

Author index

Volume 5, 1998

Allen, PG, R81
Anderson, PS, R312, 597
Apriletti, JW, 299
Arigoni, D, R221
Atkins, WM, 689
August, PR, 69
Axelsen, PH, 293
Azimioara, M, 529
Bacheler, LT, R312, 597
Bacher, A, R221
Baird, EE, 119
Baker, SI, 475
Baleja, JD, 217
Barton, JK, 413
Baxter, JD, 299
Beard, WA, R7
Bechthold, A, 647
Bedford, DJ, 647
Belshaw, PJ, 373
Benkovic, SJ, R105
Berens, C, 163
Bergstrom, RC, 475
Bernard, MP, 241
Bertozzi, CR, 447, R313
Bhakta, S, 447
Bibb, MJ, 135, 647
Bistrup, A, 447
Blattner, FR, 573
Bogyo, M, 307
Böhm, I, 407
Boone, L, 103
Bowman, KG, 447
Brady, SF, R245
Bremer, RE, 119
Breslow, R, R27
Brickner, M, 339
Burke, JM, 587
Bussiere, DE, 489
Bycroft, M, 743
Byrom, KJ, 35, 699
Cao, J, 49
Cartayrade, A, R221
Cech, TR, 539
Chan, L, 283
Chang, C-H, R312, 597
Charych, D, 619
Chaudhary, A, 273
Chen, C-hB, 283
Chen, J, 273
Chen, JP, 689
Cheng, J, 49
Chiellini, G, 299
Chin, W-C, 689
Chmielewski, J, R276, 339, 439
Ciftan, SA, 679
Clardy, J, R245
Claridge, TD, 229
Cleary, KA, 185
Cohen, FE, 345
Cohen, P, R161, 321
Coombs, GS, 475
Cooper, MA, 329
Cordova, B, R312, 597
Corey, DR, R157, 13, 475
Cortés, J, 407
Cowan, JA, 147
Cox, RJ, 35, 699
Craxton, M, 321
Crosby, J, 35, 699
Cutter, AL, 743
Dabrowski, MJ, 689
Dancer, RJ, 329
de Bizemont, T, 755
DeMoll, E, 573
Denison, C, R129
Dervan, PB, 119
Doyle, DF, R157, 13
Dunham, WR, 355
Dwarki, V, 345
Ehricht, R, 729
Ehrlich, PH, 241
Eisenreich, W, R221
Elbert, DL, 177
Ellinger, T, 729
Entress, RMH, 329
Epple, C, 209
Erickson-Viitanen, S, R312, 597
Escobedo, JA, 345
Eyers, PA, 321
Fallon, EM, R257
Famulok, M, 23
Fetherston, JD, 573
Finlay, MRV, 365
Finney, NS, R73
Fisher, DE, R29
Fitzgerald, PMD, 185
Floss, HG, 69, 647
Frost, EJ, 743
Garber, S, R312, 597
Garestier, T, 755
Gaytán, P, 519
Gehring, AM, 573
Geysen, M, R265
Ghosh, I, R276, 439
Gimble, FS, R251
Goedert, M, R161, 321
Goodman, BK, 263
Goodman, RM, R245
Gordon, EJ, R49
Gordon, S, R193
Grant, SK, 185
Greenberg, MM, 263

Author index

Greenberg, W, 397
Grover-Sharma, N, 185
Gu, Q-M, 273
Guan, W, 529
Hamer, JD, 345
Hammond, GG, 185
Han, Y, 241
Handa, S, 743
Handelsman, J, R245
Hanefeld, U, 407, 743
Harris, BR, 155
Harris, R, 743
Haugh, JM, R257
He, Y, 365
Healy, VL, 197
Hélène, C, 755
Hemmerich, S, 447
Hendrix, M, 397
Henry, PA, 529
Hermann, T, R277
Hillen, W, 163
Hitchman, TS, 35
Hoffmann, D, 69
Holzbaur, IE, 407
Hopwood, DA, 135, 647
Hoveyda, AH, R187
Huang, C-Y, 345
Huang, F, 669
Hubbell, JA, 177
Hutchins, C, 489
Hutchinson, CR, 69
Ichinose, K, 647
Imperiali, B, 427
Janmey, PA, R81
Jelinek, R, 619
Jenne, A, 23
Johnson, BL, R312, 597
Jones, M, 155
Jones, RA, 555
Jones, SJM, 155
Katz, L, 489
Keating, TA, 631
Kelleher, NL, 373
Kelley, GL, 241
Kelley, SO, 413
Kennedy, HJ, R285
Kershaw, JK, 155
Keyes, WJ, 103
Kiessling, LL, R49
Kim, C-G, 69
Kim, D, 103
Kim, S, 217
King, NP, 365
Kirkpatrick, PN, 155
Klabe, RM, R312, 597
Knight, RD, R215
Ko, SS, R312, 597
Kocz, R, 103
Kodadek, T, R129
Kolter, R, R181
Kool, ET, 59
Kozarich, JW, 185
Kurakin, A, 81
Kwiatkowski, DJ, 273
Lam, PYS, R312, 597
Landgraf, R, 283
Landweber, LF, R215
Larsen, HJ, 81
Lauffenburger, DA, R257
Leadlay, PF, 407, 743
Lee, S, 345
Lennard, NJ, 155
Lessard, IAD, 489
Leumann, C, 209
Li, T, 365
Li, Y, 1, 505
Lin, CH, 555
Lin, W, 241
Liu, H-w, 661
Liu, Y, 91
Loll, PJ, 293
Luebke, KJ, R317
Lynn, DG, 103
McCafferty, DG, 489
McCaskill, JS, 729
McGill, G, R29
Mackie, H, 519
McMaster, JS, 307
Madison, EL, 475
Mangelsdorf, DJ, 13
Marletta, MA, 255, 355
Matharu, A-L, 699
May, WJ, 185
Mayhew, GF, 573
Miller, GP, R105
Miller, R, 293
Moczydowski, E, R291
Moon, N, 355
Mori, I, 573
Morrice, N, 321
Moyle, WR, 241
Mueller, MJ, R323
Müller, R, 69
Murphy, JE, 345
Murray, JB, 587
Myers, RV, 241
Natarajan, K, 147
Navre, M, 475
Nicolaou, KC, R1, 365
Nielsen, PE, 81
Ning, S, 69
Ninkovic, S, 365
Nolan, GP, 713
Norvez, S, 619
O'Brien, DP, 329
O'Connor, SE, 427
Okada, S, 619
Olson, SH, 185
Park, I-S, 197
Patel, DJ, 555
Peet, DJ, 13

Pellequer, J-L, 475
 Perry, JM, 355
 Perry, RD, 573
 Pirring, MC, 49
 Platt, N, R193
 Ploegh, HL, 307
 Pompliano, DL, 185
 Poulos, TL, 461
 Pratt, SD, 489
 Prestwich, GD, 273
 Priestley, ES, 397
 Quadri, LEN, 631
 Radhakrishnan, R, 345
 Rao, SNV, 241
 Reid, C, R312, 597
 Revill, WP, 135, 647
 Ribeiro, RCJ, 299
 Rickles, RJ, 529
 Roddis, M, 743
 Rodgers, JD, R312, 597
 Rondon, MR, R245
 Rosen, SD, 447
 Rowe, CJ, 229
 Roy, RS, 217, 373
 Rozinov, MN, 713
 Rutter, GA, R285
 Ryan, K, 59
 Sánchez, F, 519
 Sarabia, F, 365
 Scanlan, TS, 299
 Schirmer, A, R181
 Schlonk, PM, 283
 Schreiber, SL, R1, 385
 Schroeder, R, 163
 Schwarz, M, R221
 Schweizer, M, 135
 Scott, WG, 587
 Seitz, SP, R312, 597
 Sello, J, 631
 Sen, D, 1, 505
 Seyhan, AA, 587
 Shah, K, 91
 Shakespeare, WC, 529
 Sherman, DH, 661
 Shi, H, 689
 Shin, S, 307
 Shokat, KM, 91
 Shorrock, CP, 229
 Sigman, DS, 283
 Simpson, TJ, 35, 699
 Singer, MS, 447
 Smith, MM, 475
 Soberón, X, 519
 Solenberg, PJ, 155
 Staunton, J, 407, 743
 Stockwell, BR, 385
 Stone, JR, 255
 Stossel, TP, R81
 Streicher, B, 163
 Sun, J-S, 755
 Sundaramoorthy, M, 461
 Sundelof, JG, 185
 Sutherland, JD, 229
 Szostak, JW, 609
 Tainer, JA, 475
 Tang, L, 69
 Tavaré, JM, R285
 Taylor, M, 69
 Terner, J, 461
 Terwilliger, TC, 283
 Theil, EC, 679
 Thornberry, NA, R97
 Thorp, HH, R125, 679
 Timoney, MC, 743
 Toney, JH, 185
 Tor, Y, R277
 Tornus, D, 647
 Trainor, GL, R312, 597
 Travascio, P, 505
 Tronche, C, 263
 Tropf, S, 135
 Try, AC, 329
 Uno, T, 345
 van Wageningen, AMA, 155
 Vanderwall, DE, 185
 Violette, S, 529
 von Ahsen, U, R3
 Vourloumis, D, 365
 Walsh, CT, R177, 197, 217, 373, 489, 573, 631
 Walter, NG, 587
 Walts, AD, 283
 Wang, H, R312, 597
 Wang, W, 555
 Wang, Y, 241
 Wanner, BL, 489
 Weeks, CM, 293
 Weinreb, PH, 631
 Weissman, KJ, 743
 Wells, WA, R15, R39, R63, R87, R115, R147, R165, R205, R235, R267, R303, R335
 Westhof, E, R277
 White, MRH, R285
 Williams, DH, 155, 329
 Wilson, C, 609
 Wilson, D, 661
 Wilson, SH, R7
 Winans, KA, R313
 Witke, W, 273
 Witucki, L, 91
 Wong, C-H, 397
 Wood, CD, R285
 Wright, MR, R312, 597
 Wu, JK, 185
 Xue, Y, 661
 Yañez, J, 519
 Yang, F, 91
 Yang, Z, 669
 Yarus, M, 669
 Yoon, YJ, 69
 Yoshihara, HA, 299
 Yu, T-W, 69

Author index

- Zenk, MH, R221
- Zhang, B, 539
- Zhang, X, 69
- Zhao, L, 661
- Zhao, Y, 355
- Zoller, MJ, 529
- Zuckermann, RN, 345

Subject index

Volume 5, 1998

The letters in parentheses refer to the following: P = Research paper, R = Review article, M = Minireview article, X = Crosstalk, I = Innovations

A-site RNA, aminoglycoside antibiotics, 397 (P)
N-acetyl-D-alanine (AcDA), dimerization mode for vancomycin, 293 (P)
Acquired immune deficiency syndrome (AIDS), cyclic urea HIV protease inhibitors, 597 (P)
Actin monomers, profilin I, 273 (P)
Actin-binding proteins
 gelsolin, R81 (M)
 profilin I, 273 (P)
Actinomycetes, rifamycin biosynthetic gene cluster, 69 (P)
Actinorhodin, granaticin biosynthetic gene cluster, 647 (P)
Actinorhodin polyketide synthase, malonyl CoA: *holo* acyl carrier protein transacylases (MCATs), 699 (P)
Activation-induced shedding, R49 (R)
Activators, small molecules, R134 (R)
Active oxygen species, oxidases in parasitic plant development, 103 (P)
Active-site labeling, proteasomes, 307 (P)
Active-site mutants, bacterial vancomycin-resistance phenotype, 197 (P)
Acyl carrier protein (ACP)
 rat fatty acid synthases, 135 (P)
 type II polyketide synthase, 35 (P)
Acyl transferases, ester transferase ribozyme, 23 (P)
Adaptive DNA structural transitions, amino-acid-binding pocket formation, 555 (P)
Adhesion molecules, scavenger receptors, R195 (R)
Adsorbing block copolymers, biological surfaces, 177 (P)
Affinity probes, proteasome active site labeling, 307 (P)
Agonist ligands, thyroid hormone receptor, 299 (P)
D-Ala-D-Ala dipeptidase, VanX homologs, 489 (P)
Alanine scanning, automatable codon-level mutagenesis, 519 (P)
D-alanyl-D-alanine ligase, bacterial vancomycin-resistance phenotype, 197 (P)
D-alanyl-D-serine ligase, bacterial vancomycin-resistance phenotype, 197 (P)
Alkali cation selectivity, potassium-channel proteins, R291 (R)
Alkaline-labile lesions, C1'-DNA radical, 263 (P)
Alkyl epoxides, hydrolysis, R73 (M)
Alkylation, thyroid hormone receptor, 299 (P)
Alternate-strand triple-helix formation, 755 (P)
Amino acids, codons, R215 (X)
Amino-acid substitution, SB 203580, 321 (P)
Amino-acid-binding pocket, adaptive zippering-up of DNA hairpin loop, 555 (P)
3-amino-5-hydroxy benzoic acid, rifamycin biosynthetic gene cluster, 69 (P)
Amino-terminal propeptide, microcin B17 propeptide, 217 (P)
Aminoacylation site, ester transferase ribozyme, 23 (P)
 δ -(L- α -aminoacyl)-L-cysteinyl-D- α -aminobutyrate, 229 (P)
1-aminocyclobutanecarboxylate, ethylene biosynthesis, 49 (P)
1-aminocyclopropanecarboxylic acid (ACC), ethylene biosynthesis, 49 (P)
Aminoglycosides
 A-site RNA, 397 (P)
 antibiotics, hammerhead ribozymes, R227 (X)
Amplification system, CATCH (cooperative amplification of templates by cross hybridization), 729 (P)
Amycolatopsis mediterranei, rifamycin biosynthetic gene cluster, 69 (P)
Amycolatopsis orientalis, biosynthesis of glycopeptide antibiotics, 155 (P)
Angiogenesis, R87 (I)
Ansamycin antibiotic rifamycin, rifamycin biosynthetic gene cluster, 69 (P)
Antagonists, transforming growth factor- β signaling, 385 (P)
Anti-gene agent, peptide nucleic acid binding, 81 (P)
Anti-inflammatory drugs, engineering protein kinases, R161 (M)
Antibiotics
 aminoglycoside
 A-site RNA, 397 (P)
 binding, R227 (X)
 biosynthesis
 of glycopeptide, 155 (P)
 granaticin biosynthetic gene cluster, 647 (P)
 dimerization mode, 293 (P)
 microcin B17 synthase, 373 (P)
 19 F NMR in measurement of binding affinities, 329 (P)
 pikC-encoded cytochrome P450 hydroxylase, 661 (P)
 resistance, metallo- β -lactamase inhibitors, 185 (P)
Antibody-induced shedding, protein shedding at cell surface, R54 (R)
Antigens, substrate specificity of, 475 (P)
Antimicrobial resistance, dimerization mode for vancomycin, 293 (P)
Antitumor agents, epothilones, 365 (P)
Apoplastic phenol, oxidases in parasitic plant development, 103 (P)
Apoptosis, caspases, R97 (M)
Apoptotic cells, scavenger receptors, R196 (R)
Aptamer-hemin complex, DNA-enhanced peroxidase activity, 505 (P)
Arg-Pro-Arg, inhibition of protein binding by polyamides, 119 (P)
L-argininamide-DNA aptamer complex, 555 (P)
Arginine-RNA interactions, R215 (X)
Aromatic polyketide synthases (PKSs), granaticin biosynthetic gene cluster, 647 (P)
Asparagine-linked glycosylation, glycosylation-induced conformational switching, 427 (P)
Aspergillus nidulans, isopenicillin N synthase, 229 (P)
Atomic force microscopy, protein-based nanofabrication, 689 (P)
ATP analog, engineered Src kinase nucleotide specificity, 91 (P)
Automatable codon-level mutagenesis, 519 (P)
Backbone modification, DNA analog/complementary DNA pairing, 209 (P)
Bacteria, soil, R15 (I)
Bacterial cell-wall surfaces, 19 F NMR in measurement of binding affinities, 329 (P)
Bacterial resistance, dimerization mode for vancomycin, 293 (P)
Bacterial sulfatases, modification of, R181 (X)
Bacteroides fragilis, metallo- β -lactamase inhibitors, 185 (P)
Base stacking, electron transfer in DNA, 413 (P)
Basic-helix-loop-helix (bHLH), β -sheet peptide inhibitor, 439 (P)
Benzoisochromanequinones, granaticin biosynthetic gene cluster, 647 (P)
4-benzyldihydrocinnamoyl, profilin I, 273 (P)
 β -turn structure, glycosylation-induced conformational switching, 427 (P)
Biaryl alcohol, thyroid hormone receptor, 299 (P)

Subject index

Bicyclo[3,2,1]-DNA, DNA analog/complementary DNA pairing, 209 (P)
Biogenesis, iron acquisition in *Yersinia*, 573 (P)
Bioinorganic chemistry, zinc, R125 (X)
Biological pathways, small molecules, R129 (R)
Biological surfaces, comb copolymers, 177 (P)
Biologically imposed symmetry, protein-based nanofabrication, 689 (P)
Biology/chemistry interface, R27 (R)
engineering proteins, R157 (X)
Biomimetic chemistry, R27 (R)
Biosynthesis
ethylene, 49 (P)
gene cluster, granaticin, 647 (P)
glycopeptide antibiotic, 155 (P)
isopenicillin N synthase, 229 (P)
malonyl CoA: *hōlo* acyl carrier protein transacylases (MCATs), 699 (P)
precursor-directed, 743 (P)
terpenoid, R221 (R)
Biotechnology
Caliper Technologies Corporation, R115 (I)
ChromaXome Corporation, R15 (I)
Cogentix Inc., R235 (I)
EntreMed, Inc., R87 (I)
Helicon Therapeutics, Inc., R165 (I)
Imaging Research, Inc., R205 (I)
MitoKor, R303 (I)
NemaPharm, Inc., R147 (I)
Neurex Corporation, R235 (I)
Shaman Pharmaceuticals, Inc., R63 (I)
TerraGen Diversity Inc., R15 (I)
Vertex Pharmaceuticals, Inc., R267 (I)
Biphenyl tetrazoles, metallo-β-lactamase inhibitors, 185 (P)
4,5-bisphosphate binding site, profilin I, 273 (P)
Block copolymers, biological surfaces, 177 (P)
Books, combinatorial chemistry, R265
C1'-DNA radical, generation of, 263 (P)
C12,13-cyclopropyl-epothilone A, 365 (P)
Ca²⁺
gelsolin binding, R83 (M)
calmodulin binding, flavin radical relaxation, 359 (P)
Caenorhabditis elegans, R147 (I)
Caliper Technologies Corporation, R115 (I)
Cancer, R87 (I)
Capillary electrophoresis (CE), R115 (I)
Capping, small-bisubstrate ribozymes, 669 (P)
Carbapenem antibiotics, metallo-β-lactamase inhibitors, 185 (P)
Carboxy-terminal (P1) amino acid residue, proteasome active site labeling, 307 (P)
Caspases, apoptosis, R97 (M)
Catalysis
dihydrofolate reductase, R105 (R)
isopenicillin N synthase, 229 (P)
phospholipases at conjugated lipid vesicles, 619 (P)
Catalyst discovery, R187 (M)
Catalytic DNA, DNA-enhanced peroxidase activity, 505 (P)
Catalytic RNA, monovalent cations, 587 (P)
CATCH (cooperative amplification of templates by cross hybridization), 729 (P)
Catenane, triplex-directed sliding clamp assembly, 59 (P)
Cationic lipids, cellular delivery of plasmid DNA, 345 (P)
CD36, scavenger receptors, R200 (R)
Cell surfaces,
¹⁹F NMR in measurement of binding affinities, 329 (P)
protein shedding, R49 (R)
Cephalosporins, isopenicillin N synthase, 229 (P)
Charge transport, electron transfer in DNA, 413 (P)
Chemical biology, engineering ethos, R177
Chemical nuclease, DNA scission, 283 (P)
Chemistry books, combinatorial, R265
Chemistry, biomimetic, R27 (R)
Chemistry/biology interface, engineering proteins, R157 (X)
Chiral catalysts, catalyst discovery, R187 (M)
Chloroeremomycin
biosynthesis of glycopeptide antibiotics, 155 (P)
¹⁹F NMR in measurement of binding affinities, 329 (P)
Chloroperoxidase catalysis, stereochemistry of, 461 (P)
Cholera, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)
ChromaXome Corporation, R15 (I)
Circular dichroism (CD), E47 dimerization, 439 (P)
Circular triplex-forming oligonucleotides (CTFOs), triplex-directed sliding clamp assembly, 59 (P)
Clonable fragments, DNA scission, 283 (P)
Cloning, soil microflora, R245 (X)
Codon-level mutagenesis, automatable, 519 (P)
Codon–amino-acid pairing, R215 (X)
Cogentix Inc., R235 (I)
Colorimetric detection, interfacial catalysis at conjugated lipid vesicles, 619 (P)
Comb copolymers, biological surfaces, 177 (P)
Combinatorial biosynthesis, rifamycin biosynthetic gene cluster, 69 (P)
Combinatorial chemistry
books, R265
catalyst discovery, R187 (M)
Combinatorial libraries, automatable codon-level mutagenesis, 519 (P)
Competitive inhibition, ester transferase ribozyme, 23 (P)
Computer chips, R115 (I)
Cone snails, R235 (I)
Conformational flexibility, dihydrofolate reductase, R105 (R)
Conformational restriction, DNA analog/complementary DNA pairing, 209 (P)
Conformational switching, glycosylation-induced, 427 (P)
Conjugated lipid vesicles, interfacial catalysis by phospholipases, 619 (P)
Cooperation, CATCH (cooperative amplification of templates by cross hybridization), 729 (P)
Cooperative binding, peptide nucleic acid, 81 (P)
Copolymers, biological surfaces, 177 (P)
Crystallography, chloroperoxidase catalysis, 461 (P)
Cyclic urea, HIV protease inhibitors, 597 (P)
Cyclopentanoic lipid mediators, isoprostanes, R323 (R)
Cyclopropane analog, epothilones, 365 (P)
Cysteine-knot proteins, homodimeric glycoprotein hormones, 241 (P)
Cysteine-specific sulfatase-modifying enzymes, R183 (X)
Cytochrome P450
chloroperoxidase catalysis, 461 (P)
pikC-encoded cytochrome P450 hydroxylase, 661 (P)
Cytokine engineering, R257 (R)
Cytokine receptors, protein shedding at cell surface, R56 (R)
Cytolysis, lytic peptide structure, 147 (P)
Cytoskeletal remodeling, gelsolin binding, R81 (M)
Cytosolic protein breakdown, proteasome active site labeling, 307 (P)
7-deazaguanine, electron transfer in DNA, 413 (P)
DEBS 1-TE, precursor-directed biosynthesis, 743 (P)
Dehydroproline, ethylene biosynthesis, 49 (P)
Deoxynucleoside 5'-triphosphate, DNA polymerase β fidelity, R7 (M)
Deoxyribonucleotides, C1'-DNA radical, 263 (P)
Deoxyribozymes, fluorophore-specific DNA aptamer, 609 (P)
Deoxysugar biosynthesis, granaticin biosynthetic gene cluster, 647 (P)

Deoxyxylulose phosphate, terpenoid biosynthesis, R221 (R)

Depsipeptides
binding to glycopeptides, 329 (P)
vancomycin action, 293 (P)

Dihydrofolate reductase, catalysis by, R105 (R)

Dihydrotetramethylrosamine (DHTMR), fluorophore-binding DNA aptamers, 610 (P)

Diketide analogues, precursor-directed biosynthesis, 743 (P)

Diketide synthase DKS1-2, 408 (P)

Dimerization
inhibition, *EcoRI*, 339 (P)
 β -sheet peptide inhibitor, 439 (P)
vancomycin, 293 (P)

2,6-Dimethoxy *p*-benzoquinone (DMBQ), oxidases in parasitic plant development, 103 (P)

Dimethoxytrityl-mononucleotide, automatable codon-level mutagenesis, 519 (P)

Dimethylallyl pyrophosphate (DMAPP), terpenoid biosynthesis, R221 (R)

Dimyristoylphosphatidylcholine (DMPC), interfacial catalysis at conjugated lipid vesicles, 619 (P)

Dipeptide permease, VanX homologs, 489 (P)

Dirt, R15 (I)

DMP 850, cyclic urea HIV protease inhibitor, 597 (P)

DMP 851, cyclic urea HIV protease inhibitor, 597 (P)

DNA
analog, pairing to complementary DNA, 209 (P)
bending, R29 (R)
binding, β -sheet peptide inhibitor, 439 (P)
biosynthesis of glycopeptide antibiotics, 155 (P)
cationic lipids for cellular delivery, 345 (P)
damage, 263 (P)
electron transfer, 413 (P)
inhibition of protein binding by polyamides, 119 (P)
peptide nucleic acid binding, 81 (P)
peroxidase activity, 505 (P)
polymerase β fidelity, R7 (M)
scission of, 283 (P)
substrate basicity enhancement, 1 (P)
triplex-directed sliding clamp assembly, 59 (P)

DNA aptamer, fluorophore-specific, 609 (P)

DNA aptamer–hemin complex, 505 (P)

DNA aptamer–L-argininamide complex, 555 (P)

DNA–protein interactions, small molecules, R135 (R)

DNAzyme
DNA-enhanced peroxidase activity, 505 (P)
substrate basicity enhancement, 1 (P)

Drug design, zinc, R125 (X)

Duplex DNA cleavage, DNA scission, 283 (P)

Duplex DNA invasion, peptide nucleic acid binding, 81 (P)

Dye-binding peptides, 713 (P)

E47 dimerization, β -sheet peptide inhibitor, 439 (P)

EcoRI, inhibition of, 339 (P)

EDTA titrations, metal-ion contamination, 588 (P)

Electron paramagnetic resonance, 355 (P)

Electron transfer
DNA, 413 (P)
flavin, 355 (P)

Enantioselective epoxide hydrolysis, R73 (M)

Endocytosis, scavenger receptors, R194 (R)

Endonuclease *EcoRI*, inhibition of, 339 (P)

Engineering
cytokines, R257 (R)
ethos, R177
proteins, R157 (X), R161 (M)
Src kinase nucleotide specificity, 91 (P)

Enterococcus casseliflavus, bacterial vancomycin-resistance phenotype, 197 (P)

EntreMed, Inc., R87 (I)

Enzymatic biogenesis, iron acquisition in *Yersinia*, 573 (P)

Enzyme analysis, bacterial sulfatases, R181 (X)

Enzyme detection, interfacial catalysis at conjugated lipid vesicles, 619 (P)

Enzyme inhibitors, metallo- β -lactamase inhibitors, 185 (P)

Epidermal growth factor (EGF), cytokine engineering, R258 (R)

Epothilones, 365 (P)

Epoxide hydrolysis, R73 (M)

Equilibrium constant, ester transferase ribozyme, 23 (P)

Erythromycins, precursor-directed biosynthesis, 743 (P)

Erythromycin-producing polyketide synthases, 407 (P)

Escherichia coli
acyl carrier protein of rat FAS, 135 (P)
glutamine synthetase (GS), protein-based nanofabrication, 689 (P)
microbion B17 synthase, 373 (P)
VanX homologs, 489 (P)

Ester transferase ribozyme, 23 (P)

Ethidium, electron transfer in DNA, 413 (P)

Ethylene biosynthesis, 49 (P)

Eukaryotic cells
small molecules, R129 (R)
transient protein interactions, R313

Evolution, homodimeric glycoprotein hormones, 241 (P)

Fatty acid synthases (FASs)
acyl carrier protein (ACP), 135 (P)
malonyl CoA: *holo* acyl carrier protein transacylases (MCATs), 699 (P)
type II polyketide synthase acyl carrier proteins, 35 (P)

Fenton chemistry, metal-ion-binding sites, 163 (P)

Ferric iron, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)

Ferritin iron-responsive elements, oxidation of guanines, 679 (P)

FK506, FKBP12 antagonists, 385 (P)

FKBP12 antagonists, transforming growth factor- β signaling, 385 (P)

FLASH, protein visualization, R317 (M)

Flavin, nitric oxide synthase, 355 (P)

Flavin radical relaxation
 Ca^{2+} /calmodulin binding, 359 (P)
heme spin state, 356 (P)

9-fluorenylmethoxycarbonyl, automatable codon-level mutagenesis, 519 (P)

Fluorescence spectroscopy, DNAzyme substrate basicity enhancement, 1 (P)

Fluorescence microscopy, real-time imaging of gene expression, R285 (M)

Fluorescent proteins, genetically encoded labels, R317 (M)

Fluorophore-binding DNA aptamers, 609 (P)

Fluorophore-binding peptides, 713 (P)

Fmoc, automatable codon-level mutagenesis, 519 (P)

Follitropin, homodimeric glycoprotein hormones, 241 (P)

Forskolin, function, 259 (P)

Fos transcription factor, DNA bending, R29 (R)

Free radicals, C1'-DNA radical, 263 (P)

Fyn, engineered Src kinase nucleotide specificity, 91 (P)

G-protein-coupled receptors, protein shedding at cell surface, R55 (R)

G-quartet, fluorophore-specific DNA aptamer, 609 (P)

GC-1, thyroid hormone receptor, 299 (P)

Gelsolin binding, R81 (M)

Gene disruption, rifamycin biosynthetic gene cluster, 69 (P)

Gene expression
real-time imaging, R285 (M)
small-molecule-based strategies, R129 (R)

Subject index

Gene transfer, cellular delivery of plasmid DNA, 345 (P)
Gene V protein-1–10-phenanthroline, DNA scission, 283 (P)
GlcNAc-6-O-sulfotransferase, lymphoid tissue, 447 (P)
Glutamine synthetase (GS), protein-based nanofabrication, 689 (P)
Glycopeptides
 antibiotics
 biosynthesis, 155 (P)
 dimerization mode, 293 (P)
 depsipeptides binding to, 329 (P)
 glycosylation-induced conformational switching, 427 (P)
Glycoprotein hormones, 241 (P)
Glycosylation, conformational switching, 427 (P)
Granaticin biosynthetic gene cluster, 647 (P)
Green fluorescent protein, genetically encoded labels, R317 (M)
Group I introns, metal-ion-binding sites, 163 (P)
Growth factor receptors, protein shedding at cell surface, R56 (R)
Guanines, oxidation of, 679 (P)
Guanylate cyclase, YC-1, 255 (P)

Hairpin ribozymes, monovalent cations, 587 (P)
Hammerhead ribozymes
 aminoglycoside binding, R227 (X)
 monovalent cations, 587 (P)
Harada–Frankel model, amino-acid-binding pocket formation, 564 (P)
Haustoria development, oxidases in parasitic plant development, 103 (P)
Helicon Therapeutics, Inc., R165 (I)
Hemagglutinin, glycosylation-induced conformational switching, 427 (P)
Heme spin state, flavin radical relaxation, 356 (P)
Hemin–aptamer complex, DNA-enhanced peroxidase activity, 505 (P)
Hepatitis delta ribozyme, monovalent salts, 589 (P)
Heterocyclization
 biosynthesis, microbin B17 synthase, 373 (P)
 iron acquisition in *Yersinia*, 573 (P)
 Mycobacterium tuberculosis gene cluster identification, 631 (P)
Histidine tag proteins, protein-based nanofabrication, 689 (P)
Histidine–iron bond, cleavage of, 255 (P)
HMWP1, iron acquisition in *Yersinia*, 573 (P)
HMWP2, iron acquisition in *Yersinia*, 573 (P)
Holo acyl carrier protein, malonyl CoA:holo acyl carrier protein transacylases (MCATs), 699 (P)
Homodimeric glycoprotein hormones, 241 (P)
Homodimeric nitric oxide synthase, 355 (P)
Homopyrimidine peptide nucleic acids, cooperative binding by, 81 (P)
Hormones, homodimeric glycoprotein, 241 (P)
Host defence, scavenger receptors, R195 (R)
Host recognition, oxidases in parasitic plant development, 103 (P)
Human CD36, scavenger receptors, R200 (R)
Human chorionic gonadotropin (hCG), homodimeric glycoprotein hormones, 241 (P)
Human immunodeficiency virus (HIV) protease inhibitors, cyclic urea, 597 (P)
Human profilin I, photoaffinity labeling of, 273 (P)
Hydrogen bonds, inhibition of protein binding by polyamides, 119 (P)
Hydrolysis
 epoxide, R73 (M)
 proteasome active site labeling, 307 (P)
Hydrolytic kinetic resolution (HKR), epoxide hydrolysis, R74 (M)
Hydroxamic acid, protein shedding, R52 (R)
N-hydroxyaminoacid, ethylene biosynthesis, 49 (P)
Hydroxyaryloxazoline, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)

Hydroxylation
 ethylene biosynthesis, 49 (P)
 pikC-encoded cytochrome P450 hydroxylase, 661 (P)
3-(5'-hydroxymethyl-2'-furyl)-1-benzylindazole (YC-1), activating guanylate cyclase, 255 (P)

Imaging, gene expression, R285 (M)
Imaging Research, Inc., R205 (I)
Imidazole–pyrrole polyamides, inhibition of protein binding by polyamides, 119 (P)
Imipenem, metallo-β-lactamase inhibitors, 185 (P)
Inflammation
 GlcNAc-6-O-sulfotransferase, 447 (P)
 isoprostanes, R323 (R)
 SB 203580, 321 (P)
Infrared thermography, catalyst discovery, R187 (M)
Inhibition
 caspases, R101 (M)
 cyclic urea HIV protease, 597 (P)
 E47 dimerization, 439 (P)
 EcoRI, 339 (P)
 engineering protein kinases, R161 (M)
 metallo-β-lactamase, 185 (P)
 proteasome active site labeling, 307 (P)
 protein binding by polyamides, 119 (P)
Inositol lipids, gelsolin binding, R83 (M)
Intercalation, electron transfer in DNA, 413 (P)
Interfacial catalysis, conjugated lipid vesicles, 619 (P)
Interfacial peptides, *EcoRI*, 339 (P)
Interleukin-2, cytokine engineering, R261 (R)
in vitro selection, ester transferase ribozyme, 23 (P)
Ion-channel proteins, alkali cation selectivity, R291 (R)
Ionic strength, peptide nucleic acid binding, 81 (P)
Iron acquisition, *Yersinia pestis*, 573 (P)
Iron(II)-mediated Fenton reactions, 163 (P)
Iron-chelating siderophores, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)
Iron-responsive element RNA, oxidation of guanines, 679 (P)
Iron–histidine bond, cleavage of, 255 (P)
Iron–oxo intermediate, ethylene biosynthesis, 49 (P)
IRORI, R39 (I)
Isopenicillin N synthase catalysis, 229 (P)
Isopentenyl pyrophosphate (IPP), terpenoid biosynthesis, R221 (R)
Isoprenoid derivatives, terpenoid biosynthesis, R221 (R)
Isoprostanes, R323 (R)
Isothermal amplification, CATCH (cooperative amplification of templates by cross hybridization), 729 (P)

Jasmonic acid, isoprostanes, R323 (R)
Jun transcription factor, DNA bending, R29 (R)

β-ketoacyl synthase (KS), type II polyketide synthase acyl carrier proteins, 35 (P)
Killer lymphocytes, lytic peptide structure, 147 (P)

L-selectin, GlcNAc-6-O-sulfotransferase activity, 447 (P)
Leader, microcin B17 propeptide, 217 (P)
Leishmania tarentola, DNA bending, R29 (R)
Leu223, isopenicillin N synthase, 229 (P)
Leucine zipper (bZIP) transcription factors, DNA bending, R29 (R)
Ligand binding domain (LBD)
 nuclear hormone receptor RXR, 13 (P)
 thyroid hormone receptor, 299 (P)
Ligand complexes, chloroperoxidase catalysis, 462 (P)
Ligand-activated transcription, nuclear hormone receptor RXR, 13 (P)
Ligand-induced proteolysis, protein shedding at cell surface, R55 (R)
Ligand-mediated dimerization, vancomycin, 293 (P)

Ligand/receptor trafficking dynamics, cytokine engineering, R257 (R)

Lipid vesicles, interfacial catalysis by phospholipases, 619 (P)

Lipids, cellular delivery of plasmid DNA, 345 (P)

Lipitoids, cellular delivery of plasmid DNA, 345 (P)

Lipoproteins, scavenger receptors, R194 (R)

Luminescence microscopy, real-time imaging of gene expression, R285 (M)

Lutropin receptors, homodimeric glycoprotein hormones, 241 (P)

Lymphocyte homing, GlcNAc-6-O-sulfotransferase, 447 (P)

Lymphoid tissue, GlcNAc-6-O-sulfotransferase, 447 (P)

Lytic peptide, structure, 147 (P)

M-13 gene V protein (GVP), DNA scission, 283 (P)

Macrolactone YC-17, hydroxylation, 661 (P)

Macrolide antibiotics, 661 (P)

MALDI-TOF, profilin I, 273 (P)

Malonyl CoA: *holo* acyl carrier protein transacylases (MCATs), 699 (P)

Malonyl transferase

- malonyl CoA: *holo* acyl carrier protein transacylases (MCATs), 699 (P)
- type II polyketide synthase acyl carrier proteins, 35 (P)

Matrix metalloproteinases (MMPs), protein shedding, R52 (R)

Mechanism-based cellular assay, SH2-domain-specific protein–protein inhibitors, 529 (P)

Membranes, lytic peptide structure, 147 (P)

Memory, enhanced, R165 (I)

Mesoporphyrin IX (MPIX), DNAzyme substrate basicity enhancement, 1 (P)

Mesoscale science, R177

Metal ions

- binding sites, group I introns, 163 (P)
- monovalent cations, 587 (P)
- peptidyl-transferase ribozymes, 539 (P)

Metal-mediated drug efficacy, zinc, R125 (X)

Metallo-β-lactamase inhibitors, 185 (P)

Metalloenzyme, monovalent cations, 587 (P)

Metalloporphyrins, DNA-enhanced peroxidase activity, 505 (P)

Metalloproteinase inhibitors, protein shedding, R52 (R)

Methicillin resistance, biosynthesis of glycopeptide antibiotics, 155 (P)

N-methylmesoporphyrin (NMM), DNAzyme substrate basicity enhancement, 1 (P)

N-methylmesoporphyrin IX (NMM), DNA-enhanced peroxidase activity, 505 (P)

Methymycin, *pikC*-encoded cytochrome P450 hydroxylase, 661 (P)

Mevalonate pathways, terpenoid biosynthesis, R229 (R)

Microcin B17 propeptide, 217 (P)

Microcin B17 synthase, heterocycle biosynthesis by, 373 (P)

Microtubules, epothilones, 365 (P)

Minimal polyketide synthase, 407 (P)

Minor groove

- base encapsulation, amino-acid-binding pocket formation, 555 (P)
- inhibition of protein binding by polyamides, 119 (P)

Mitochondria, R303 (I)

MitoKor, R303 (I)

Model bacterial cell-wall surfaces, ¹⁹F NMR in measurement of binding affinities, 329 (P)

Modular polyketide synthase, 407 (P)

- rifamycin biosynthetic gene cluster, 69 (P)

Molecular biology, soil microflora, R245 (X)

Molecular dynamics, chloroperoxidase catalysis, 461 (P)

Molecular evolution, CATCH (cooperative amplification of templates by cross hybridization), 729 (P)

Molecular recognition

- dimerization mode for vancomycin, 293 (P)
- inhibition of protein binding by polyamides, 119 (P)

Molecular self-assembly, protein-based nanofabrication, 689 (P)

Monomethoxy polyethylene glycol, 177 (P)

Monovalent cations, ribozymes, 587 (P)

Multi-sulfatase deficiency, R181 (X)

Mutagenesis

- automatable codon-level, 519 (P)
- microcin B17 propeptide, 217 (P)

Mycobacterium tuberculosis, gene cluster, 631 (P)

Mycobactin, gene cluster identification, 631 (P)

Nanofabrication, Ni²⁺-NTA in biologically imposed symmetry, 689 (P)

Narbomycin, *pikC*-encoded cytochrome P450 hydroxylase, 661 (P)

Natural products

- drugs, R63 (I)
- as gene expression regulators, R129 (R)

NemaPharm, Inc., R147 (I)

Nematodes, R147 (I)

Neomethymycin, *pikC*-encoded cytochrome P450 hydroxylase, 661 (P)

Neurex Corporation, R235 (I)

Ni²⁺-NTA, protein-based nanofabrication, 689 (P)

Nitric oxide, and iron–histidine bond cleavage, 255 (P)

Nitric oxide synthase, flavin, 355 (P)

Nonribosomal peptide synthetase, iron acquisition in *Yersinia*, 573 (P)

Nonviral gene therapy, cellular delivery of plasmid DNA, 345 (P)

Novel cationic lipids, cellular delivery of plasmid DNA, 345 (P)

Nuclear hormone receptor RXR, 13 (P)

Nuclear magnetic resonance (NMR)

- glycopeptide binding, 329 (P)
- interfacial catalysis at conjugated lipid vesicles, 619 (P)
- lytic peptide structure, 147 (P)
- microcin B17 propeptide, 217 (P)
- oxidation of guanines, 679 (P)

Nucleic acids

- fluorophore-binding DNA aptamers, 609 (P)
- homopyrimidine peptide, 85 (P)

Nucleosides, DNA analog/complementary DNA pairing, 209 (P)

Nucleotide specificity, engineered Src kinase, 91 (P)

Oligonucleotides

- alternate-strand triple-helix formation, 755 (P)
- automatable codon-level mutagenesis, 519 (P)
- C1'-DNA radical, 263 (P)
- DNA analog/complementary DNA pairing, 209 (P)

Oligopurine strands, alternate-strand triple-helix formation, 755 (P)

Optics, R205 (I)

Oxazole heterocycles

- microcin B17 propeptide, 217 (P)
- microcin B17 synthase, 373 (P)

Oxidases, parasitic plant development, 103 (P)

Oxidation, guanines, 679 (P)

Oxoruthenium, oxidation of guanines, 679 (P)

Oxygen species, oxidases in parasitic plant development, 103 (P)

P450, see cytochrome P450

Parasite evolution, oxidases in parasitic plant development, 103 (P)

Parasitic plant development, oxidases, 103 (P)

Paromomycin, aminoglycoside specificity, 399 (P)

Pathway-specific activator gene, granaticin biosynthetic gene cluster, 647 (P)

Penicillin, isopenicillin N synthase, 229 (P)

Peptide, lytic, 147 (P)

Peptide antibiotic microcin B17, 217 (P)

Peptide binding to fluorophore dyes, 713 (P)

Subject index

Peptide conformation, glycosylation-induced conformational switching, 427 (P)

Peptide nucleic acids (PNA)
cooperative binding by, 81 (P)
triplex-directed sliding clamp assembly, 59 (P)

Peptide synthetase, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)

Peptide-to-heterocycle conversions, microbin B17 synthase, 373 (P)

Peptidoglycan recycling, VanX homologs, 489 (P)

Peptidyl-transferase ribozymes, 539 (P)

Peptoids, cellular delivery of plasmid DNA, 345 (P)

Perforin amino terminus, structure, 147 (P)

Peroxidases
activity, catalytic DNA, 505 (P)
chloroperoxidase catalysis, 461 (P)
oxidases in parasitic plant development, 103 (P)

Phage display, prostate-specific antigen, 475 (P)

1,10-phenanthroline-copper, DNA scission, 283 (P)

Phenol, oxidases in parasitic plant development, 103 (P)

Phenylmethylsulphonyl fluoride (PMSF), type II polyketide synthase acyl carrier proteins, 39 (P)

Phosphate–sugar backbone, DNA analog/complementary DNA pairing, 209 (P)

Phosphatidylinositol, profilin I, 273 (P)

Phosphoinositides, gelsolin binding, R81 (M)

Phospholipases
conjugated lipid vesicles, 619 (P)
interfacial catalysis at conjugated lipid vesicles, 619 (P)

Phosphoramidites, automatable codon-level mutagenesis, 519 (P)

Phosphorylation, engineered Src kinase nucleotide specificity, 91 (P)

Photoaffinity labeling, profilin I, 273 (P)

Photooxidation, electron transfer in DNA, 415 (P)

Pikromycin, *pikC*-encoded cytochrome P450 hydroxylase, 661 (P)

Plague, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)

Plant development, oxidases, 103 (P)

Plasmid DNA, cationic lipids for cellular delivery, 345 (P)

Poly(L-proline) binding, profilin I, 273 (P)

Poly-L-lysine (PLL), biological surfaces, 177 (P)

Polyamides, inhibition of protein binding, 119 (P)

Polyanionic ligands, scavenger receptors, R193 (R)

Polydiacetylene (PDA), interfacial catalysis at conjugated lipid vesicles, 619 (P)

Polyethylene glycol (PEG), biological surfaces, 177 (P)

Polyketide synthases (PKSs)
acyl carrier proteins, 35 (P)
granaticin biosynthetic gene cluster, 647 (P)
iron acquisition in *Yersinia*, 573 (P)
minimal, 407 (P)
pikC-encoded cytochrome P450 hydroxylase, 661 (P)
precursor-directed biosynthesis, 743 (P)
rat fatty acid synthases, 135 (P)
rifamycin biosynthetic gene cluster, 69 (P)

Polyketide synthesis, malonyl CoA: *holo* acyl carrier protein transacylases (MCATs), 699 (P)

Polyketide/nonribosomal peptides, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)

Polymerase β fidelity, DNA, R7 (M)

Polyphosphoinositol lipids, profilin I, 273 (P)

Porphyrin
DNAzyme substrate basicity enhancement, 1 (P)
metallation reactions, DNA-enhanced peroxidase activity, 505 (P)

Potassium-channel proteins, alkali cation selectivity, R291 (R)

Profilin I, photoaffinity labeling, 273 (P)

Propeptide, microcin B17, 217 (P)

Prostaglandins, isoprostanes, R323 (R)

Prostate-specific antigen, substrate specificity of, 475 (P)

Protease specificity, prostate-specific antigen, 475 (P)

Protease-activated receptors (PARS), protein shedding at cell surface, R55 (R)

Proteasome active site, labeling of, 307 (P)

Protein engineering, R157 (X)
binding, inhibition by polyamides, 119 (P)
nuclear hormone receptor RXR, 13 (P)
protein-based nanofabrication, 689 (P)
Src kinase nucleotide specificity, 91 (P)

Protein kinases
engineered Src kinase nucleotide specificity, 91 (P)
engineering, R161 (M)
inhibitors, SB 203580, 321 (P)

Protein kinase C (PKC), protein shedding, R49 (R)

Protein minimization, homodimeric glycoprotein hormones, 241 (P)

Protein shedding, cell surface, R49 (R)

Protein splicing, R251 (M)

Protein visualization, genetically encoded labels, R317 (M)

Protein-based nanofabrication, Ni²⁺-NTA in biologically imposed symmetry, 689 (P)

Protein–DNA interactions, R29 (R)
inhibition of protein binding by polyamides, 119 (P)
small molecules, R135 (R)

Protein–nucleic acid, ester transferase ribozyme, 23 (P)

Protein–protein inhibitors, mammalian cell assay for identification, 529 (P)

Protein–protein interactions, small molecules, R138 (R)

Protein–RNA complex, translational fidelity, R3 (M)

Proteolysis, cell surface and, R49 (R)

Protoporphyrin IX (PPIX), DNAzyme substrate basicity enhancement, 1 (P)

Provir, R63 (I)

PS2.M–hemin complex, DNA-enhanced peroxidase activity, 507 (P)

PS5.M, DNAzyme substrate basicity enhancement, 1 (P)

Pseudorotaxane, triplex-directed sliding clamp assembly, 59 (P)

Pyrophosphatase, small-bisubstrate ribozymes, 669 (P)

Pyrrole–imidazole polyamides, inhibition of protein binding by polyamides, 119 (P)

Racemic epoxide, hydrolysis, R73 (M)

Radiofrequency (rf) tags, R39 (I)

Rainforest drugs, R63 (I)

Rapamycin, FKBP12 antagonists, 385 (P)

Rat fatty acid synthase, acyl carrier protein domain of, 135 (P)

Real-time imaging, gene expression, R285 (M)

Receptor shedding mechanisms, protein shedding at cell surface, R59 (R)

Receptor/ligand trafficking dynamics, cytokine engineering, R257 (R)

Red blood cells, biological surfaces, 177 (P)

Redox activity, fluorophore-specific DNA aptamer, 609 (P)

Repressors, small molecules, R134 (R)

Retinoid X receptor (RXR), ligand-activated transcription, 13 (P)

Reversed specificity, bacterial vancomycin-resistance phenotype, 197 (P)

Ribosomes
translational fidelity, R3 (M)
RNA, aminoglycoside specificity, 397 (P)

Ribozymes
aminoglycoside binding, R227 (X)
divalent cations, 587 (P)
DNA-enhanced peroxidase activity, 505 (P)
DNAzyme substrate basicity enhancement, 1 (P)
ester transferase, 23 (P)
metal-ion-binding sites, 163 (P)
peptidyl-transferase, 539 (P)
small-bisubstrates, 669 (P)

Rifamycin biosynthetic gene cluster, 69 (P)

RNA catalysis
ester transferase ribozyme, 23 (P)
peptidyl-transferase ribozymes, 539 (P)

RNA enzymes
monovalent cations, 587 (P)
small-molecule substrates, 669 (P)

RNA group I introns, metal-ion-binding sites, 163 (P)

RNA recognition
aminoglycoside binding, R227 (X)
aminoglycoside specificity, 397 (P)

RNA-arginine interactions, R215 (X)

RNA-protein complex, translational fidelity, R3 (M)

Rous sarcoma virus (RSV), engineered Src kinase nucleotide specificity, 91 (P)

RpoS-dependent genes, VanX homologs, 489 (P)

Saccharopolyspora erythraea, polyketide synthase, 407 (P)

Salicylic acid, iron acquisition in *Yersinia*, 577 (P)

SB 203580
engineering protein kinases, R163 (M)
mechanism of action, 321 (P)

Scavenger receptors, polyanionic ligands, R193 (R)

Scission, DNA, 283 (P)

Selective alkylation, thyroid hormone receptor, 299 (P)

Self-acylation, type II polyketide synthase acyl carrier proteins, 35 (P)

Self-cleaving RNA, monovalent cations, 587 (P)

Sequence-dictation, DNA scission, 283 (P)

Serine-specific inhibitor phenylmethylsulphonyl fluoride (PMSF), type II polyketide synthase acyl carrier proteins, 39 (P)

Serine-specific sulfatase-modifying enzymes, R182 (X)

Shaman Pharmaceuticals, Inc., R63 (I)

Sheared G.A triple alignments, amino-acid-binding pocket formation, 555 (P)

Shikimate pathway, rifamycin biosynthetic gene cluster, 69 (P)

Siderophore, iron acquisition in *Yersinia*, 573 (P)

Signal transduction research, engineering protein kinases, R161 (M)

Sliding clamp assembly, triplex-directed, 59 (P)

Smad, FKBP12 antagonists, 385 (P)

Small molecules
chiral catalysts, catalyst discovery, R187 (M)
gene expression, R129 (R)
substrates, RNA enzymes, 669 (P)
fluorophores bound to peptides, 713 (P)

Snails, R235 (I)

Sodium dodecyl sulfate, lytic peptide structure, 147 (P)

Soil bacteria, R15 (I)

Soil organisms, genetic content, R245 (X)

Specificity, nuclear hormone receptor RXR, 13 (P)

Src kinase nucleotide specificity, 91 (P)

Src-homology 2 (SH2) domain, mammalian cell assay for identification, 529 (P)

Staphylococcus aureus, biosynthesis of glycopeptide antibiotics, 155 (P)

Stereochemistry, chloroperoxidase catalysis, 461 (P)

Steric stabilization, biological surfaces, 177 (P)

Stopped-flow, guanylate cyclase, 255 (P)

Strand breaks, C1'-DNA radical, 263 (P)

Strand-switch targeting, peptide nucleic acid binding, 85 (P)

Streptomyces, polyketide synthase, 407 (P)

Streptomyces coelicolor
acyl carrier protein of rat FAS, 135 (P)
polyketide synthesis, 699 (P)

Streptomyces lividans, potassium-channel proteins, R291 (R)

Streptomyces toyocaensis, VanX homologs, 489 (P)

Streptomyces venezuelae, *pikC*-encoded cytochrome P450 hydroxylase, 661 (P)

Streptomyces violaceoruber Tü22, granaticin biosynthetic gene cluster, 647 (P)

Stress-activated protein (SAP) kinases, SB 203580, 321 (P)

Stretching exercises, dihydrofolate reductase, R105 (R)

Striga asiatica, oxidases in parasitic plant development, 103 (P)

Subsite occupancy, prostate-specific antigen, 475 (P)

Substrate basicity, DNAzyme, 1 (P)

Substrate phage display, prostate-specific antigen, 475 (P)

Substrate specificity
prostate-specific antigen, 475 (P)
proteasome active site labeling, 307 (P)

Subtype selectivity, thyroid hormone receptor, 299 (P)

Sugar-phosphate backbone, DNA analog/complementary DNA pairing, 209 (P)

Sulfatases, modification of, R181 (X)

Sulfated carbohydrates, GlcNAc-6-O-sulfotransferase, 447 (P)

Sulforhodamine B, fluorophore-specific DNA aptamer, 609 (P)

Sulfotransferase, 447 (P)

Surface plasmon resonance, aminoglycoside specificity, 397 (P)

Surface-enhanced binding, ¹⁹F NMR in measurement of binding affinities, 329 (P)

Switching, glycosylation-induced, 427 (P)

Synechocystis, VanX homologs, 489 (P)

Synergistic activation, guanylate cyclase, 255 (P)

T cells, lytic peptide structure, 147 (P)

Taxol, epothilones, 365 (P)

Terpenoid biosynthesis, R221 (R)

TerraGen Diversity Inc., R15 (I)

Tetrahydrofolate, dihydrofolate reductase, R105 (R)

Texas red, binding of peptides, 713 (P)

Thiazole
heterocycles, microcin B17 propeptide, 217 (P)
microcin B17 synthase, 373 (P)

Thyroid hormone receptor, agonist ligand, 299 (P)

Thyromimetic compounds, thyroid hormone receptor, 299 (P)

Thyrotropin, homodimeric glycoprotein hormones, 241 (P)

Thyrotropin receptor (TSHR), protein shedding at cell surface, R55 (R)

trans reactions, peptidyl-transferase ribozymes, 539 (P)

Transcription, nuclear hormone receptor RXR, 13 (P)

Transcription cycle, small molecules, R132 (R)

Transcription factors, inhibition of protein binding by polyamides, 119 (P)

Transcriptional regulation, small molecules, R129 (R)

Transforming growth factor- β (TGF β)
FKBP12 antagonists, 385 (P)
SB 203580 action, 321 (P)

Transient protein interactions, R313

Translational fidelity, R3 (M)

Trinucleotides, automatable codon-level mutagenesis, 519 (P)

Triple-helix formation, alternate-strand, 755 (P)

Triplex-directed sliding clamp assembly, 59 (P)

Triton X-100, DNA-enhanced peroxidase activity, 507 (P)

Tuberculosis, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)

Tubulin polymerization, epothilones, 365 (P)

Tumor necrosis factor- α converting enzyme (TACE), protein shedding, R53 (R)

Ultraviolet-visible spectroscopy, DNAzyme substrate basicity enhancement, 1 (P)

VanA-resistant bacteria, 329 (P)

VanB-resistant bacteria, 329 (P)

Vancomycin, dimerization mode for, 293 (P)

Vancomycin resistance
bacterial phenotype, 197 (P)
biosynthesis of glycopeptide antibiotics, 155 (P)

Subject index

- dipeptidase (VanX) homologs, 489 (P)
- enterococci, 197 (P) , 489 (P)
- ^{19}F NMR in measurement of binding affinities, 329 (P)
- VanX homologs, 489 (P)
- Vertex Pharmaceuticals, Inc., R267 (I)
- Vesicles, interfacial catalysis by phospholipases, 619 (P)
- Vibriobactin siderophores, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)
- Vinyl sulfones, proteasome active site labeling, 307 (P)
- Virulence factors, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)
- VS ribozymes, monovalent cations, 587 (P)
- Water-soluble copolymers, biological surfaces, 177 (P)
- Watson–Crick alignments, amino-acid-binding pocket formation, 556 (P)
- Worms, R147 (I)
- Xenognosis, oxidases in parasitic plant development, 103 (P)
- YC-1, activating guanylate cyclase, 255 (P)
- YC-17, hydroxylation, 661 (P)
- Yersinia pestis*, iron acquisition, 573 (P)
- Yersiniabactin
 - iron acquisition in *Yersinia*, 573 (P)
 - siderophores, *Mycobacterium tuberculosis* gene cluster identification, 631 (P)
- ZAP-70 SH2-domain-dependent two-hybrid assay, mammalian cell assay for identification, 531 (P)
- Zinc biochemistry, R125 (X)
- Zippering-up, amino-acid-binding pocket formation, 555 (P)