

# 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
- Bachelor, 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  
Moczydlowski, 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  
 Pirrung, 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  
 Schlölk, 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)  
 $\delta$ -(L- $\alpha$ -aminoadipoyl)-L-cysteinyl-D- $\alpha$ -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- $\beta$  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)  
  microbin B17 synthase, 373 (P)  
   $^{19}\text{F}$  NMR in measurement of binding affinities, 329 (P)  
  *pikC*-encoded cytochrome P450 hydroxylase, 661 (P)  
  resistance, metallo- $\beta$ -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)  
Apoptotic 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,  $^{19}\text{F}$  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- $\beta$ -lactamase inhibitors, 185 (P)  
Base stacking, electron transfer in DNA, 413 (P)  
Basic-helix-loop-helix (bHLH),  $\beta$ -sheet peptide inhibitor, 439 (P)  
Benzoisochromanequinones, granaticin biosynthetic gene cluster, 647 (P)  
4-benzoyldihydrocinnamoyl, profilin I, 273 (P)  
 $\beta$ -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: *holo* acyl carrier protein transacylases (MCATs), 699 (P)
- precursor-directed, 743 (P)
- terpenoid, R221 (R)
- Biotechnology
- Caliper Technologies Corporation, R115 (I)
- ChromaXome Corporation, R15 (I)
- Cognetix 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- $\beta$ -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)
- Ca<sup>2+</sup>
- 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- $\beta$ -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,
- <sup>19</sup>F 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)
- <sup>19</sup>F 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)
- Cognetix 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  $\beta$  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)  
    $\beta$ -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,  $\beta$ -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  $\beta$  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,  $\beta$ -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- $\beta$ -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)  
   microbin 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- $\beta$  signaling, 385 (P)
- FLASH, protein visualization, R317 (M)
- Flavin, nitric oxide synthase, 355 (P)
- Flavin radical relaxation  
   Ca<sup>2+</sup>/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)
- Hastoria 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- $\beta$ -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- $\beta$ -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)
- $\beta$ -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- $\beta$ -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,  $^{19}\text{F}$  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,  $\text{Ni}^{2+}$ -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)
- $\text{Ni}^{2+}$ -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  $\beta$  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, Ni<sup>2+</sup>-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 phenylmethylsulfonyl 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, <sup>19</sup>F 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)
  - microbin 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- $\beta$  (TGF $\beta$ )
- 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- $\alpha$  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)  
<sup>19</sup>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)