Index

The bold numbers indicate the definition or explanation of the term.

abortive complex **20**
acetylcholine 5, 6
acetylcholine esterase **5**, 32, 149
acrylamide 138, 224
activation energy **3**, 4, 65, 237
activation volume **67**, 71, 72
activationless ground state H-tunneling 239
active site **117**
active transport **7**
adenylate cyclase 180
adenylyl imidodiphosphate (AMP-PNP) 190
affinity chromatography 221, 222
agarose **219**
agarose gel electrophoresis 10–12
alcohol dehydrogenase 9–10, 50
aldehyde dehydrogenase 9–12, 50
allosteric effector 161, **166**, 167
allosteric site **166**, 167, 173
α,ß-methylene adenosine diphosphate (AMP-PCP) 190
α helix 103
amino acid, 21st, 22nd **91**
amino acid residue **92**, 93
amino group 146
ammonium sulfate 217, 218, 230, 231
AMP-PCP 190
AMP-PNP 190
ampholite 225
apoenzyme 118
  apoprotein 118
Arrhenius equation **3**, 65, 236
Arrhenius pre-exponential factor 238
aspartic transcarbamoylase (ATCase) 165
association constant **22**
asymmetric or chiral carbon **87**

β pleated sheet (β sheet) **103**, 104
biotin 118, **125**

calmodulin **109**, 110
cAMP 179, **180**, 182
cAMP-dependent protein kinase 179, 180
carbonic anhydrase **6**, 7
carbonyl group 146
carboxyl group **88**, 125, 147, 175
catalysis **1**, 87
catalytic subunit 181, 182, 184, 185
cellulose 219, 226, 230, 231
channeling of substrates and products 195
  in tryptophan synthase 200
  in heterotetrameric sarcosine oxidase 201
chemical modification **6**, 145
  of *Pseudomonas* Phe oxidase 152
  of *Aspergillus* amine oxidase 156
chiral carbon **87**

chymotrypsin **68**–72
chymotrypsinogen **68**, 173, 174
circular dichroism (CD) 25, 77, **105**, 106
cleavage of peptide bond **95**, 173, 174
coenzyme A **118**–120, 127
cofactor 118
  protein-derived 127
coiled coil **109**–111
column chromatography **218**, 219, 230
competitive inhibition **44**–48
concerted model (MWC model) **169**
continuous-flow method **76**
covalent modification 141, **173**, 178
CTQ **128**, 134
  cysteine tryptophylquinone **128**, 134
  lysine ε-oxidase 134
  quinohemoprotein amine dehydrogenase 134
cysteine sulfinic acid, cysteine sulfenic acid **138**, 139
  in nitrile hydratase, NHase 139
  claw setting for NO in the active site of NHase **139**

de Broglie wavelength 236
dehydrogenase **120**
dextran **219**
dideoxy method **96**, 98
diethypyrocarbonate 150
diffusion-controlled 32
diisopropylfluorophosphate (DFP) 149
dimethylglycine oxidase, DMGO 202, 208, 209
dissociation constant **21**, 22, 42, 45–47, 53, 55, 64, 182, 186, 235, 239
DNA polymerase 9–11, 98, 151
DNA sequencing 96, 98
DNP method **93**
domain 8, **172**, **173**, 182, 183, 242
DTNB {5,5′-dithiobis(2-nitrobenzoic acid)} 146, **148**
  Ellman reagent 148, 160

Eadie plot 40
Edman degradation **93**, 94
EF hand motif 109, **110**
electron crystallography 8, **9**
electrophoresis 12, 98, 155, **223**, 226, 231
electrostatic interaction 99
enthalpy of activation 69
entropy of activation 69–70
enzyme kinetics **17**
enzyme specificity **2**, 31
enzyme-substrate (ES) complex **18**, 20, 55, 58
Eyring equation **64**
Eyring plot **239**

feedback inhibition 165, **166**
feedforward activation **166**
first-order rate constant 18, 77, **83**, **84**, 154
first-order reaction **80**, 83, 154
flavin adenine dinucleotide (FAD) 118, 120–121
flavin mononucleotide (FMN) 118, 120–121

flow method **25**, 75, 79, 190
folate 118, 122–124
formylglycine **137**, 138
  biogenesis 138
  sulfatase **138**
free energy of activation **63**

G protein **179**, 180
gel filtration chromatography 220, **221**
genetic testing 10
glucose 12, 13, 17, 18, 170
glucose oxidase **12**, 13, 42
Greek key **109**, 111
Greek numbers and alphabets 255
guanine nucleotide-binding protein 179
guanine nucleotide exchange factor 180
Guggenheim plot **84**

H^+, K^+-ATPase **7**, 8
hairpin β **111**
Hanes plot 40
heme 25, 118, **121**
hemoglobin 76, **121**, 166, 169, 170, 226, 263
heterotetrameric sarcosine oxidase, HTSO 201
  oxidation-reduction-dependent conformation change of 204, 207, 211
  channeling of substrates and products in 202–211
  tunnel analysis of 203
heterotropic effect **167**
heterotropic interaction **166**
Hill coefficient **168**–**169**, 171, 182
Hill equation **168**, 192
Hill plot **168**, 171
His-tagged recombinant enzyme 222
holoenzyme 118
  holoprotein 118
homeostasis **165**
homology-modeling 107
homotropic effect **166**
homotropic interaction **167**
hydrogen bond 68, **100**, 103, 104
hydrogen quantum tunneling (hydrogen tunneling) **236**
hydrophobic interaction **100**, 183, 231

initial burst **186**–188
iodoacetamide, iodoacetate 147
ion exchangers 219
isoelectric focusing **225**, 226
isoelectric point **225**, 231

k_{cat} **30**, 234, 235
k_{cat}/K_m **31**, 112
kinetic isotope effect **236**, 238, 249
King–Altman's method **253**

lactate dehydrogenase 59, 77, **112**, 119, 121, 161
Law of coulomb **99**
leucine zipper 110
Lineweaver–Burk plot **40**
loop 108, 109, **111**–113, 260

LTQ **128**, 132
lysyl tyrosylquinone **128**, 132
biogenesis 133
lysyl oxidase 132, 133

Michaelis–Menten equation **20**, 23–24, 35, 40, 50
Michaelis–Menten mechanism 17, 31, **35**, 53, 60, 64, 75, 253
MIO **128**, 136
4-methylidene-5-imidazole-5-one **128**, 136
biogenesis 136
histidine ammonia lyase 137
phenyalanine ammonia lyase 136
mixed type inhibition **46**, 49
mutarotation 17,**18**, 21

N-ethymaleimide (NEM) 148
NAD^+ 112, 118, **119**
$NADP^+$ 26, 118, **119**
neurotransmission 5
non-competitive inhibition **45**–48

obligatory complex 20
ordered bi-bi mechanism **41**
overlapping method **96**–97
oxidase **120**
oxidative deamination 152, 229, **232**, 233, 244, 246, 248
oxygenation 232, 248
oxygenative decarboxylation 152, 229, **232**, 233, 244, 246, 249

L-phenylalanine oxidase (deaminating and decarboxylating) 229

phenylglyoxal 146, 150, 153
phenylhydrazine, PH **146**
modification of carbonyl group by 146, 157–159
phosphoryl transfer reaction 188–190, 191
phosphorylation 8, 173, **178**, 181, 183, 184, 188
physical constants 255
Ping-Pong bi-bi mechanism **42**–43, 50
p*K*a 58, 90
polyacrylamide **219**, 223, 224
polyacrylamide gel electrophoresis (PAGE) 98, 220, **223**
polypeptide **92**–95, 97, 102–104, 106, 109, 173, 227
PQQ **128**, 129
pyrroloquinoline quinone **128**, 129
biogenesis 129
in glucose dehydrogenase 130
primary structure **92**, 105, 107
proenzyme 107, **173**
prosequence **173**, 175, 229, 241–243
prosthetic group 25, 62, **118**, 120
protein kinase 109, **179**–181
protein kinase A **179**–181, 189
proton pump 6–7
pseudo-first-order treatment 79, **82**, 83
pyridoxal phosphate (PLP) 118, **122**, 123
pyrrolyysine **91**, 128

pyruvate kinase 166, **171**–173
pyruvoyl (pyruvate) **128**, 135
  biogegesis 135
  pyruvoyl-dependent decarboxylase 135

quantum tunneling 62, **236**

random bi-bi mechanism 41–42
rapid equilibrium (or quasi-equilibrium) 21, 42, 45, 46, 169, 192
rapid freezing method 77, 78
reaction specificity **2**, 244, 246–249
regulatory subunit 181, 182
RS notation (Cahn–Ingold–Prelog notation) **89**

salting out **216**, 217
sarin 6
Schiff base **122**
SDS-PAGE 220, **223**–227, 231
second-order reaction 79, 81–83
selenocysteine **91**, 128
sequential model (KNF model) 169
site-directed mutagenesis 145, 151, **152**, 161
sodium dodecyl sulfate (SDS) 155, 220, **223**
sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) 220, 223–227, 231
specificity constant **31**
steady state **27**
steady state method **24**, 29
stoichiometry 8, 156, **232**
stopped-flow method **25**, 77, 234
substrate specificity **2**, 244–246
sulfhydryl group 120, 147–149
supersecondary structure (motif) 108

tertiary structure 106
tetrahedron 87
5,6,7,8-tetrahydrofolate (THF) 124
tetranitoromethane (TNM) 149
thiamine diphosphate (TDP) 124, **125**
thiamine pyrophosphate (TPP) 118, 124, **125**
TPQ **128**, 130
  topaquinone **128**, 130
  biogenesis of 131
  in copper amine oxidase 130, 132, 156
transition state analogue **62**
transition state theory 4, **61**, 62
triose phosphate isomerase 4, 111
trypsin 101, 173–178
trypsinogen 101, 173–178
tryptophan synthase, TRPS 195
  allosteric regulation of 199
  catalytic mechanism of 196, 197
  3D structural change of 196, 197
  channeling of substrates and products in 196, 197, 200
TTQ **128**, 133
  tryptophan tryptophyl quinone **128**, 133
  biogenesis of 133, 134
  methylamine dehydrogenase 133, 134

two-dimensional gel electrophoresis 226
Tyr-tRNA synthetase reaction 78–79

uncompetitive inhibition **46**, 47, 49, 50
useful software and data banks 256

van der Waals force 99, **101**–102
van der Waals radius 102

zero-order reaction **79**, **80**
the zero point energy 236, 249
zinc finger 109–111
zymogen 173

"*The relationship between the structure and the function of enzymes, despite their efficient and superior catalytic function, has been a mystery. Through the recent precise analysis of the structure of the active site, this book presents an easy-to-understand and visual explanation of the mechanism by which the catalytic function is generated. It provides a deep insight into the further development of enzyme science and the practical use of enzymes.*"

Professor Emeritus Hidehiko Kumagai
Ishikawa Prefectural University, Japan

"*This book carefully describes the basics of enzymology, including the derivation of rate equations in enzyme kinetics. Regarding the molecular mechanism of enzyme reaction based on structural analysis, the new research results obtained by Prof. Suzuki and his colleagues make it possible to touch the forefront of research. The book will be useful not only for undergraduate students interested in enzymes but also for researchers. Rich literature and end-of-chapter problems are very helpful for the readers who want to learn more deeply.*"

Former Professor Yasuzo Nishina
Kumamoto University, Japan

The first edition of this book covered the basic treatment of the enzyme reaction using the overall reaction kinetics and stopped-flow method, the general properties of protein and cofactors, the control of enzyme reaction, and the preparation of enzyme protein. These topics are the basis of enzyme research and thus suitable for the beginner in the field. The second edition presents the cofactors produced via the post-translational modification of the enzyme's active site. These cofactors expand the function of enzymes and open a new research field. The carbonyl reagent phenylhydrazine and related compounds have been useful in finding some of the newly discovered cofactors and thus have been discussed in this edition. The topic of the control of enzyme activity through the channel of substrates and products in polyfunctional enzymes has also been expanded in this book.

Haruo Suzuki is professor emeritus at Kitasato University, Tokyo, Japan. He graduated from Tokyo Metropolitan University in 1966. Then he majored in biochemistry from the Graduate School of the University of Tokyo in 1971 and received a DSci degree in the same year. After postdoc in the United States, Dr. Suzuki worked at Aichi Prefectural Colony, Japan, and then at Kitasato University. His research was on the structure–function relationship of enzymes and on the control of hemoglobin biosynthesis.

V714
ISBN 978-981-4800-66-2
9 789814 800662

JENNY STANFORD
PUBLISHING