cyclin-dependent kinase studies, 235–239
- Eμ-myc* mutations, 84
- of hepatocellular carcinoma, 251–259
- of human cancer epigenetics, 338–340
- human chromosome translocation mimics, 275–281
- imaging technology and, 243–245
- of liver tumors, genomic progression in, 217–223
- of neurofibromatosis type 1 tumors, 173–175
- of non-small-cell lung cancer, 2–3, 5, 241–248
- Npm* mutations, 87–89
- in p53 research, 490–491
- of pancreatic ductal and intraepithelial neoplasms, 67–70
- with pRb pathway inactivation, 283–289
- of prostatic adenocarcinoma, 283, 287–289
- of small-cell lung cancer, 225–231
- of telomere dysfunction, 202–203
- transgenic, with inducible oncogenes, 1–3
- VHL* mutations, 160–161
- MRI. *See* Magnetic resonance imaging
- mtDNA variations in disease and climatic adaptation, 365–367
- MTOR inhibitors, 480–481
- Multiple mole and melanoma syndrome, familial atypical, 66
- Myc protein
- dMyc transcriptional regulation, 299–305
- in intrinsic tumor suppression and tumor maintenance, 264–269
- L-myc, in mouse model of SCLC, 225–231
- c-Myc transcription, 210–211
- c-myc proto-oncogene
- inactivation of, and increased thrombospondin-1 expression, 393–394
- role in tumorigenesis, 83–84
- MYC*-oncogene family, in small-cell lung cancer, 226
- Myelogenous leukemia, chronic (CML). *See* Chronic myelogenous leukemia
- Myeloid leukemia, acute (AML), 193
- Myelomonocytic leukemia, chronic (CMML), 479–480
- N**
- NBS1 protein, in recruitment of ATM, 106–108
- NC160 cancer cell line, 25–32
- Neoplastic transformation. *See* Tumorigenesis
- Neovascularization. *See also* Angiogenesis
- mechanisms and control of, 399–400
- Network-targeted combination therapy, 521–522
- Neural crest cell factor, in melanocytes, 295
- Neuroendocrine differentiation, in small-cell lung cancer, 225–231

- Neurofibromatosis type 1, mouse models for, 173–175
- Neurofibromin, 173–175
- Nexavar (sorafenib), 465–467, 500
- NFX1-91 protein, as repressor of hTERT transcription, 211–214
- NFX1-123 protein, in hTERT transcription, 213–214
- Nonhomologous end-joining repair pathway, in telomere-related genome instability, 198–199
- Non-small-cell lung cancer (NSCLC) chemotherapeutic resistance in, 3, 73–79, 480–483, 526
- and kinase screening in tissue culture, 455–456
- EGFR* gene and *EGFR* protein in, 3–5, 242–243, 419–425
- EGFR* inhibitor response in, 3–4, 419–425
- EGFR* inhibitor therapy, and markers of predicted benefit, 483–486
- essential kinase screening in tissue culture, 454–455
- genomic profiles of, 11–22
- mouse models of, 2–3, 5, 241–248
- resequencing of protein kinase gene family in, 43–48
- subtypes of, and pulmonary cell niches, 247–248
- Npm* gene and *Npm* protein, 87–90
- NPM* (nucleophosmin; B23), 86–89, 132–133
- NPM1* gene, 86
- NPM-RARα* fusion protein, 86–89
- NSCLC. *See* Non-small-cell lung cancer
- Nuclear export inhibitor activation of p53 protein, 494
- Nucleophosmin. *See* *NPM*
- Nutrient uptake in metazoan cells, 357–361
- O**
- Ocular disease, VEGF Trap antiangiogenic therapy for, 411, 414–415
- Oncogene addiction
- angiogenesis and, 389–396
- gefitinib response and, 422–423
- in human lung adenocarcinoma, 3–5
- overview, 1–5
- protein kinase inhibitors and, 43–44
- and tumor dependency, 25–26
- Oncogene cooperation, 263–264
- Oncogene-dependent tumor suppression, 177–182, 263–272
- Organ-specific metastatic colonization, 149–158
- Organ-specific tumorigenesis, 344
- Ovarian epithelial cells, pRb pathway inactivation in, 283
- Oxidative phosphorylation, alterations of, in cancer, 363–367, 370–372
- P**
- p15ink4b/CDKN2B* silencing in leukemia, 329–330
- P16ink4a* gene, epigenetic inactivation of, 330
- p16^{Ink4a}* protein
- and carcinogenesis in mammary epithelial cells, 317–326
- in stem cell self-renewal and cancer cell proliferation, 179–181
- p19^{Arf}* protein. *See also Arf* gene
- biochemistry of, 132–133
- p53 induction by, 129–130
- p53-independent functions of, 133–134
- in regulation of *Arf/p53* tumor surveillance network, 310–313
- in stem cell self-renewal and cancer cell proliferation, 179–181
- sumoylation induced by, 134–135
- p21WAF1* gene, p53 activation of, 121–127
- p53* gene
- deletion of, in mouse model of SCLC, 225–231
- sequencing of, 492
- p53 Mdm2 interaction, blockage of, 493
- p53* protein
- antibodies against, staining of, 491–492
- in apoptosis, 470
- in astrocytoma, 284
- dependent transcription profile, 492–493
- dependent tumor suppression, and telomere attrition, 201–203
- K-ras cooperative effects, 243
- as mediator of aging, 181
- mutant, reactivation of, 493
- nuclear export inhibitor activation of, 494
- p19^{Arf}* induction of, 129–130
- in prostatic adenocarcinoma, 283, 288–289
- in response to radiation and chemotherapy, 491
- RNAi suppression of, 256–257
- structure, homologs, and activity of, 489–490
- transcriptional elongation inhibitor activation of, 494
- transcriptional regulation by, compared to p73, 121–127
- wild-type, activation of, 493
- p53* tumor surveillance network
- and *Arf* tumor suppressor function, 129–135
- in diagnostics and therapy, 489–495
- E2F transcription factor in regulation of, 309–315
- gene single-nucleotide polymorphisms in, 111–118
- in tumor maintenance, 269–272
- p53AIP1* gene, p53 activation of, 121–127
- p73* gene, epigenetic inactivation of, 330
- p73* protein, transcriptional regulation by, 121–127
- p107 expression in cancer, 234
- p130 expression in cancer, 234
- Pancreatic β cells, Myc activation in, 265–267
- Pancreatic ductal adenocarcinoma
- compared to non-small-cell lung cancer, 17–21
- epidemiology, genetics, and clinical considerations, 65–67
- mouse models of, 67–70
- Pancreatic intraepithelial neoplasms
- genetics of, 65–66
- mouse models of, 67–70
- Parent-of-origin-specific transmission, in Beckwith-Wiedemann syndrome, 336–337
- Patient biopsies, proteomic profiling of, 517–523
- Patient-tailored therapy. *See* Personalized molecular cancer therapeutics/diagnostics
- Perp* gene, single-nucleotide polymorphism in, 114–118
- Personalized molecular cancer therapeutics/diagnostics
- for *EGFR* inhibitor therapy, in lung adenocarcinoma, 73–79
- p53-selective, 517–523
- progress and challenges in development of, 499–510
- proteomic profiling of patient biopsies, 517–523
- Peutz-Jeghers syndrome, 66
- Phenotypic expression
- of Cdk family alterations, 234
- epigenetic silencing of regulatory genes and, 331
- of mutations in a mouse model for small-cell lung cancer, 225–231
- screens for, in mammalian tissue culture, 449–458
- Pheochromocytoma, hereditary, pVHL tumor suppressor protein and, 159, 161–162
- Phosphoinositide 3-kinase inhibitors, 504–505
- PML-RARα fusion protein, 85–86
- Podosomes, Tks5 and, 167–170
- Poly (ADP-ribose) polymerase-1 inhibition, in treatment of *BRCA1/2* cancer, 142–146
- Polygenic inheritance, and breast cancer, 35–40
- Poor prognosis signatures
- in breast cancer, 150, 152, 156–157
- and metastasis mechanism theories, 292–294
- pRB
- in cell cycle regulation, 233
- E2F transcription factor regulation by, 309–315
- expression of, in cancer, 234
- pRb pathway inactivation, in mouse models of astrocytoma and prostatic adenocarcinoma, 283–289
- Preneoplasia, epigenetic changes in, 329–332, 335, 339–340
- Primary CNS lymphoma, epigenetic silencing in, 331
- Prognostic tools. *See also* Biomarkers of cancer; Poor prognosis signatures
- breast cancer
- gene signatures in primary tumors, 150, 152, 154–157
- ROMA CGH and FISH analysis of, 59–61
- EGFR* inhibitor response in NSCLC, 483–486
- Promoter region methylation, 329–332
- Promyelocytic leukemia, acute (APL), 85
- Prostaglandin-endoperoxide synthase 2 (COX-2), association with p16Ink4a hypermethylation, 322–324

- Prostate cancer
 adenocarcinoma, mouse models of, 283, 287–289
 hormone-refractory, 192–193
 kinase inhibitor therapy for, 480
 prostate stem cells and, 187–194
- Prostatic stem cells
 identification of, 188–190
 niche of, 190–192
 and prostate cancer, 192–194
- Pro-survival proteins of Bcl-2 family, and apoptosis, 469–475
- Protein kinase family. *See also names of specific kinases*
 identification by genetic modifier screens, 455–457
 RNAi and cDNA screening for, 449–458
 sequencing of somatic mutations in human cancer, 43–48, 527
- Protein kinase inhibitor therapy. *See also specific drugs and drug classes*
 acquired resistance to, 3, 73–79, 419–425, 480–481, 525–526
 review of application of, 479–481
- Protein microarrays, in protein signaling network analysis, 517–519
- Proteins, microenvironmental, in tumor induction and progression, 346, 352–353
- Protein-signaling network models, clinical proteomic analysis of, 517–523
- Proteomics, clinical
 and lung cancer biomarker identification, 246
 protein signaling network analysis in, 517–523
- Proto-oncogene activation, in stem cell self-renewal and cancer cell proliferation, 177–182
- Pten tumor suppressor
 inactivation, in tumor progression, 283, 286–287
 in prostate cancer suppression, 287
- PTEN tumor suppressor
 genetic mutations of gene for, 502
 and kinase inhibitor response, 480–481
 in neoplastic proliferation and aging, 181–182
- PTEN/AKT signaling pathway
 dysregulation, in human prostate cancer, 187, 194
- pVHL, in cancer and oxygen sensing, 159–162
- R**
- Radiation. *See Irradiation*
- Raf kinase inhibitors, 465–467, 500–501
- Raf proteins, 461–467
- Ranibizumab (Lucentis), 411
- Rapamycin, 480
- RARα* gene fusions, 84
- Ras effector pathways. *See also K-ras*
 murine models of lung cancer; K-ras protein
 activation, in tumor progression, 283, 285–286
 cancer targets in, 461–467
 deregulation of in neurofibromatosis type 1, 174–175
 in tumorigenesis, 245
- RASSF1a* gene, epigenetic inactivation of, 330
- Rbl* gene
 deletion of, in mouse model of SCLC, 225–231
 epigenetic inactivation of, 330
- Reactive oxygen species (ROS)
 mitochondrial alterations and, 363, 365, 368, 370–372
 phenotypic alterations and genomic instability due to, 350–351
- Renal cell carcinoma
 clear-cell, pVHL tumor suppressor protein and, 159, 161
 sorafenib for, 465
- Representational oligonucleotide microarray analysis (ROMA), 51–62
- Retinoblastoma proteins. *See pRB*
- Retroviral vectors
Cre-expressing, for T₁₂₁ induction, 286–287, 289
 in RNAi and cDNA screening, 451–454
- Reverse phase microarray, 518–519
- RNA interference (RNAi)
 in cancer-signaling network studies, 435–441
 in gene suppression studies, 256–257
 as research tool, 527–528
 screens using, in mammalian tissue culture, 449–458
 synthetic lethal screens, 447–448
- ROMA (representational oligonucleotide microarray analysis), 51–62
- ROS. *See Reactive oxygen species*
- R-Roscovitin* (seliciclib; CYC202), 502–504
- Rous sarcoma virus, 1, 344–345
- S**
- Sca-1 antigen, as prostatic stem cell marker, 187–194
- SCC. *See Squamous cell carcinoma*
- SCLC (small-cell lung cancer), mouse models for, 225–231
- Screens. *See also Biomarkers of cancer*
 cell-based, for novel p53 activators, 494
 genetic modifier, for kinase identification, 455–457
 synthetic lethal, 438–441, 445–448
 using RNAi and cDNA expression, 449–458
- SDF-1 α (stromal-cell derived factor 1 α ; CXCL-12), 384
- Secreted frizzled related proteins (SFRPs), 428–429
- Seed and soil hypothesis of metastasis, 149
- Seliciclib (CYC202; *R-roscovitin*), 502–504
- Serum protein biomarkers, 481
- SFRPs (secreted frizzled related proteins), 428–429
- Shelterin, 198, 202
- Short hairpin RNAs (shRNAs)
 in cancer-signaling network studies, 435–441
 screens using, in mammalian tissue culture, 449–458
 in synthetic lethal screens, 447–448
- Signaling pathways. *See Cancer-signaling networks*
- Single-nucleotide polymorphism (SNP) arrays, 25–32
- Single-nucleotide polymorphisms (SNPs)
 in genes encoding microenvironmental proteins, 346, 352–353
 in p53 pathway, 111–118
- siRNAs. *See Small interfering RNAs*
- Site-specific metastatic colonization, genes mediating, 149–158
- Site-specific tumorigenesis, 344
- Slug neural crest cell factor, in melanocytes, 295
- Small interfering RNAs (siRNAs)
 in synthetic lethal screens, 447–448
 use in mammalian cells, 435–436
- Small molecule drugs. *See Erlotinib; Gefitinib; Imatinib*
- Small-cell lung cancer (SCLC), mouse models for, 225–231
- SMC1 protein
 in cellular response to DNA damage, 102–105
 and mechanisms of DNA repair, 106–108
- Smoking history in NSCLC, and response to EGFR inhibitors, 485–486
- SNPs. *See Single-nucleotide polymorphisms*
- Somatic mutations in human cancer, 43–48
- Sorafenib (Nexavar), 465–467, 500
- Sporadic cancers
 “BRCA-ness” of, 144–145
 inactive X chromosome abnormalities in basal-like breast cancer, 93–96
- Squamous cell carcinoma (SCC)
 of esophagus, promoter region methylation and progression of, 332
 of lung, genomic profile of, 11, 16–17, 20
- v-src* gene, 1, 344
- Src protein tyrosine kinase, 167–170
- Stem cells
 adult
 assays for enrichment of, 188
 hematopoietic, 187, 193
 prostatic, 187–194
 self-renewal of, proto-oncogene and tumor suppressor activation and, 177–182
 in tissue regeneration, 188
 tumorigenesis potential of, 187, 192–193, 527
 cancer
 in lung cancer, 247–248
 telomerase activity in, 205–207
 in tumorigenesis, 193, 225
 embryonic murine, homologous recombination techniques in, 275–281
- Stem cell theory of cancer, telomerase activity and, 205–207
- Stroma, in tumor induction and progression, 343–352, 383–387
- Stromal-cell derived factor 1 α (SDF-1 α ; CXCL-12), 384
- Stromelysin-1 (MMP-3), 343, 350–351

- Sumoylation, Arf induction of, 129, 134–135
- Synthetic lethal screens, 438–441, 445–448
- T**
- T₁₂₁
induction of, new systems for, 284–286
induction of using *Cre*-expressing lentivirus vectors, 286–287
pRb inactivation by, 283–289
- T790M mutation of *EGFR*, 423
- TAp73 expression, in colorectal adenocarcinoma cell lines, 121–127
- Tarceva (erlotinib). *See* Erlotinib
- Telomerase
cancer stem cells and, 205–207
human papillomavirus regulation of, 209–214
up-regulation of, and telomere dysfunction, 202–203
- Telomere dysfunction induced foci, 200–201
- Telomere hypothesis of cancer, 205–207
- Telomeres
dysfunction of, and genomic instability in human cancer, 197–203, 320–321
human, molecular structure of, 197–198
length of, in neoplastic proliferation and aging, 181
- TERT* gene and *TERT* protein, human. *See hTERT* gene and hTERT protein
- Testicular germ-cell tumors, resequencing of protein kinase gene family in, 43–48
- Tetraploidy, telomere-related, 200–201
- TGF- β (transforming growth factor β)
and cancer progression, 384–385
in wound healing and tumorigenesis, 345
- Therapeutic strategies for cancer. *See also* Chemotherapeutic drugs; Chemotherapeutic resistance
Bcl-2 life/death switch in, 469, 473, 475
BH3 mimetics in, 469, 473–475
in *BRCA1/2* carriers, 139–146, 526
combination therapy, network-targeted, 521–522
kinase inhibitors, 3, 479–481
p53-selective therapies, 489–495
personalized. *See* Personalized molecular cancer therapeutics/diagnostics
progress and challenges in development of, 499–510
- Thrombospondin-1/2
overexpression of, and suppression of tumor growth, 392–393
structure and mechanism of action of, 400, 404–406
- Tissue polarity, in regulation of chemotherapeutic resistance, 349
- Tissue structure and function regulators, in tumor induction and progression, 343–352, 526–527
- Tissue-culture cells, mammalian
aneuploidy of p53 knockout mouse cells, 490–491
chemotherapeutic resistance in breast cancer, and kinase screening, 455–456
proteomic profiling of, 519–520
RNAi and cDNA screening in, 449–458
siRNA use in, 435–436
- Tks4 protein, 167–168
- Tks5 protein, and cancer cell invasiveness, 167–170
- TP53. *See* p53 gene; p53 protein
- TR gene and TR protein, human. *See hTR* gene and hTR protein
- Transcription profile, p53-dependent, 492–493
- Transcriptional elongation inhibitor
activation of p53 protein, 494
- Transcriptional regulation
by *Drosophila* Myc and Mnt transcription factors, 299–305
by human papillomavirus, 446
by p53 and p73 proteins, 121–127
- Transforming growth factor β (TGF- β)
and cancer progression, 384–385
in wound healing and tumorigenesis, 345
- Translocator mouse model, 275, 277–279, 281
- Trp53* gene deletion, in mouse model of SCLC, 225–231
- Tumor progression. *See also* Angiogenesis; Metastasis
aberrant gene silencing in, 427–431
Darwinian model of, 291–293
extracellular matrix in, 343–352, 526–527
fibroblasts and, 383–387
microenvironmental proteins in, 346, 352–353
need for studies on, 6–7
promoter region methylation and, 329, 331–332
Pten inactivation in, 283, 286–287
Ras effector pathways in, 285–286
- Tumor suppression, oncogene-dependent, 263–272
- Tumor suppressors. *See also names of specific tumor suppressors*
activation of, in stem cell self-renewal and cancer cell proliferation, 177–182
and kinase inhibitor response, 480
pleiotropic, 85–86
- Tumor-associated macrophages, 344
- Tumorigenesis
Bcl-2 life/death switch in, 469, 472–473
extracellular matrix in, 343–352, 526–527
leukemia/lymphoma genes and, 83–90
c-myc proto-oncogene and, 83–84
organ-specific metastasis genes in breast cancer and, 155–156
promoter region methylation and, 329–332
stem cell potential in, 187, 192–193, 527
telomerase activity in cancer stem cells and, 205–207
telomere-related genome instability in, 197–203
viral oncoproteins in, 209–214, 217
- Tumstatin, structure and mechanism of action, 400, 402–404
- Type 1 collagen, and cancer progression, 385
- Tyrosine kinase inhibitors. *See also specific drugs and drug classes*
differential sensitivity to, in lung adenocarcinoma, 3–5, 73–79
oncogene addiction and, 25–26, 43–44
- V**
- Vascular basement membrane, in angiogenesis, 400
- VEGF and VEGF family, 411–412
- VEGF receptors, 412
- VEGF Trap, as antiangiogenic treatment, 411–415
- VEGF-R2 inhibitors, 465–467
- VelociGene-based discovery of angiogenesis targets, 415
- VHL* gene, 159–162, 330
- Viral oncogenes, 1, 344
- Viral oncoproteins
in liver tumor development, 217
and telomerase regulation disruption, 209–214
- Viral vectors
Cre-expressing, for T₁₂₁ induction, 286–287, 289
in RNAi and cDNA screening, 451–454
- von Hippel-Lindau tumor suppressor protein (pVHL), in cancer and oxygen sensing, 159–162
- Von Recklinghausen's neurofibromatosis, 173–175
- W**
- Wilms' tumors, 335–337
- Wound healing, and tumorigenesis, 345
- X**
- X chromosome, inactive (Xi), abnormalities in *BRCA1* mutant and sporadic basal-like breast cancer, 93–96
- Y**
- Yeast, synthetic lethal screens in, 446

Cold Spring Harbor Symposia on Quantitative Biology

Subject Index

Cold Spring Harb Symp Quant Biol 2005 70: 531-538

Access the most recent version at doi:[10.1101/sqb.2005.70.062](https://doi.org/10.1101/sqb.2005.70.062)

License

Email Alerting Service

Receive free email alerts when new articles cite this article - sign up in the box at the top right corner of the article or [click here](#).

To subscribe to *Cold Spring Harbor Symposia on Quantitative Biology* go to:
<http://symposium.cshlp.org/subscriptions>