

Key word index Volume 11, 1998

- aggregation, 461
antisense RNA, 463
automated assignment, 31
automated resonance assignment, 387
- backbone angle γ , 103
 β -sheet, 407
bidirectional coherence transfer, 185
Binase, 185
BPTI, 415
- calcium-myristoyl switch, 135
carbon-carbon J coupling, 199
cell-free protein synthesis, 295
chemical shift, 45, 459
chemical shift anisotropy, 213
chemical shift indices, 363
CLEANEX-PM, 221
combinatorial minimization, 31
comparison to X-ray structure, 153
complete assignments, 119
confirmation filter, 241
constant time evolution, 451
coupling constant, 329
cross-correlation, 213
cryoprotective mixtures, 415
CspA, 461
- detergents, 381
deuteration, 279
deuterium labelling, 307
distance geometry, 241
DNA, 103
DnaB helicase, 233
DNA-binding domain, 457, 459
DNA-binding protein, 265
DNA gyrase B, 279
dynamic NMR, 355
- E. coli* arginine repressor, 445
E. COSY, 199
E2, ^1H , ^{15}N , and ^{13}C NMR resonance assignments, 457
excitation sculpting, 437
- FHMQC, 279
FHSQC, 279
fibril formation, 461
 ^{15}N relaxation, 279
 ^{15}N relaxation measurements, 407
FimC, 229
flexibility, 415
- gradient coherence selection, 185
Grb2, 153
- heme, 119
heme protein, 119
hemoproteins, 423
heteronuclear, 329
heteronuclear NMR, 97, 289, 451, 459
heteronuclear NMR relaxation, 265
heteronuclear NOE, 289
heteronuclear triple-resonance NMR, 363
HMQC, 279
HMQC- α/β , 445
HMQC-J, 329
HNHCACO, 185
homonuclear, 319
HPr, 205
HSQC, 279
HSQC- α/β , 445
hydration, 437
hydrogen bonds, 1
hydrogen exchange, 221
- isotope-editing efficiency, 17
isotope effects, 423
isotope labeling, 97
- Karplus equation, 199
kinetics, 355
- lactose, 289
leukemia, 337
line shape simulation, 355
linewidth, 329
lipase, 363
lipolytic enzyme, 363
Lyme disease, 407
- magnetization exchange network editing, 85
maquette, 227
membrane proteins, 381
micelles, 381
mixed micelles, 381
model compounds, 423
model-free approach, 265

- Mrf-2, 459
- multidimensional heteronuclear magnetic resonance, 135
- multiple-solvents suppression, 437
- multiple-quantum, 319
- multi-quantum, 191
- NMR assignments, 227, 229, 233, 319, 387, 463
- NMR structural refinement, 17
- NOE, 221
- NOESY, 85
- NOESY-HSQC, 17
- oligosaccharide, 289
- oncogenic protein, 337
- one-bond coupling constants, 445
- ^1H , 457
- organic solvents, 437
- outer surface proteins, 407
- papillomavirus, 457
- parallel computing, 241
- partially deuterated proteins, 191
- periplasmic chaperone, 229
- ϕ angle, 199
- polypeptide, 329
- protein, 221, 231
- protein design, 227
- protein-DNA interaction, 465
- protein-DNA interactions, 307
- protein dynamics, 165, 265
- protein expression, 97
- protein folding, 355, 461
- protein hydration, 1
- protein NMR, 153
- protein-protein interactions, 307
- proteins, 31, 451
- protein structural homology, 45
- protein structure, 337
- proton side-chain assignment, 191
- ψ , 213
- pulsed field gradients, 221, 437
- recoverin, 135
- reduced-dimensionality triple-resonance experiments, 387
- resolution enhancement in NMR, 387
- resonance assignment, 363
- resonance assignments, 45, 407
- ribonuclease T₁, 1, 165
- RNA, 85, 319
- RNA-protein complex, 463
- RNA-protein interactions, 59
- RNP domain, 59
- ROP, 463
- rotational diffusion, 265
- secondary chemical shift, 45
- secondary structure, 119
- selective labeling, 295
- sequence homology, 45
- sequential assignments, 451
- SH2 domain, 153
- side-chain amide proton, 205
- side chain motion, 165
- simultaneous ^{15}N and $^{13}\text{C}^\alpha$ acquisition, 185
- site-directed labeling, 295
- solution structure, 135, 153
- solvent exchange rates, 205
- spectral simulation, 17
- spin diffusion structure, 85
- spin system editing, 191
- stable isotope, 295
- stereospecific assignment of 5'-methylene protons, 103
- stereospecific deuterium labeling, 103
- sweet, 231
- systematic search, 241
- temperature coefficients, 205
- thermostability, 231
- thioredoxin, 17
- ^{13}C relaxation times, 165
- ^{13}C shieldings, 423
- three-dimensional, 319
- 3D ^{15}N -HMQC-NOESY- ^{15}N -HMQC, 279
- 3D NMR, 199
- 3D NOESY- ^{15}N -HMQC, 279
- threshold accepting, 31
- translational diffusion, 381
- translocations, 337
- triple resonance, 451
- triple resonance NMR spectroscopy, 407
- type I pili, 229
- ubiquitin, 199
- U1A protein, 59
- viscosity, 415
- water, 221
- water residence time, 1