

Key word index Volume 34, 2006

- ^{13}C & ^{15}N direct detection, 63
 ^{15}N -HSQC, 13
 ^{19}F , 221
- amyloid, 75
apoptosis, 221
automated assignment, 41
automated protein NMR structure determination
with ATNOS and CANDID, 3
- backbone assignment, 41
Bcl-xL, 229
BMRB, 153
- calcineurin, 197
calmodulin, 197
CCC 3D, 245
CD3 ϵ , 203
cell-free protein synthesis, 13
chemical exchange, 129, 209
chemical shift distribution analysis, 261
cis peptides, 153
CNS, 153
combinatorial ^{15}N -labelling, 13
computational docking, 237
conformational change, 209
CPMG NMR relaxation dispersion, 129
cross-saturation, 167
CSA, 245
CYANA, 153
- density functional theory, 229
deuteration, 167
deuterium isotope shift, 229
dispersion, 245
DNA, 229
DNA polymerase III, 13
dynamical averaging, 101
- fast multidimensional NMR, 179
- HET-s, 75
homology modeling, 117
hydrogen bond, 229
- ICMD, 153
immunophilins, 197
- immunosuppression, 197
incomplete factorial design, 137
isotope labeling, 23
- K63, 89
- logistic regression analysis, 261
- magnetic alignment, 117
metalloenzyme, 117
methyl protons, 167
methyl-TROSY, 167
mms2, 89
model free approach, 101
Monte-Carlo simulation, 129
- Nck, 203
network anchoring, 3
nickel enzyme, 117
NMR, 23, 41, 153, 203, 209, 221, 229
NMR relaxation, 237
NMR spectroscopy, 63
NOESY, 31
NRPS, 31
nuclear magnetic resonance (NMR), 101
nuclear magnetic resonance, 31
- paramagnetic NMR, 63
paramagnetic, 117
peptide, 23
phage library, 23
polyubiquitination, 89
PPIases, 197
PR-CALC, 179
prions, 75
PR-NMR, 179
processing software, 179
projection-reconstruction NMR, 179
protein complex, 237
protein folding, 129
protein structure, 31
protein–protein complex, 167
pseudo-contact shifts, 63
- R_2 , 209
RECOORD, 153

274

relaxation, 209
residual dipolar couplings (rdcs), 101
resolution, 245
resonance assignment, 13
ribosomal protein, 153
RNA, 229

sample preparation, 137
selective pulse, 245
sequence specific assignment, 63
sequential assignment, 41
SH3 domain, 129, 203
solid-state NMR, 75,245
solubility, 137
solution structure determination, 63
stability, 137

structure, 221
structural proteomics, 3
structure calculation, 153, 237
subunit τ , 13

Thermotoga maritima, 3
time-shared, 31
torsion angle space, 153
triple resonance experiments, 41

ubiquitin binding motif, 89
ubiquitin, 89, 101
UEV, 89

XPLOR-NIH, 153

Zn-ligated cysteine, 261