# The Enzymes of Biological Membranes

## Volume 3 Membrane Transport

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### **Preface**

Much of the information currently available on the transport systems of bacterial and animal cell membranes and their mode of coupling to metabolic supply of energy can be found in this volume. Consideration of the participating enzymes dictated the choice of topics: Several transport systems where little information is available on the enzymology of the process are not included, while separate chapters deal with  $\gamma$ -glutamyl transpeptidase and intestinal disaccharidases which meet many of the requirements of transport enzymes. The volume also includes two chapters on photosynthetic membranes as a general introduction to the topic. Other aspects of biological transport and photosynthesis will be developed in detail in a forthcoming volume now in preparation.

These chapters reveal the excitement and rapid advance of the field, the daily reports of new concepts, new techniques, and new experimental findings which instantly interact to generate further progress. Our aim was to provide a starting point for those who are just beginning, and an opportunity for others to stop, take stock, and start in a new direction.

My warmest thanks to all who contributed to this volume.

St. Louis, Missouri January, 1976 ANTHONY N. MARTONOSI

### Contents

### PART A MEMBRANE TRANSPORT IN MICROORGANISMS

1	Bacterial Membrane Transport Proteins 3
	Adam Kepes
	<ul> <li>I. Introduction 3</li> <li>II. Transport Proteins as Membrane-Bound Proteins 4</li> <li>III. Time and Place of Deposition of Membrane-Bound Transport Protein in the Membrane 8</li> <li>IV. Lateral Mobility of Membrane Proteins in Escherichia coli 13</li> <li>V. Transmembrane Mobility of Transport Proteins 14</li> <li>VI. Substrate Binding Sites, Energization, and Conformational Change 18</li> <li>VII. The Coupling of Metabolic Energy to Active Transport 22</li> <li>VIII. Mechanics and Energization of Desmoprotein-Dependent Transport Systems 25</li> <li>IX. Conclusions 25</li> <li>References 26</li> </ul>
2	The Bacterial Phosphoenolpyruvate Phosphotransferase
_	System 31
	Werner Kundig
	<ul> <li>I. Introduction 31</li> <li>II. The Phosphotransferase System in Enterobacteriaceae 33 <ul> <li>A. The Formation of Phospho-HPr 34 · B. Enzyme II Complexes 35</li> <li>C. Genetics of the Phosphotransferase System 45 · D. The Physiological Functions of the Phosphotransferase System 47</li> </ul> </li> <li>III. The Phosphotransferase System in Staphylococcus aureus 49</li> <li>IV. The Distribution of the Phosphotransferase System in Other</li> </ul>
	Organisms 50 References 52

References

3	Structure and	Function	of Membrane-Bound ATPase
	in Bacteria	57	

- Adolph Abrams
  - I. Introduction 57
  - II. Molecular Properties 58
     A. Solubilization and Purification 58 · B. Molecular Weight and Subunits 60 · C. Amino Acid Composition 62 · D. Nucleotide Binding 63
  - III. Kinetic Properties 65
  - IV. Reassembly 66
  - V. Inhibitory Action of Dicyclohexylcarbodiimide (DCCD) 67
  - VI. Physiological Functions 69
    - A. Function in E. coli 69 · B. Function in S. faecalis 70 References 71
- 4 Respiration and Energy Transduction in

Escherichia coli 75

#### RICHARD W. HENDLER

- I. Introduction 75
- II. The Electron Transport Chain of E. coli 76
- III. Solubilization and Fractionation of the Electron-Transport Chain 81
- IV. The Multiplicity of Cytochromes and Their Possible Involvement in Energy Transduction 83
- V. Oxidative Phosphorylation in E. coli 86
- VI. On the Direct Use of Energy from Respiration-Linked p-Lactate
  Oxidation for Active Transport 93
- VII. On the Role of Mg<sup>2+</sup>, Ca<sup>2+</sup> Adenosine Triphosphatase in Energy Transduction 100 References 103
- 5 Membrane-Bound Enzymes from Mycobacterium phlei; Malate Vitamin K Reductase 111

### RAJENDRA PRASAD AND ARNOLD F. BRODIE

- I. Introduction 111
- II. Membrane Orientation 112
- III. Nature of Respiratory Chain 114
- IV. Malate Vitamin K Reductase 116
   A. Assay of Malate Vitamin K Reductase Activity 116 B. Localization of Malate Vitamin K Reductase 117 C. Separation of NAD+-Linked Dehydrogenase from Malate Vitamin K Reductase 118 D. Purification

of Malate Vitamin K Reductase 118 · E. Absorption Spectrum and Amino Acid Composition 119 · F. Stability of Malate Vitamin K Reductase 119 G. Phospholipid Requirement 119 · H. Nature of Phospholipid Binding to Malate Vitamin K Reductase 124 · I. FAD Requirement of Malate Vitamin K Reductase 125 · J. Quinone Specificity of Malate Vitamin K Reductase 126 · K. Nonheme Iron: A Component of Malate Vitamin K Reductase 127 · L. Transmembrane Electron Transfer 129

V. Membrane-Bound Latent ATPase Coupling Factor 130
 A. Localization of Latent ATPase 131 · B. Solubilization and Purification of Latent ATPase Activity 132 · C. Properties of Latent ATPase 132
 D. Role of Latent ATPase in Oxidative Phosphorylation and Active Transport 134 · E. Lipid Requirement for Latent ATPase Activity 135

VI. Nature of Cytochromes from M. phlei 135

VII. Conclusion 135 References 136

### PART B PHOTOSYNTHETIC APPARATUS

### 6 The Organization of Photosynthetic Enzymes on the Chloroplast Membrane 143

DAVID W. KROGMANN

- I. Introduction 143
- II. Organization of the Catalysts in a Functional Sequence 144
- III. Functional and Structural Subunits of the Chloroplast Membrane 148
- IV. Individual Catalysts and Their Interactions with the Membrane and Each Other 149

A. NADP: Ferredoxin Oxidoreductase 149 · B. Ferredoxin 151 · C. X and  $P_{700}$  152 · D. Plastocyanin 153 · E. Cytochrome f 155 · F. Plastoquinone and Cytochrome  $b_{559}$  155 · G. Photosystem II and Oxygen Evolution 156 · H. Coupling Factor 156 References 158

### 7 Chlorophyll-Proteins: Membrane-Bound Photoreceptor Complexes in Plants 163

- J. PHILIP THORNBER AND RANDALL S. ALBERTE
  - I. Introduction 163
  - II. Demonstration of Existence of Multiple Chlorophyll-Proteins in Higher Plants 164
  - III. The P<sub>700</sub> Chlorophyll a-Protein 167
     A. Isolation 167 · B. Characteristics 168 · C. Function 170
  - IV. Light-Harvesting Chlorophyll a/b-Protein
     A. Isolation 171 · B. Characteristics 172 · C. Function 173

V. Content of Chlorophyll-Proteins in Photosynthetic
Membranes 174
VI. Biosynthesis of the Chlorophyll-Protein Complexes 177
VII. Chloroplast Membrane Polypeptides 178  A. Characteristics 179 · B. Function 180 · C. Biosynthesis 182
VIII. Summary and Concluding Remarks 183
References 186
PART C SOLUTE TRANSPORT IN MAMMALIAN CELLS
8 Binding Proteins and Membrane Transport 193
ERNESTO CARAFOLI AND MARTIN CROMPTON
I. Introduction 193
II. Nonmammalian Cells 195
A. Periplasmic Proteins 195 · B. The Phosphotransferase System 199
C. The Lactose Permease 200 · D. The Dicarboxylate-Transporting System 201  III. Mammalian Cells 202
A. The Ca ATPase of Erythrocytes 202 · B. The Ca-Binding Protein from
Intestinal Mucosa 203 · C. The Sucrase-Isomaltase Complex 205
IV. Mitochondria 205  A. The Ca-Binding Proteins 205 · B. Anions 207
V. Conclusions 211
References 212
. —— 0.0
9 The Calcium Transport ATPase of Sarcoplasmic
Reticulum 221
DAVID H. MACLENNAN AND PAUL C. HOLLAND
I. Structure of the Sarcotubular System 221
II. Function of the Sarcotubular System 222
III. Isolation of the Sarcoplasmic Reticulum 223
IV Protein Composition 225
V. Purification of the Membrane-Bound ATPase Enzyme 226
A. Lipid Composition of ATPase 228 · B. Proteolipid 230 C. Reconstitution of Calcium Transport 230
VI. Ultrastructure of Isolated Sarcoplasmic Reticulum Vesicles and
of ATPase 232
A. Tryptic Fragmentation of ATPase 233 · B. Ionophoric Activity in the
A. Tryphic Fragilic Itation of State of Function through Phosphorylation 236 D. Membrane-Binding Sites for Calcium 236
VII. Biosynthesis of Sarcoplasmic Reticulum 239

· 10

11

VIII.	Reaction Mechanism 240
	A. The Phosphorylated Intermediate 241 · B. Formation of the
	Phosphorylated Intermediate (EP) 242 · C. Decomposition of EP 245  D. Substrate Specificity 246 · E. Inhibitors of Ca <sup>2+</sup> -Dependent ATPase
	Activity and Ca <sup>2+</sup> Transport 246
IX.	Model for ATP-Driven Ca <sup>2+</sup> Transport 247
	Conformational Probes 249
	A. Spin Labels 249 · B. Chromophoric Probes 249 · C. Hydrogen
	Exchange 250 · D. Circular Dichroism 250
XI.	Summary 251
	References 251
Plasr	na Membrane Calcium Transport and
	nbrane-Bound Enzymes 261
IVICII	ibranc-bound Enzymes 201
FRANK	K F. VINCENZI AND THOMAS R. HINDS
I.	Introduction 261
	A. Red Blood Cell Membrane Preparations 262 · B. Red Blood Cell
	Membrane-Bound ATPases 263
11.	Plasma Membrane Calcium Transport 265
	A. Calcium Transport in Red Blood Cells 265 · B. Calcium Transport in Other Systems 269 · C. Cellular Significance of Plasma Membrane
	Calcium Transport 270 · D. Active Ca <sup>2+</sup> Transport and Na <sup>+</sup> -Ca <sup>2+</sup>
	Exchange 272
	Calcium Transport and Disease 273
IV.	Summary 274
	References 276
The	(Sodium plus Potassium)-Transport ATPase 283
	(Source plus 1 statisfically 1 tampert 111 2 asserting
R. W	Albers
	Physiological Background 283
II.	Characteristics of Ouabain-Sensitive Na+ and K+ Fluxes 284
III.	General Properties of the ATPase 285
IV.	Molecular Events 286
V.	The Ionophoric Process 288
VI.	Reversal of the (Na <sup>+</sup> + K <sup>+</sup> )-ATPase Reaction 290
VII.	Arguments Against a Sequential Transport Model 292
	Regulation of Na <sup>+</sup> and K <sup>+</sup> Active Transport 293
IX.	Hormonal Control 294
$\mathbf{X}$	Regulation at the Cellular Level 295
	Enzyme Preparations 295
	Properties of Purified (Na + K +) ATPases 296
	. Conclusion 296
	References 297

XIV	CONTENT
12	Potassium-Activated Phosphatase 303
	Alcides F. Rega and Patricio J. Garrahan
	<ul> <li>I. Introduction 303 <ul> <li>A. K-Activated Phosphatase and (Na<sup>+</sup> + K<sup>+</sup>) ATPase 303</li> </ul> </li> <li>II. Estimation of Phosphatase Activity 305</li> <li>III. Substrate Requirements 305</li> <li>IV. Effects of Cations 307 <ul> <li>A. Magnesium 307 · B. Potassium 307 · C. Sodium 308</li> </ul> </li> <li>V. Effects of Inhibitors 309</li> <li>VI. Effects of ATP 310 <ul> <li>References 312</li> </ul> </li> </ul>
13	Membrane-Bound γ-Glutamyl Transpeptidase 315
	ALTON MEISTER, SURESH S. TATE, AND LEONARD L. ROSS
	<ul> <li>I. Introduction 315</li> <li>II. Background 316</li> <li>III. Histochemical Studies 320</li> <li>IV. Studies on Purified γ-Glutamyl Transpeptidase 327  A. Methods of Purification 327 · B. Some Chemical and Physical Properties of the "Light" and "Heavy" Forms of the Enzyme 329  C. Specificity 330 · D. Inhibition 333 · E. Ontogeny 335</li> <li>V. Physiological Function of γ-Glutamyl Transpeptidase 337</li> <li>References 343</li> </ul>
14	Small Intestinal Disaccharidases: Their Properties and
17	Role as Sugar Translocators across Natural and
	Artificial Membranes 349
	Giorgio Semenza
	<ul> <li>I. Small Intestinal Oligo- and Disaccharidases 349</li> <li>A. Maltases-Glucoamylases 350 · B. Sucrase-Isomaltase Complex 351</li> <li>C. Trehalase 352 · D. β-Glycosidase Complex 353</li> <li>II. Some Molecular Properties of the Sucrase-Isomaltase Complex from Rabbit Small Intestine 354</li> <li>III. The Hydrolytic Mechanism of Sucrase and Isomaltase 358</li> <li>A. The Kinetic Mechanism 358 · B. The Configuration of C<sub>1</sub> of Glucose in the Products 359 · C. The Participation of a Carboxylate Group 359</li> <li>D. The Bond Split by Sucrase and Isomaltase 362 · E. The Effect of Para</li> </ul>

Substituents in the Aglycone Moiety: the Hammett-Hansch Equation 362

F. The Secondary Deuterium Effect 363

G. A Minimal Reaction Mechanism 363

IV.	The Role of Brush-Border-Bound	Disaccharidases in Intestina
	Sugar Transport in Intact Cells	367

 V. Reconstitution of the Sucrase-Dependent Sugar-Transport System into Artificial Membranes 369
 References 376

### 15 The ADP-ATP Carrier in Mitochondrial

Membranes

383

#### MARTIN KLINGENBERG

- I. Introduction 383
- II. Fundamentals of Defining Mitochondrial ADP-ATP Transport 384

A. Metabolic Localization of ADP-ATP Transport 384 · B. The Mitochondrial Adenine Nucleotide Pool 385 · C. The Carrier Concept 387

III. Kinetics 388

A. Specificity 389 · B. Temperature Dependence 390

IV. Regulation of Carrier Activity 391

A. Concentration Dependence of ADP-ATP Transport 392

A. Concentration Dependence of ADP-ATP Transport 392 · B. Energy Control of Reversed and Forward Rates 393 · C. Electrical Charge Movement and Exchange 395

- V. Inhibitors of ADP-ATP Transport 397
- VI. Definition of the Carrier Sites 399
   A. Binding of ADP and Interaction with ATR 399
   B. Binding of ADP and Interaction with Bongkrekate 402
   C. The Reorientation Mechanism 405
   D. Endogenous ADP, ATP under the Influence of BKA 406

VII. Conformational Changes of the Membrane on Binding of ADP 407

- VIII. The Binding of [35S]ATR and [35S]CAT and the Interaction with Other Ligands 412
  - IX. The Sensitivity of ADP-ATP Carrier to Maleimide 419

X. The ADP-ATP Carrier in Submitochondrial (Sonic) Particles 421

XI. Carrier Mechanisms 425
 A. Translocation Step 426 B. Activation Step 428

XII. Isolation of the Carrier Protein

A. [35S]CAT as a Marker for Carrier Isolation 430 · B. NEM as a Marker of the Carrier Protein 434 · C. Conclusions

References 435

Author Index 439

Subject Index 453

# Part A $\mathbf{M}_{\text{EMBRANE}} \ T_{\text{RANSPORT IN}} \ \mathbf{M}_{\text{ICROORGANISMS}}$



### Bacterial Membrane Transport Proteins

### ADAM KEPES

### I. Introduction

Bacterial transport systems are historically associated with the acceptance of the idea that the crossing of the cell membrane by a physiologically significant solute was mediated by the specialized operation of a protein or an array of molecules including specific proteins. This idea was in opposition to the predominant-view of permeability, a membrane property, as the principal factor governing the passage of solutes.

The concept of the specialized transport protein gained general recognition primarily because of the possibility of varying the amount of transport protein separately from that of surface area of the membrane through specific genetic change and through inductive or repressive regulation of its biosynthesis (Cohen and Monod, 1957). The word "permease" (Rickenberg et al., 1956) stirred up considerable discussion which served to emphasize the transport proteins. It suggested in a condensed form the involvement of a protein with enzyme-like specificity and catalytic (i.e., cyclic) activity. Unfortunately, it failed to stress distinction between permeability and active transport which later was recognized to be a nearly universal feature of all transport systems to which the term has ever been applied (Kepes, 1964). The enzyme-like denomination "-ase" can be justified on the ground that a typically enzymatic event, the breakdown of chemical (or electrochemical) energy, is partly or totally dependent on the transport protein. The phosphoenolpyruvate sugar phosphotransferase system (Kundig et al., 1964) (see also Kundig, this volume) is an illustration of this statement, although since the discovery of its chemical

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mechanism it has seldom been included among permeases. Presumably, once similarly well-defined biochemical mechanisms have been established for all transport systems, the term permease will have completely lost its usefulness.

In this chapter both old and recent evidence concerning the membrane location of transport proteins will be reviewed. This view is supported by their limited freedom of movement along the membrane surface. Some facts will be reported which permit speculation about the insertion of membrane protein into membrane during biosynthesis; other facts and speculations will be relevant to the possibility of transmembrane movements.

The likelihood of multiple configurational changes during the transport cycle will be documented by several lines of indirect evidence. The energy coupling to active transport will be discussed briefly on the basis of experiments with inhibitors (Kepes, 1974) and isolated membrane vesicles (Kaback, 1971, 1972). The chemiosmotic theory and its methodology (Harold, 1972; West, 1970; West and Mitchell, 1972, 1973; Rosen, 1973) and the genetic analysis of the energy pathways in bacterial transport will be briefly reviewed (Haddock and Schairer, 1973; Devor et al., 1974; Simoni and Shallenberger, 1972). For a large class of transport systems the results can be tentatively summarized as the utilization of an energized state of the membrane to fuel active transport. Finally, recent evidence for transport systems utilizing chemical-bond energy independent from the energized state of the membrane will be briefly described (Berger, 1973).

### II. Transport Proteins as Membrane-Bound Proteins

The plasma membrane is the main diffusion barrier to penetration of hydrophilic solutes from the medium and to the escape of many hydrophilic metabolites from the cell. This basic impermeability is the cause of the inaccessibility of intracellular metabolic enzymes to their substrates dissolved in the medium (Deere et al., 1939). This inaccessibility (termed crypticity) helped establish the generalized requirement for transport systems to carry out the uptake of all exogenously furnished nutrients (Cohen and Monod, 1957).

The logical counterpart of the virtual impermeability of the plasma membrane is the necessary location within its hydrophobic fabric of essential parts of the transport machinery. Some of these must either encompass the thickness of the barrier permanently or be able to shuttle occasionally or periodically from one face to another. Such logic does not unambiguously designate a membrane protein. The best examples of nonprotein carriers are the polyisoprenoid molecules which help the hydrophilic building blocks of murein or lipopolysaccharide to cross the hydrophobic membrane. The logic is somewhat tightened when a transport process is performed in isolated membranes in the absence of cytoplasmic factors, since only structures permanently linked to the membrane can participate in the translocation process from the recognition of the solute to its release on the other side. Such a sequence implies a stereospecific site for the transport substrate and strongly supports the presence of the key protein.