Index

absorption, 38
activation energy, 246, 247
adiabatic following, 100
antenna complex, 62
antibunching, 100, 110, 111
atomic force microscope, 330
autocorrelation, 45
autocorrelation function (ACF), 196
autofluorescence of cells, 204
bacterial photosynthesis, 62
biorelevant reaction kinetics, 130, 134, 135
blinking, 51
Bloch, 100, 101, 104–106, 108
chemical analysis, 242
cleavage, 334
clusters of receptor, 208
coherent dynamics, 277
collection reporters, 55
confocal, 167, 169
Confocal Fluorescence Coincidence Analysis (CFCA), 212
confocal fluorescence detection, 167
confocal scanning optical microscope, 328
conformational, 277
conformational dynamics, 237
conformational rearrangements, 89
cross-correlation, 56
cryptography, 99
Cy3, 327
cysteine, 330
cytochrome P-450 dependent monooxygenase, 277
dark states, 343
DBATT, 102, 104, 107
DC Stark effect measurements, 89
DNA, 144
DNA base, 154
delocalization, 76
denaturing, 330
Dextran-SNARF-1, 56
diagonal disorder, 68
dibenzanthanthrene (DBATT), 102
diffusion, 50
dipole–dipole interaction, 63, 75
docking, 336
dual-color cross-correlation, 211
dynamic disorder, 228
electrofusion, 136, 139
electroporation, 131, 136, 139, 142, 143
emission spectra, 48
energy landscape, 329
energy transfer, 63, 74
energy transfer efficiency, 328
ensemble averaging, 33
enzyme kinetics, 227
evolutionary biotechnology, 219
exciton model, 76
Förster transfer, 75
FCS, 345
fluctuations, 56
fluorescein, 327
fluorescence, 100, 102–104, 107–109, 112
fluorescence correlation spectroscopy (FCS), 195, 211, 345
fluorescence decay, 163
fluorescence excitation, 38
fluorescence lifetime, 162, 163
fluorescence quenching, 329
fluorescence resonant energy transfer (FRET), 55, 326
fluorescence spectroscopy, 211
fluorescence-excitation spectroscopy, 64
FM spectroscopy, 36
foldability, 328
four-level system, 348
frequency-modulation, 38
Gaussian, 154
Green Fluorescent Protein (GFP), 51, 53, 338
guanosine, 334
Hanbury-Brown and Twiss, 103
HEK293, 198
hexadecane, 102
high-throughput screening, 217
hole-burning, 44, 82
hole-burning spectroscopy, 342
homogeneous linewidths, 40, 83
hyper Raman, 156
immobilization, 330
inhomogeneous distribution, 83
intercomplex heterogeneity, 68
intra-domain quenching, 331
intracomplex heterogeneity, 68
kinetics, 44
labeling efficiency, 330
LH1, 62
LH2, 62
light-harvesting (LH) complexes, 62
light-induced frequency jumps, 94
lipid domains, 130, 140
lookup table, 165
magnetic resonance, 47
metabolic pathways, 278
metal colloids, 146
micropipette, 131, 136–139
microsphere, 50
misfolded state, 333
molecular heterogeneity, 251
molecular individualism, 326
molecular networks, 278
morphology-dependent resonances, 50
n-hexadecane, 102, 104
nanoenvironment, 33
near-field probe, 50
nile red, 51
nonphotochemical hole-burning, 82
ODMR, 47
on-time distributions, 55
optical switching, 82
optical trap, 134, 136, 142
Oregon Green, 332
p-terphenyl, 36, 83
p-terphenyl crystal, 83
p-terphenyl matrix, 93
paraboloid, 102, 103
pentacene, 36, 93
persistent spectral hole-burning, 82
photobleaching, 207, 344
photon antibunching, 46
photon-counting image acquisition system, 169
photosynthetic purple bacteria, 62
Poisson, 154
polarization, 52
polarization anisotropy, 328
poly(acrylamide) gels, 51
protein folding, 329
protein machines, 277
pulsed excitation, 168
quantum electrodynamic, 50
quantum Monte Carlo, 105, 109
quantum optics, 57
rapid adiabatic passage, 100, 101, 107, 112
Raman effect, 144
rate constants, 336
receptor–ligand, 195
refolding, 330
ribosomal protein S15, 326
RNA conformational change, 326
RNA folding, 332
Rps. acidophila, 62
saturation, 41
SFS, 36
Shpol’skii matrices, 43, 102
signal-to-noise ratio (SNR), 35
single molecule, 99, 227
single photons, 51, 99
single-molecule enzymology, 244
single-molecule fluorescence spectroscopy, 327
single-molecule hole-burning, 86
single-molecule imaging, 343
single-molecule spectroscopy (SMS), 32, 343
single-photon source, 57
small volumes, 277
spectral diffusion, 41, 43, 71
spectral hole-burning, 36
spiking, 283
squeezed light, 99
Stark effect, 102
start–stop, 103, 105, 106, 110, 111
statistical fine structure, 36
stochastic model, 278
stoichiometry of ligand binding, 200
substrate cycles, 278
surface-enhanced Raman scattering (SERS), 144
synchronization, 277
terpylene, 57, 83
terpylene in poly(ethylene), 49
tertiary structure, 330
Tetrahymena ribozyme, 333
thermal denaturation, 252–254
30 S ribosomal subunit, 326
three-dimensional orientation, 53
time-correlated single-photon counting (TCSPC), 162, 167
titin, 329
total internal reflection (TIR) microscopy, 51, 334
transmembrane protein, 195
turnover cycles, 277
two-color excitation, 346
two-state model, 328
undocking, 336
unfolding, 330
vibrational spectrum, 49