

## Key word index Volume 12, 1998

- $\alpha/\beta$ -HSQC, 435
- $\alpha/\beta$ -HSQC- $\alpha/\beta$ , 435
- antibiotic resistance, 201
- assignment, 39, 373, 423, 461, 559
  - homology programs, 395
- automatic, 395
  
- backbone assignments, 453
- bacteriocin AS-48, 173
- $\beta$ -lactoglobulin, 89
- $\beta$ -sheet, 535
- bicelle, 443, 447
- bicelles, 325
- binding, 51
- biosynthetic peptide, 109
  
- $^{13}\text{C}^{\alpha}\text{-}^1\text{H}^{\alpha}$  dipolar couplings, 325
- $^{13}\text{C}$  block labelled RNA, 223
- $^{13}\text{C}$ -edited NMR, 209
- $^{13}\text{C}$ -labeled carbohydrate, 209
- carbohydrate, 385
- $\text{Ca}^{2+}$ -binding protein, 465
- CD, 183
- chain, 385
- charged lipids, 447
- chemical shift, 51
  - index, 197
- chemical synthesis, 223
- CHIFIT, 277
- chromomycin, 243
- cobalt, 243
- cold shock domain, 463
- colicin, 145, 567
- complex, 51
- compressibility, 535
- computer simulation, 501
- conformational dynamics, 145
- core binding factor, 459
- coupling constants, 223
- cross-correlation, 509
- cross-relaxation, 333
- cryptogin, 523
- CT-HMQC-HA, 319
- CT-HMQC-HN, 319
- cyclic protein, 173
- cytochrome P 450, 407
  
- 3D NMR, 197
- deuteration, 189, 333
- differential relaxation, 319
- distance restraints, 543
- DLVO theory, 447
- DNA, 51, 243
- DnaB, 435
- DNA-binding, 357
- Donovan transition, 193
- dsRNA binding domain, 349
- dynamics, 73
  
- E. coli*, 189
  - arginine repressor, 319, 435
  - flavodoxin, 319
- editing, 339
- EH domain, 465
- eIEF4E, 73
- electrostatics, 523
- elicitin, 523
- E9 DNase, 145
- enteropathogenic, 189
- Eps15, 465
- EPSP synthase, 417
- exchange broadening, 549
- EXSY, 145
  
- fast freezing, 417
- fatty acid-binding protein, 197
- Fc, 385
- ferredoxin, 407
- fully  $^{13}\text{C}/^{15}\text{N}$ -labelled biomolecules, 39
  
- grid search, 543
- glutaredoxin, 353
- glycoprotein, 385
- G proteins, 467
- guanine nucleotide exchange, 467
- gurmarin, 535
- Gymnema sylvestre*, 535
  
- $^1\text{H}$  and  $^{15}\text{N}$  assignments, 569
- $^1\text{H}$  relaxation, 259
- $^1\text{H}$ -resonance assignments, 571
- HACACO- $\alpha/\beta$ , 435

- hanging drop, 493
- HCCH-COSY-TOCSY, 559
- HDV, 183
- heavy metal ion sensing, 453
- heteronuclear, 201
  - correlation, 39
- high pressure NMR, 535
- histocompatibility antigens class II, 299
- HMQC-trNOESY, 123
- HNCO, 325
- homeodomain, 357
- homonuclear decoupling, 39
- HSQC- $\alpha/\beta$ , 435
- hydrogen bond, 161, 535
- hydrophobic membrane core, 549
- hydroxyl protons, 209
- hyperfine shift, 243
  
- IgG, 385
- internal dynamics, 135
- intimin, 189
- isl-1, 357
- isotope
  - effect, 161, 339
  - exchange, 333
  - labeled proteins, 345
  - labeling, 25, 299
  - shifts, 259
- isotopic enrichment, 197
  - $\{^{15}\text{N}, ^2\text{H}\}$ , 259
- ISP, 339
  
- J-coupling constants, 501
  
- Kdo, 123
  
- labeled RNA, 373
- lactam, 201
- lipid binding and transfer, 571
- liquid crystal, 443
  - NMR, 447
- local conformation analysis, 543
  
- magnetic orientation, 447
- mannose binding protein, 209
- mastoparan-X, 109
- maximum likelihood, 277
- membrane penetration, 549
- methyl-containing residues, 89
- micellar-aqueous boundary, 549
- model-free
  - approach, 135
  - formalism, 471
- modified HCCH-TOCSY, 89
- module-2, 569
- molecular dynamics, 501
- monoclonal antibody, 123
- multidimensional NMR, 339
  - analysis, 277
  
- $^{15}\text{N}$  relaxation, 73
- narrowing line widths, 417
- neural cell adhesion molecule, 569
- nitrogen-15 NMR, 307
- NMR
  - assignments, 173, 193, 357, 455, 463, 465
  - relaxation, 471
  - sample preparation, 493
  - structure determination, 543
- ns-LTP, 571
- nucleic acids, 25
  
- OB-fold, 463
- oligomeric proteins, 299
- oligonucleotide, 373
- oligosaccharide conformation, 161
- one-bond coupling constants, 435
- order parameter, 471
- order parameters, 135
- ovomuroid, 193
  
- $^{31}\text{P}$  NMR, 417
- palmitate, 571
- paramagnetic, 243
  - metalloproteins, 553
  - relaxation, 243
- paramagnetism, 407
- partially folded form, 89
- PDZ2, 455
- peptides, 135
- pKa, 523
- PKR, 349
- protein, 357, 559
  - alignment, 443
  - dynamics, 307, 407, 471, 509
  - solubility, 493
  - structure, 231, 299
  - synthesis, 467
  - tyrosine kinase, 461
  - tyrosine phosphatase hPTP1E, 455
- protein:protein complex, 567

- protein-DNA complex, 25
- proteinase inhibitor, 193
- pseudocontact shifts, 553
- pseudoknot, 423
  
- QUIET-trNOESY, 123
  
- REDOR, 231
- relaxation, 135
- residual dipolar coupling, 443
- resolution enhancement, 39
- resonance assignments, 197, 349, 565
- RNA, 423, 559
  - binding, 183
- RN4 structure determination, 223
- rotating-frame relaxation, 307
- rotational correlation time, 177
  
- sarcoplasmic calcium-binding protein, 565
- scalar three-bond coupling constant, 319
- secondary structure, 173, 197, 353, 459
- sensitivity enhancement, 345
- sequence-specific assignments, 353, 459
- sequential resonance assignment, 25
- side chain, 559
- side-chain assignment, 89
- SmtB, 453
- solid state NMR, 39
- solution
  - conformation, 183
  - structures, 553
- solvent accessible surface area, 177
- solid-state NMR, 231, 417
- solvent interactions, 259
- spectral deconvolution, 277
- spider silk, 231
- spin-diffusion, 333, 509
  
- Src homology 3 domain, 461
- stable isotope
  - enrichment, 109
  - labeling, 385
- stereospecific assignment, 543
- structure, 51, 523
  - and dynamics, 177
  - calculations, 259
  - refinement, 501, 553
- susceptibility, 243
  
- tec kinase, 461
- tertiary structure, 535
- TFIIIA, 51
- time-averaging restraints, 501
- torsion angle restraints, 543
- torsion angles, 423
- transcriptional factor, 453
- translation, 73
- transverse relaxation-optimized spectroscopy, 345
- trehalose, 417
- triple resonance, 373
  - NMR, 109, 189
- trNOESY, 123
- trROESY, 123
  
- ubiquitin fusion system, 109
  
- vapor diffusion, 493
  
- Y-box protein, 463
- yeast ubiquitin hydrolase, 109
  
- zinc finger, 51
- zinc protein, 201