

Index

Page numbers in italics refer to figures. Page numbers in bold denotes entries in tables.

- absorbing boundary conditions 148, 184, 198, 208, 213, 406
- accommodation 449
- acetylcholine 118, 119, 205
 - binding 120, 192
 - charges 34, 34
- acetylcholine receptor 34, 132, 133, 133, 192, 234, 241, 362, 374
 - channel structural parameters and conductances **371**
 - ligand association rate **204**
- acetylcholinesterase 34, 205–206, 206
 - ligand association rate **204**
- acid-base catalysis 268–270
 - β -galactosidase 270–271, 271
 - general-acid catalysts 269, 270, 271
 - general-base catalysts 269, 269
- acidic phosphate groups in nucleic acids 53, 302
- action potentials 434
 - axon geometry and conduction 455–457, 456
 - channel diversity 457–458
 - current-voltage curves and thresholds 447–450, 448
 - definition 434–439, 435, 437, 438
 - dendritic integration 466–468, 467
 - Hodgkin-Huxley equations 442–446, 444, 447
 - myelin 453, 453–455
 - oscillations 461–466
 - propagation 450–453, 452
 - repetitive activity and the A-current 458–461, 459, 460
 - voltage clamp 439, 439–441, 440
- activation energies 169–170, 264, 274
- activation of ion channels 442
- active transport across membranes 351–352, 386
- activity coefficient for ions 279, 279–283, 353
 - definition 280
 - infinite dilution 281, 281
- A-current 458–461, 459, 460, 468
- additivity 128, 129
- adenine–thymine base pairs, hydrogen bonding 52
- ADP 130
- alanine (ala) 8, 38, 81, 85, 119
- helix continuation parameter **81**
- alcohols 48
- alkaline phosphatase 211
- allosteric enzymes 130–132, 257–258
- allosteric interactions 111
 - allosteric transition 112
 - binding and response 115–116
 - binding site interactions 121, 121–122
- energy balance in one-site model 116–117, 117
- G-protein coupled receptors 117–121, 120
- hemoglobin 126, 126–127
- ligand-gated channels 132–133, 133
- macroscopic and microscopic additivity 128–130
- Monod-Wyman-Changeux (MWC) model 123–126
 - energetics 127, 127–128, 128
 - enzymes 257
- one binding site and one allosteric interaction 112–115, 113
- phosphofructokinase 130–132, 131, 132
- subunit-subunit interactions 134, 134–136
- Szabo-Karplus (SK) model 137–140, 139
- α -helices 49, 73, 85
 - capping 81
 - mathematical analysis 74
 - proteins 49, 49, 50
 - stability 73
- amino acids
 - helix continuation parameters **81**
 - side chains 268
- Anisidoris* snail 459, 461
- arginine 17, 18, 119, 283
- arginine (arg), helix continuation parameter **81**
- Arrhenius equation 169
- Arrhenius plot 170
- asparagine (asn), helix continuation parameter **81**
- aspartate 8, 42, 119, 206, 272
- aspartic acid (asp), helix continuation parameter **81**
- ATP 130
- axial resistivity 401
- axons
 - geometry and conduction 455–457, 456
 - reflections 457
 - speed and size 452
 - supernormal 449
 - varicosities 456, 456, 457
- bacteriorhodopsin 208
- barnacle muscle fibers 462, 464
- barnase 86, 189, 189, 190, 192
- β -sheets in proteins 49, 68–71, 70, 189
- binding energy in enzymes 258–259
- binomial distribution 154, 156, 243, 309, 320
- binomial expansion 124, 138, 155, 471
- Bohr effect 127, 140
- Boltzmann constant 4
- Boltzmann distribution 2, 4, 5, 17, 56, 161, 182, 260, 277, 288, 307, 313, 362, 378
 - activation energies 169
 - reaction coordinate 179
- Boltzmann equation 17, 22, 293, 443, 462
- Boltzmann weight 2, 32, 57, 74, 96
- bond vibrations 3
 - frequency 44
 - kinetic energy 3
 - normal modes 46, 102, 103
- Born energy 28
- Briggs-Haldane mechanism 254
- Brønsted equation 174, 270
- Brønsted slopes 268–270
- Brownian motion 142, 283, 336
- buffers 269, 269
- burst analysis 232, 232
- n*-butane 56–58, 57
- cable equation 403, 403–406, 454
- cable length constant (λ) 405
- cable theory 400
 - analysis of neurons 418, 418–422, 420, 421
 - branches and equivalent cylinder representation 412–413, 413
 - steady-state 413–415, 415
 - time constants 415–418

- cable parameters **406**
- compartmental models 428, 428–431, 450, 467
- current steps in a finite cable 411–412
- current through membranes and cytoplasm 401, 401–403
- steady-state in a finite cable 406–407, 408
- synaptic integration in dendrites
 - analytical models 422–423, 423
 - compartmental models 430–433, 431, 432
 - impulse responses 423–425, 424
 - realistic synaptic inputs 425–428, 427
- calcium chloride, activity coefficient 281, 281
- calcium ion channels **207**, 208, 392, 458, 462
- calmodulin, ligand association rate **204**
- capacitance
 - circuit 329
 - ionic layers 290
- carbamylcholine 118, 119
- carbon-carbon bonds 44
 - force constant 261
- carbonic anhydrase 177, 273–275, 274, 355
- carboxypeptidase 268
- catalytic efficiency of enzymes 253
- cation- π interactions 33, 33–35, 47
- central-limit theorem 65, 156
- channel noise 186, 321, 323, 327–328, 328
- channel structure 367
 - Eisenman selectivity sequences 374–376, 375, 398
 - energy barriers and channel properties 371–374, 372
 - gramicidin A 370, 378–380, 384, 393
 - KcsA channel 71, 394, 394–399, 396
 - Ohmic channels 370, 370–371, 372, 376, 384
 - rate theory for multibarrier channels 380, 380–384, 383
 - single-file channels 371, 390, 390–394, 397
 - single-ion channels 384–390
 - structural parameters and conductances **371**
- characteristic equation of a matrix 223, 242, 475
- characteristic ratio 62, 63
 - charge-dipole interactions 31, 31–32
- choline 291, 441
- chymotrypsin 248, 250, 256, 258, 259, 272
 - hydrolysis rates **250**
 - ligand association rate **204**
- chymotrypsin inhibitor-2 190, 191, 192
- circuit noise 329, 329–331
 - mean-square voltage 329
- classical configuration integral 3, 46, 301
- closed-time distribution 185, 232, 233, 236, 237, 240, 241
- coils, random 72, 73, 106, 107, 163–164
 - frictional coefficients 163
 - molecular behavior 68
 - statistics 60, 60–62
 - stretching 67–68
- collision frequency 198, 200
- compartmental models 428, 428–430
 - synaptic integration in dendrites 430–433, 431, 432, 450, 467
- concerted binding 91–93
- configurational entropy 71, 72, 107
- configurational free energy 94, 106–107, 107, 129
- configurational partition functions 58–60
- conservation of total number of moles 227, 228
 - loss of 237–240, 240
- constant-field equation 353, 360
 - extended form 361
- cooperative units 11, 16, 79, 123, 303
- cooperativity within systems
 - allostoric transitions 123, 130
 - helix-coil transitions 53, 78, 79, 79
 - hydrogen bonds 41, 43
 - molecular associations 91
 - concerted binding 91–93
 - nearest-neighbor interactions 94
 - sequential binding 93–94
 - protein folding 72, 86–87
 - thermal transitions 11–12
 - voltage-induced transitions 19–21, 20
- correlation function 322–328, 331–338
- Coulomb's law 25
 - contribution to potential energy 280
- Coulomb potential 25–27, 31, 276, 277, 279–282, 298, 300, 302, 375
 - Coulombic interactions 32, 34, 177, 206, 398
- counterions *see* ions and counterions
- cratic contribution 100
- creatine kinase 334, 335, 335
- critical assessment of protein structure prediction (CASP) 52
- cysteine (cys), helix continuation parameter **81**
- cytoplasm 401, 401–403
 - resistance 401, 429
 - viscosity 335, 406
- de Broglie wavelength, thermal 99, 179
- Debye length 277–278, 287, 289
- Debye-Hückel limiting law 281, 282
 - dilute solutions 282
 - exact at infinite dilution 283
 - ionic atmospheres 281, 282
- Debye-Hückel screening 297–305
- degeneracy 57, 75, 84, 138
- delta function 144, 423, 479
- denaturants of proteins 11, 13, 48, 187–192
- dendrites 419
 - action potentials 466–468, 467
 - synaptic integration
 - analytical models 422–423, 423
 - compartmental models 430–433, 431, 432
 - impulse responses 423–425, 424
 - realistic synaptic inputs 425–428, 427
- desensitization 133
- detailed balance 116
 - kinetics of multi-state systems 228
 - loss of 237–240, 240
 - rate processes 170–182
- dielectric constant 25, 30, 31, 35, 36, 38, 41, 47, 51, 272, 276, 287, 363, 368, 376, 402, 406
- diffusion 142
 - diffusion equation 66
 - from microscopic theory 159–160
 - diffusion-limited associations 197–200, 198
 - diffusion-limited dissociations 200–201
 - friction 160–162, 336

- diffusion (cont.)
 Gaussian distribution 156–159, 157
 lateral diffusion in membranes 164–165
 macromolecules, diffusion
 constants 163–164, 164
 deviation from Stokes–Einstein relation 163
 macroscopic diffusion and Fick's laws 142–143
 solving the diffusion equation 143–144
 diffusion across an interface 146–148, 147, 148
 diffusion with boundary conditions 148–150, 149
 one-dimensional diffusion from a point 144–146, 145
 three-dimensional diffusion from a point 146
 steady-state 150–151
 long pipe 151
 porous membrane 153–154
 small hole 152, 152–153
 Stoke's law 162, 162–163
 dimensionality, reduction in 107–108, 108, 212–214
 dipicrylamine 369, 369
 dipole–dipole interactions 32, 49, 398
 dipole moment 26, 31, 31, 32, 35, 49, 395, 396
 dipoles
 induced dipoles 32–33
 interactions with charges 31, 31–32
 dispersion force (London force) 35, 39, 43, 52
 lipid bilayers 54
 DNA 52–53, 62
 binding 94, 112, 214
 electrostatic repulsion 298, 298
 flexibility parameters 63
 formation of circular form from linear form 67
 melting 302–305, 305
 random coil behavior 68
 Donnan potentials 341–343, 342, 344, 346
 effective segment length of macromolecules 62–63
 eigenvalues 46, 223, 474–476
 multisubunit kinetics 244
 eigenvectors 223, 224, 474–476
 three-state model 225
 Einstein's equation for diffusion and friction 161, 267, 347
 Eisenman theory of selectivity 374–376, 375, 376, 398
 elastase 248, 250
 electrogenic membrane pumps 354, 355
 electroneutrality 288, 342, 343, 346
 electrophoresis 294–297, 295
 mobility of ions 295
 sheer force 295
 velocity of ions 294
 electrostatic self-energy 27–29
 electrostatic stress 267
 elementary weight 57
 partition function 58
 enthalpy 6, 37, 41
 Coulomb's law 26
 hydration 28, 28
 ions in water 27
 thermal denaturation of proteins 9–12, 10, 72, 87
 entropy 6
 of electrostatic interactions 26
 ions in water 27
 protein denaturation 71–73
 unfolding entropy 72
 rotational entropy 263–264
 translational entropy 260, 260–263, 263
 enzyme catalysis 248
 acid–base catalysis 268–270
 β -galactosidase 270–271, 271
 allosteric enzymes 257–258
 friction in an enzyme–substrate complex 267–268
 hydrolysis rates **250**
 Kramers rate theory 259–260
 Michaelis–Menten kinetics 251–254
 pre-steady-state kinetics 256–257
 proton transfer in carbonic anhydrase 273–275, 274
 proximity and translational entropy 260, 260–263, 263
 rotational entropy 263–264
 serine proteases 272–273
 steady-state approximations 254–256
 transition state complementarity 264–267, 266
 utilization of binding energy 258–259
 equipartition of energy 23, 104, 313–317, 329
 equivalent cylinder representation 412–413, 413
 steady-state 413–415, 415
 time constants 415–418
 Euler's formula 479
 excluded volume effect 43, 63, 64, 70, 72, 281
 theta solvents 65
 exponential relaxations 167–169, 169
 extended constant-field equation 361
 eye, light detection 311–313, 312, 313
 Eyring theory 179–180
 Fick's laws 142–143
 first law 142
 second law 143
 fluctuations 307
 channel noise 327, 328
 circuit noise 329, 329–331
 deviations from the mean 307–308
 energy fluctuations in macromolecules 315–317
 equipartition of energy 313–315
 fluorescence correlation spectroscopy 164, 332, 332
 friction and the fluctuation-dissipation theorem 336, 338
 Poisson distribution 309, 309–311, 310
 protein ionization 317–319
 single-channel current 320–322, 321
 statistics of light detection by the eye 311–313, 312, 313
 two-state systems 319–320
 correlation function 322–324
 Wiener–Khinchine theorem 324–327, 331
 fluorescence correlation spectroscopy 164, 332, 332, 335
 fluorescence recovery after photobleaching (FRAP) 164, 165
 fluorescent proteins 334, 335
 flux 198, 200, 347
 Ussing flux ratio 351–352, 390
 definition 352
 folding of proteins 46, 82–86
 cooperativity 86–87
 good-folding amino acid sequences 84

- hydrophobic interactions 47, 48
 native state 46, 71, 82, 85, 85
 jigsaw puzzle picture 86
 molten-globule 82
 oil droplet picture 86
 time taken 72
 Fourier analysis 477, 477–480, 478
 Fourier integral 324, 423
 Fourier transform 144, 149,
 150, 324, 325, 408,
 410, 423
 additive noise 324, 325
 fluctuations 324, 326
 inverse 327
 Lorentzian 328
 free energy
 change in 5
 electrostatic 15
 pressure-induced transitions 12
 protein ionization 284
 thermal denaturation of
 proteins 6
 configurational free energy 94,
 106–107, 107
 global states of proteins 2, 3, 4
 interactions 21
 linear analysis 192
 linear relations 172–175,
 173, 175
 Marcus relation 177–178, 178
 molar free energy 5
 standard state 95
 rotational free energy 101–102, 263
 translational free energy 98–101,
 260–263
 change in 101
 translation contribution to ΔG°
 99, 100
 vibrational free energy 102–104
 change in 104
 vibrational contribution 102
 freely jointed chains 60, 60
 freely rotating chains 61
 friction 160–162
 electrophoretic mobility 294
 enzyme–substrate complexes
 267–268
 fluctuation–dissipation theorem
 336, 338
 frictional coefficients 163
 Stoke's law 162, 162–163
 fructose-1,6-diphosphate 130
 fructose-6-phosphate 130, 131
 fura-2 196, 197
 GABA 183, 236, 374
 β -galactosidase 270, 271
 gas constant 4
 gating current 18, 18–19
 gating particle 442
gauche conformation of *n*-butane 56,
 57, 57
 Gaussian distribution
 polymers 65
 random walks 156–159, 157
 Gaussian integrals 481–482
 geometric series 471
 Gibbs–Helmholtz equation 10
 global states of proteins 1, 4
 allosteric transitions 112, 113, 117,
 121, 174
 compliance 21–23, 22
 definition 2–4
 equilibrium between two global
 states 4–5
 free energy 2, 3, 4
 partition function 3
 transitions 12–14
 transitions induced by
 denaturants 13
 transitions induced by temperature
 5–7, 6
 transitions induced by voltage 14,
 14–17
 cooperativity 19–21, 20
 steepness factor 16, 16
 transition voltage 16, 16
 glutamate 85, 206, 270–271, 271, 283,
 292, 355
 glutamic acid (glu), helix
 continuation parameter **81**
 glutamine 17, 18, 85
 glutamine (gln), helix continuation
 parameter **81**
 glycine (gly) 38, 81, 85, 394
 helix continuation parameter **81**
 glycine receptors 374
 Goldman–Hodgkin–Katz current
 equation 348, 357–360,
 359, 361, 362, 363, 364,
 372, 434
 Goldman–Hodgkin–Katz voltage
 equation 349, 350, 352–354,
 354, 357, 360, 387
 good-folding amino acid sequences 84
 Gouy–Chapman equation 287
 Gouy–Chapman theory 285–288, 294,
 296–297, 302
 Stern's improvements 288–291
 G-protein coupled receptors
 117–121, 120, 122
 gramicidin A 374, 378–380, 393
 channel structural parameters and
 conductances **371**
 green fluorescent protein (GFP) 70, 71
 guanine–cytosine basepairs,
 hydrogen bonding 52
 harmonic oscillators 21, 44, 100,
 103, 104
 harmonic potentials 22, 44–46
 heat capacity 37, 41, 315, 316
 helix–coil transition/theory 53, 60,
 73–74, 74, 87, 94, 303
 helical propensities 80–82
 mathematical analysis 74–78
 mean number of helical
 residues 76
 results 78, 78–79
 Helmholtz–Smoluchowski
 equation 296
 hemoglobin 70, 70, 137–140, 164,
 267, 319
 allosteric interactions 126, 126–127
 iron–heme binding sites 140
 linear free energy relation 174, 174
 oxygen binding 92
 pH sensitivity 140
 Hill coefficient 92, 93, 94, 125–126
 sequential binding 93
 Hill equation 92, 92, 126, 126, 135, 136
 Hill plot 92
 hippocampal neuron **406**, 430, 431
 histidine (his) 249–251, 266, 272,
 272–275
 helix continuation parameter **81**
 Hodgkin–Huxley equations 442–446,
 444, 447
 Hodgkin–Keynes model 390, 392
 horseradish peroxidase 206–207
 ligand association rate **204**
 H-P (hydrophobic–polar amino acids)
 lattice model 83
 modeling 83, 83
 oil droplet picture 86
 sequences 84
 good-folding 84
 hydration force 39
 hydrogen bonds 39–43
 energies **42**
 enzyme–substrate 41, 42
 energies **42**
 force constant 261

- hydrogen bonds (cont.)
 nucleic acids 52
 adenine–thymine base pairs 52
 double-helix formation 52
 guanine–cytosine base pairs 52
 proteins 48, 49, 83
 α -helices 49, 49, 50
 β -sheets 49
 stretching force constant 45
 strong bonds 272–273
 histidine–aspartate 272
 pK of histidine 272, 273
 water 41, 82
 hydrophobic forces 36–39, 38, 48, 54,
 85, 105–106
 protein folding 47, 72, 83–86, 190
 hydrophobic matching 53
- ideal polymer chains 64
 central-limit theorem 65
- ideal solutions
 deviation from 279
 infinite dilution 281
- inactivation of ion channels 442
- insulin 103, 104
- image forces 29, 29–31, 30, 38, 283, 363,
 368–371, 377, 377, 379, 395
- internal motions in proteins 267
- inverse Fourier transform 480
- ion hydration energy 28, 28
 ion size 376
- ion hydration shell 281
- ion permeation 339, 368 *see also*
 channel structure
 Donnan potentials 341–343, 342
 forces within ion channels 376,
 376–378, 377
 Nernst potentials 339–341, 340
 permeation without channels
 367–369, 369
- ionic atmosphere 279, 282
 Debye–Hückel limiting law 281
- ionic double layer 287
- ions and counterions 276–277
 activity coefficient 279,
 279–283, 353
 contribution of screening to
 potential energy 280
 counterion condensation 300–302
 Debye–Hückel screening 297–305
 DNA melting 302–305, 305
 electrophoretic mobility
 294–297, 295
 velocity 294
- ionization of proteins 283–285
 membrane surface charge 285–288,
 361–362
 Stern's improvements of
 Gouy–Chapman theory
 288–291
 Poisson–Boltzmann equation and
 Debye length 277–278
 surface charge and channel
 conductance 291–293
 surface charge and voltage gating
 293–294, 294
- isoleucine (ile), helix continuation
 parameter 8, 9, **81**
- jigsaw puzzle picture for protein
 folding 86
- Johnson noise 331
- K system of enzymes 257, 258
- KcsA channel 71, 71, 394, 394–399, 396
- kinetics of associations 194
 bimolecular associations 194–195
 binding to DNA 214
 binding to membrane receptors
 208–211, 209
 diffusion-limited associations
 197–200, 198
 diffusion-limited dissociations
 200–201
 protein–ligand association rates
 203–205, **204**
 acetylcholinesterase
 205–206, 206
 evolution of speed 205
 horseradish peroxidase 206–207
 proton transfer 207–208
 rates **207**
 reduction in dimensionality
 212–214
 site binding 201–203, 202
 small perturbations 195–196, 197
- kinetics of multi-state models 216
 general solution to multi-state
 systems 221–225
 general treatment of single-channel
 kinetics 234–236, 236
 initial conditions 219–220, 220
 loss of stationarity, conservation
 and detailed balance
 237–240
 multisubunit kinetics 242–244, 243
 random walks and stretched
 kinetics 244–246, 246
- relation between single-channel
 and macroscopic kinetics
 236–237
 separation of time scales 220–221
 single-channel kinetics 232, 232
 single-channel correlations
 240–242, 241
 stationarity, conservation and
 detailed balance 226–228
 three-state model 216–219
 matrix notation 225
 single-channel kinetics
 229–232, 231
- Kirchoff's law 404
- Koshland–Nemethy–Filmer (KNF)
 model 134, 134–136
- Kramers' theory 180–183
 enzymes 259–260, 267–268
 ion channels 445
- β -lactamase, ligand association
 rate **204**
- Langevin equation 336, 397
- Laplacian differential operator 143,
 146, 285, 485
- Lennard–Jones potential 43, 44,
 51, 95
- leucine 38, 85, 86
- leucine (leu), helix continuation
 parameter **81**
- Levinthal's paradox 73
- ligand-gated channels 132–133, 133
- ligands 202, 203
 frequency of binding to receptors
 211
 protein–ligand association rates
 203–205, **204**
 acetylcholinesterase
 205–206, 206
 evolution of speed 205
 horseradish peroxidase 206–207
 reduction in dimensionality
 212–214
- light detection by the eye 311–313,
 312, 313
- like–dissolves–like rule 36
- Linderstrøm–Lang model of protein
 ionization 283
- linear transformations of matrices
 472–473
- linkage 122
- lipid bilayers 14, 23, 30, 39, 53–54, 54,
 108, 164–165, 357, 363,
 367–369

- dispersion force (London force)
 - 36, 54
- hydration forces 39
- melting 54
- lobster axon **406**
- lock-and-key stereospecific
 - interactions 43
- London force *see* dispersion force
- loop formation 66–67
- Lorentzian 328
- lysine 18, 85, **250**, 283
- lysine (lys), helix continuation
 - parameter **81**
- lysozyme 70, 71, 156, 264
 - diffusion constant 156, 164
 - unfolding by thermal denaturation
 - 7–9, 8, 12
 - melting curves 8, 9
- macromolecules, conformations of 56
 - backbone rotations in proteins
 - 68–71, 69
 - n*-butane 56–58
 - trans* and *gauche* conformations
 - 56, 57, 57
 - configurational partition functions
 - and polymer chains 58–60
 - effective segment length 62–63
 - energy fluctuations 315–317
 - entropy of protein denaturation
 - 71–73
 - flexibility parameters for chain
 - molecules **63**
 - helix continuation parameters for
 - amino acids **81**
 - helix-coil theory 78, 78–79
 - helical propensities 80–82
 - helix-coil transition 73–74, 74
 - mathematical analysis 74–78
 - loop formation 66–67
 - nonideal polymer chains and theta
 - solvents 63–65
 - probability distributions 65–66
 - protein folding 82–86
 - cooperativity within 86–87
 - random coil behavior of
 - molecules 68
 - statistics of random coils 60–62
 - stretching of random coils 67–68
- macroscopic additivity 128–130
- Marcus theory 177–178, 178
 - enzyme catalysis 273–275, 274
- Markov processes 160, 184
- matrix algebra
- determinants 473–474
- eigenvalues, eigenvectors and
 - diagonalization 46, 77, 225, 474–476
- linear transformations 472–473
 - positive semidefinite 45
- Maxwell time constant 402, 403
- mean capture time 213
- mean number of helical residues 76
- mean-square displacement 23, 145, 155, 160, 314
- mean-square end-to-end length 61
- membrane capacitance 402, 405, 428, 429, 452, 456
- membrane conductance 21, 348, 370, 400, 429, 440
- membrane potentials 339, 343
 - cells 343–344
 - muscle, skeletal 345–346
 - neurons 345, 345, 350–351
- divalent ions 360–361
- Goldman-Hodgkin-Katz current
 - equation 357–360, 359, 360–363, 364
- Goldman-Hodgkin-Katz voltage
 - equation 350, 352–354, 354, 360
- membrane pumps 354–355
- membrane transporters 355, 358
- permeability to sodium and
 - potassium ions 347, 347–349
- rate theory 362–365, 363
- surface charge 361–362
- Ussing flux ratio and active
 - transport 351–352
- membrane time constant 405
- membranes
 - binding 108–109, 109
 - current flow 401, 401–403
 - lateral diffusion 164–165
 - protein associations 107–108, 108
 - proteins 53–54, 54
 - hydrophobic matching 53
 - pumps 354–355
 - receptor binding 208–211, 209
 - resistance 401
 - surface charge 285–288, 361–362
 - Stern's improvements of
 - Gouy-Chapman theory
 - 288–291
 - transmembrane voltage 14, 14
 - transporters 355, 358
- methionine (met), helix continuation
 - parameter **81**
- Michaelis-Menten equation 91, 252, 253
 - enzyme catalysis 251
- microscopic additivity 128–130
- microstates of proteins 2, 3
 - entropy 3
 - partition function 2, 3
 - thermal denaturation 6, 6
- minimum potential energy
 - conformation of
 - polypeptides 70, 71
- mitochondria 355
- molecular associations 89
 - association equilibrium in solution
 - 89–91, 90
 - binding to membranes 108–109, 109
 - configurational free energy 94, 106–107, 107
 - contact formation 95–96
 - cooperativity 91
 - concerted binding 91–93
 - nearest-neighbor interactions 94
 - sequential binding 93–94
 - protein association in membranes
 - 107–108, 108
 - rotational free energy 101–102
 - solvation effects 105–106
 - statistical mechanics of association
 - 96–98
 - thermodynamics of associations
 - 94–95
 - translational free energy 98–101
 - change in 101
 - translation contribution to ΔG°
 - 99, 100
 - vibrational free energy 102–104
 - change in 104
 - vibrational contribution 102
- molecular crowding 165
- molecular forces 25
 - bond flexing and harmonic
 - potentials 44–46
 - cation- π interactions 33, 33–35, 47
 - charge-dipole interactions 31–32
 - Coulomb potential 25–27
 - dispersive forces 35–36
 - electrostatic self-energy 27–29
 - hydration forces 39
 - hydrogen bonds 39–43
 - hydrophobic forces 36–39, 38
 - image energy 29–31
 - induced dipoles 32–33
 - protein force fields 50–52

- molecular forces (cont.)
 stabilizing forces in nucleic acids 52–53
 stabilizing forces in proteins 46–50
 steric repulsions 43
 molten-globule native state 82
 Monod-Wyman-Changeux (MWC) model 123–126, 126, 284
 energetics 127, 127–128, 128
 enzymes 257
 hemoglobin 126, 139–140
 phosphofructokinase 130–132
 ligand-gated channels 133
 Morris-Lecar model 462, 464
 muscle, membrane potentials 345–346
 myelin 453, 453–455
- native states of proteins 46, 71, 82, 85, 85
 jigsaw puzzle picture 86
 molten-globule 82
 oil droplet picture 86
 Neher-Steinbach model 234
 Nernst equation 340, 356
 Nernst potentials 339–341, 340, 344, 344, 356, 357, 364
 Nernst-Planck equation 162
 NEURON computer program 430, 467
 neurons *see also* axons; dendrites
 cable analysis 418, 418–422, 420, 421
 compartmental model 428, 428
 membrane potentials 345, 345, 350–351
 neurotransmitters 34, 89, 118, 184, 205, 235, 351, 355, 393, 423, 457
 neutrophils 355
 Newton's equation of motion 51, 397
 nodes of Ranvier 453
 nonideal behavior of ionic solutions 279, 280, 300, 353–354
 nonideal polymer chains 63–65
 normal modes of vibration 46, 102, 103
 nucleic acids
 acidic phosphate groups 53
 stabilizing forces 52–53
 hydrogen bonds 52
 nullclines 464, 465
 Nyquist's theorem 331
- Ohmic channels 370, 370–371, 372, 372, 376, 384
 smallest channels 371
 Ohm's law 359, 403, 404
 oil droplet picture for protein folding 86
 open-time distribution 184, 185, 229, 231, 234, 235, 236, 238, 240, 323
 orotidine monophosphate decarboxylase 266
 ouabain 355
 Overton theory 367
 oxycarbenium intermediate 264
- pancreatic trypsin inhibitor 267
 Parseval's theorem 326
 partition coefficient
 ion permeation 368
 inorganic ions 368
 partition function 58
 association mechanics 96
 N residue chain 76
 polymers and monomers 59
 protein global states 3
 protein microstates 2, 3
 thermodynamic stability 3
 sum over elementary weights 58
 translational partition function 99
 passive voltage changes 400
 pathway counting 240–242, 241, 387–388
 Pauli exclusion principle 43
 permeability ratio 350, 352–353, 360, 362, 387, 387–388, 389, 436
 persistence length 53, 63, 298
 phenylalanine 34, 38, 42, 42, 119, 205
 phenylalanine (phe), helix continuation parameter **81**
 phosphofructokinase 130–132, 131, 132
 photoreceptor cells 312, 313
 pi-electrons, interactions with cations 33, 33–35, 34, 47
 Poisson distribution 309, 309–311, 310
 definition 309
 fluctuations in molecule number 311, 333
 photon absorption 312
 RMS deviations 311
 Poisson equation 26, 277, 296, 402
 Poisson-Boltzmann equation 277–278, 283, 292, 293
 linearized form 279, 282, 283
 membranes 285, 286
 uniformly charged cylinder 297
- polar and spherical coordinates 484, 484–485
 polarizability of molecules 33, 35
 poly-L-alanine, flexibility parameters **63**
 polyelectrolyte solutions
 counterion condensation 300–302
 Debye-Hückel screening 297–305
 polyethylene 59, 62
 flexibility parameters **63**
 polymer chains
 configurational partition functions 58–60
 nonideal 63–65
 polypeptide backbone of proteins 68, 69
 minimum potential energy conformation 70, 71
 rotations 69
 poly proline 70, 70, 72
 positive semidefinite matrices 45
 potassium ion channels 136, 291, 292, 292, 294, 437, 439, 439–441, 440, 463
 power spectrum 326, 328, 328
 proline 81, 250, 265
 proline (pro), helix continuation parameter **81**
 proline racemase 265, 265
 protein engineering 192
 proteins
 allosteric proteins 115
 α -helices 49, 49, 50
 associations in membranes 107–108, 108
 backbone rotations 68–71, 69
 β -sheets 49
 conformational states 1
 denaturation by other variables 12–14
 denaturants 13
 denaturation by temperature 5–7, 6
 cooperativity 11–12
 entropy 71–73
 lysozyme unfolding 7–9
 melting curves 8, 8, 9
 number of global transitions 11
 rate 188
 steepness and enthalpy 9–11, 10
 thermal unfolding 106
 transition temperature (T^*) 6
 energy fluctuations 317
 fluorescence 334, 335
 folding 46, 82–86

- cooperativity 86–87
- good-folding amino acid sequences 84
- hydrophobic interactions 47, 48
- jigsaw puzzle picture 86
- native state 46, 71, 82, 85, 85
- oil droplet picture 86
- time taken 72
- force fields 50–52
- global states 1, 4
 - compliance 21–23, 22
 - definition 2–4
 - equilibrium between two global states 4–5
 - free energy 2, 3, 4
 - microstates 2, 3, 6
 - partition function 2, 3
 - transitions induced by temperature 5–7
 - transitions induced by voltage 14, 14–17, 16, 16, 19–21, 20
- global transitions 1–2
- ionization 283–285
 - fluctuations 317–319
- membrane proteins 53–54, 54
 - hydrophobic matching 53
- predicting structure 51
 - critical assessment of protein structure prediction (CASP) 52
- protein–ligand association rates 203–205, **204**
 - acetylcholinesterase 205–206
 - evolution of speed 205
 - horseradish peroxidase 206–207
- random coil behavior 68
- stabilizing forces 46–50
 - electrostatic contributions 47
 - hydrogen bonds 48, 49
- voltage-gated channels 17–18, 18
 - gating current 18, 18–19
 - S4 amino acid segment 17, 18
- proton transfer 207–208
 - rates **207**
- quantum effects on bonds 3, 314
- quantum mechanics 40, 99–101, 179, 264
- Rall branching rules 412, 417, 418
- Rall model for neurons 418, 418, 420, 421, 421, 422
- Ramachandran plots 69, 70
- random walks 154–156
- binding to membrane receptors 210, 210
- Gaussian distribution 156–159, 157
- kinetics of multi-states 244–246, 246
- rate processes 167
 - activation energies 169–170
 - diffusion over a barrier 180–183
 - exponential relaxations 167–169, 169
- Eyring theory 179–180
- ion movements within ion channels 377
- linear free energy relations 172–175, 173, 174, 175
- Marcus free energy relation 177–178, 178
- membrane potentials 362–365, 363
- multibarrier channels 380, 380–384, 383
- reaction coordinate and detailed balance 170–182, 171, 172
- reaction coordinate for global transitions 186–193, 187
- single-channel kinetics 183, 183–186, 185
- voltage-dependent rate constants 175–176, 176, 177
- reaction coordinate 170–182, 171, 172, 173, 204, 249, 258–262, 260, 267–268, 274
- global transitions 186–193, 187
- rectification 373, 374
- red blood cells 355
- reflecting boundary conditions 150, 213, 407, 411
- refractive index 35
- relaxed (R) state 112, 113, 117
 - hemoglobin 126
- repetitive activity 458–461, 459, 460
- resting potential of cells 343
- retina 312
- rhodopsin 312
- ribonuclease A 107
- root-mean-square (rms) end-to-end distance 64
- root-mean-square (rms) length 58
- root-mean-square (rms) velocity of a molecule 156, 336
- rotational entropy 263–264
- rotational free energy 101–102
- rotational isomer model 61, 62
- rubber and elastic molecules 13, 68
- S4 amino acid segment in voltage-gated channels 17, 18
- saddle points 186, 187
- Saffman–Delbrück equation 165
- saltatory conduction 454
- selectivity filters 374, 395, 398
- self-energy (Born encag) 27–31, 30, 177, 280, 283
- sequential binding 93–94
- serine (ser) 12, 81, 248, 272, 272
 - helix continuation parameter **81**
- serine proteases 248–251, 249, 260, 272–273
 - hydroxyl group 272
- serotonin 393
- sheer force 295
- simple elastic spring 68
- single-channel current and conductance 132, 183, 232, 320–322, 321, 370, 378, 390, 443
- single-file channels 371, 390, 390–394
- single-ion channels 384–390, 385, 387
- sink of diffusion 151
- sodium chloride 276, 278
 - activity coefficient 281, 281
 - osmolarity of solutions 279
- sodium ion channels 293, 436, 437, 439, 439–441, 440
 - activation 442
- solvation effects on molecular associations 105–106
- solvents 47, 64, 368
- source of diffusion 151
- space constant (λ) 405
- spectral density 326
- S-peptide 107
- spherical and polar coordinates 484, 484–485
- squid giant axon **406**, 439, 439, 440, 443, 444, 446
 - firing 458, 459
 - frequency response 458
 - speed and size 452
- stability 226
- stabilizing forces in proteins 46–50
- stacking interaction 52
 - double-helix formation 52
- standard state, molar free energy 95
- state counting 234–236, 236
- stationarity 226, 228
 - loss of 237–240, 240

- statistics
 - light detection by the eye 311–313, 312, 313
 - random coils 60, 60–62
- steady-state diffusion 151
 - long pipe 151
 - porous membrane 153–154
 - small hole 152, 152–153
- steepness factor 16, 16
- steric repulsions 43
- Stern layer 289, 289, 290
- Stern's improvements of Gouy–Chapman theory 288–291
- Stirling's approximation 157
- Stoke's law 162, 162–163, 165, 295, 297
- Stokes–Einstein relation 163, 199, 203, 335
- stretched kinetics 244–246, 246
- supernormal axons 449
- superoxide dismutase 206
 - ligand association rate **204**
- surface potential 287, 290, 292, 293, 294, 361–362
- synapses 184, 468
 - integration in dendrites
 - analytical models 422–423, 423
 - compartmental models 430–433, 431, 432
 - impulse responses 423–425, 424
 - realistic synaptic inputs 425–428, 427
 - synaptic current 186
- Szabo–Karplus (SK) model 123, 126, 137–140, 139
- Tanford β_T value 188
- Taylor series 470, 470
- tense (T) state 112, 113, 117
 - hemoglobin 126
- thermal de Broglie wavelength 99, 179
- thermodynamics in molecular associations 94–95
- theta solvents 65
- threonine (thr) 7–9, 12, 81, 119, 266, 394
 - helix continuation parameter **81**
- threonine–valine–glycine–tyrosine–glycine (TVGYG) sequence 394, 395, 398
- threshold stimulus 436
- trans* conformation of *n*-butane 56, 57, 57
- transition states 169
 - complimentarity 264–267, 266
- transition temperature (T^*) 6
 - DNA melting 302–305
 - melting curves 8
 - steepness and enthalpy 9–12, 10
- transition voltage 16, 16
- translational entropy 260, 260–263, 263
- translational free energy 98–101
 - change in 101
 - translation contribution to ΔG° 99, 100
- translational partition function 99
- transmembrane voltage 14, 14, 339
- transmission coefficient 180
- transverse resistivity 402
- triose phosphate isomerase **204**
- trypsin 248, 250
 - hydrolysis rates **250**
- tryptophan 34, 47, 205, **250**
- tryptophan (trp), helix continuation parameter **81**
- tubulin 334, 335, 335
- turnover number of enzymes 252
- tyrosine 34, 41, 42, 119, 205, 266, 267, 394
- tyrosine (tyr), helix continuation parameter **81**
- tyrosyl-tRNA synthase 41, 42, 265, 266
- unfolding of proteins 6, 12, 106
 - denaturants 13
 - entropy 72
- lysozyme 7–9
 - melting curves 8, 8, 9
 - rate 188
- Ussing flux ratio 351–352, 390
 - definition 352
- V system of enzymes 257, 258
- valine (val) 8, 38, 81, 394
 - helix continuation parameter **81**
- van't Hoff enthalpy 10
- van't Hoff equation 10
- varicosities on axons 456, 456, 457
- vibrational energy of bonds 3
 - frequency of vibration 44
 - kinetic energy 3
 - normal modes 46, 102, 103
- vibrational free energy 102–104, 129
- voltage clamp 439, 439–441, 440
- voltage-dependent rate constants 175–176, 176, 177
- voltage-gated channels 17–18, 18, 293–294, 294, 439–450, 457–458
 - dendritic 466–468
 - gating current 18, 18–19
 - S4 amino acid segment 17, 18
- water
 - dielectric constant 26
 - temperature dependence 27
 - enthalpy of solvated ions 27
 - entropy of solvated ions 27
 - hydration energy 28, 28
 - ion size 376
 - hydration forces 39
 - hydrogen bonds 41, 82
 - hydrophobic force 37, 37, 38
- wave equation 451
- Wiener–Khinchine theorem 324, 331
- zeta-potential 296