

Keyword index Volume 13, 1999

- α -ketobutyrate, 369
- α -ketoisovalerate, 369
- accuracy, 51
- acidic fibroblast growth factor, 11
- adenylate kinase, 93, 195
- adiabatic
 - fast passage, 213
 - pulses, 275
- AIDS, 343
- alignment, 187
- amide, 25
- anisotropic overall motion, 139
- anti-gp 120 antibody, 193
- artifact suppression, 73
- assignments, 197
- automated assignment, 311

- backbone angles, 289
- band-selective pulses, 67
- Bayesian, 133
- bicelle, 187, 387
- build-up curves, 61

- ^{13}C , 83
- ^{13}C -glucose, 149
- calcitonin, 161
- calcium-binding protein, 233
- calcyclin, 233
- calsequestrin, 357
- carbon-13 chemical shifts, 199
- cell cycle, 397
- cell division, 395
- chain recombination, 193
- CHAPS, 303
- chemical exchange, 275
- chemical exchange-relay, 67
- chemical shift, 289
 - anisotropy, 101, 139
- Chlamydomonas*, 309
- coat protein, 337
- coherence transfer selection by gradients, 3
- conformational flexibility, 161
- correlation time, 101
- coupling constants, 91
- CPMG, 275
- cross-correlation, 375
- C-terminal domain, 197

- Desulfovibrio vulgaris* flavodoxin, 263
- detergents, 31
- deuteration, 369
- diffusion, 25, 223
- dihedral angles, 375
- dipolar interactions, 375
- dipolar coupling, 175, 187
- distance geometry, 311
- disulfide bond, 149, 357
- DNA
 - recombinase, 307
 - repair, 393
 - structure, 119
- DNA-binding protein, 275
- DtxR, 197
- DYANA, 161, 343
- dynamics, 83
- dynamic properties and enzyme function, 195
- dynein, 309

- E.COSY, 263
- error restraints, 325
- ether-lipid, 387
- exchange, 25

- filamentous bacteriophage, 337
- FK506, 325
- force fields, 51

- GATA-1, 249
- genetic algorithm, 325
- glycosylation, 149
- gramicidin A, 31

- ^1H , ^{13}C , ^{15}N assignments, 11
- helix chirality, 161
- heteronuclear
 - filtration, 223
 - relaxation, 213
- heparin binding, 11
- hepatitis C protease, 175
- heteronuclear
 - cross-polarization, 61
 - NMR, 89, 193, 197
- HIV-1, 343
- homodimer, 395

homology of chemical shift, 289
hydration, 67
hydrogen bonding, 199

Interleukin 4, 51

leucine-rich repeat protein, 309
LFA-1, 43
ligand hydration, 43
liquid crystal, 187, 387
lysozyme, 67

mbp1, 397
membrane protein, 31, 91
methyl protonation, 369
microtubule, 309
MinE, 395
molecular dynamics, 119, 161
molecular surface, 31
multidimensional NMR, 77

NADP(H), 305
¹⁵N NMR, 213
¹⁵N relaxation, 101
(¹⁵NH₄)₂SO₄, 149
NMR
– assignments, 195, 303, 397
– relaxation, 133, 139
– structure, 343

NOE, 67
NOESY-TROSY, 77
normalization of NOE, 61
nuclear Overhauser effect, 101
nucleotide-binding, 305

off-resonance relaxation, 275
1D, 2D and 3D ¹³C/¹⁵N ω_2 half-filter experiments, 43
one-bond J coupling, 175
order parameters, 181
oriented samples, 337
oxytocin, 73

packing density, 181
particle mesh Ewald, 119
peptide binding, 223
peptide deformylase, 311
pH, 187
 φ angle, 289
 φ_{29} , 303
 φ -torsion angle, 263
Pichia farinosa, 113

PISEMA, 337
precision, 51
proline, 381
proline-rich, 381
protein, 223
– alignment, 387
– disulfide isomerase, 357
– dynamics, 181, 213, 275
– expression, 149
– folding, 357
– NMR, 101
– structure, 199, 233, 289, 311
– unfolding, 113

protein-protein interactions, 249
proteins, 77, 83
proton translocation, 305
 ψ angle, 289
pulsed field gradients, 43
pulsed-gradient spin-echo, 113

radiation damping, 73
refinement, 325
relaxation, 83
residual dipolar coupling, 387
resonance assignments, 89, 93, 193, 337
retinoid X receptor, 275
ribonuclease H, 343
RNA-DNA hybrid, 343

S100 protein, 233
salt-mediated killer toxin, 113
secondary shifts, 91
secondary structure, 11
selective
– excitation, 31
– NOE, 61
– pulses, 381
– water excitation, 73
sensitivity enhancement, 77, 175
sequence homology, 289
sequential assignment, 381
SH3, 223
solid-state NMR spectroscopy, 337
solution structure, 51, 249
solvated refinement, 119
spectral density, 83
spin-lattice relaxation, 101
spin-spin relaxation, 101
ssDNA, 303
stability, 187

- structure
 - refinement, 199, 311
 - validation, 51
- sub-unit rotation, 307
- surface accessibility, 181

- $T_{1\rho}$ -dispersion, 213
- TALOS, 289
- thioredoxin, 357
- 3D NMR, 307, 393
- three-bond coupling constants, 263
- three-dimensional NMR, 31
- three-dimensional structure, 11
- TOCSY-TROSY, 77
- topological specificity, 395
- torsion-angle dynamics, 161, 343
- transhydrogenase, 305
- translational self-diffusion, 113

- transposition, 307
- triple resonance NMR, 3, 11, 93
- triple-resonance, 337, 381
- TROSY, 3, 77, 139

- UBC9, 89
- ubiquitin, 187
- ubiquitination, 89

- viomycin, 25

- water, 67
 - flip-back, 77
- water-solute NOEs, 73

- X-ray induced DNA damage, 393

- zinc finger, 249, 275