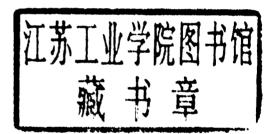


# Essays in Biochemistry

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# Essays in Biochemistry

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### **Abbreviations**

A<sub>2</sub>pm diaminopimelic acid

Ac<sub>2</sub>KAA  $N^{\alpha}$ ,  $N^{\epsilon}$ -diacetyl-L-lysyl-D-alanyl-D-alanine

AcKAA  $N^{\alpha}$ -acetyl-L-lysyl-D-alanyl-D-alanine

ADA adenosine deaminase

ADH horse liver alcohol dehydrogenase

ADRP autosomal dominant retinitis pigmentosa

apo E apolipoprotein E

**ASVB** Avocado sun-blotch virus

a.t.r.-f.t.i.r. attenuated total reflection Fourier transform infrared

spectroscopy

BHprotonated base

bis(NAD+)  $N_2$ ,  $N_2$ '-(adipodihydrazide)-bis( $N^6$ -

carbonylmethyl)NAD+

**BPD** bronchopulmonary dysplasia

BSE bovine spongiform encephalopathy CAT chloramphenicol acetyltransferase

c.d. circular dichroism

CID Creutzfeld-Jakob disease CLD chronic lung disease

chaperonin cpn

DD-peptidase D-alanyl-D-alanine peptidase

**DMSO** dimethylsulphoxide **ECM** extracellular matrix EGF epidermal growth factor ER endoplasmic reticulum **GDH** glutamate dehydrogenase **GPI** glycosylphosphatidylinositol GSS

**HDV** hepatitis delta virus

h.p.l.c. high-performance liquid chromatography

Gerstmann-Sträussler syndrome

Н,О, hydrogen peroxide

HIV human immunodeficiency virus

HLA human leukocyte antigen **HMM** high molecular mass hsp heat-shock protein IgG immunoglobulin G

**IVH** intraventricular haemorrhage

**IVS** intervening sequence LCR ligase chain reaction
LDH lactate dehydrogenase
LDL low-density lipoprotein
LMM low molecular mass

MHC major histocompatibility complex

n.m.r. nuclear magnetic resonance
NEC necrotizing enterocolitis
NIPAM N-isopropyl acrylamide

NO nitric oxide nt nucleotide

O<sub>2</sub>-- superoxide radical

PBP penicillin-binding protein PCR polymerase chain reaction

PEG polyethylene glycol PFK phosphofructokinase

PrP prion protein RNase P ribonuclease P

ROP retinopathy of prematurity SAP sphingolipid activator protein

snRNA small nuclear RNA

snRNP small nuclear ribonucleoprotein

STRSV satellite RNA of tobacco ringspot virus

ss single stranded
TRiC TCP ring complex
VLBW very low birth weight

YADH yeast alcohol dehydrogenase

### **Contents**

A	uthors	i×
A	bbreviations	xii
Ва	acterial DD-transpeptidases and penicillin	
	Marc Jamin, Jean-Marc Wilkin and Jean-Marie Frère	
	Introduction: the bacterial DD-transpeptidases and the peptidoglyc	anl
	How penicillin kills bacteria	
	The physiological DD-transpeptidases	
	The DD-peptidases of Streptomyces R61, Streptomyces K15 and Actinomadura R39	
	DD-Peptidases and β-lactamases	
	Ester and thiolester substrates	
	Modification of the Streptomyces R61 enzyme by site-directed mutagenesis	
	The search for a general base	
	Penicillin-resistant PBPs	
	Conclusion: does penicillin behave as a substrate analogue?	
	References	
Sp	phingolipid activator proteins	
	Kunihiko Suzuki	
	Introduction	25
	Brief history	27
	Nomenclature	28
	Molecular genetics	28
	Activator function in vitro	30
	Physiological activator function in vivo and genetic disorders	31
	Other possible functions	33
	Future investigations	34
	References	36

# Oxygen toxicity, free radicals and antioxidants in human disease: biochemical implications in atherosclerosis and the problems of premature neonates

Catherine A. Rice-Evans and Vimala Gopinathan

	*	
	Introduction	39
	Antioxidants in the maintenance of health and protection	
	against disease	43
	Atherosclerosis: oxidants and antioxidants	47
	Hyperoxia and oxygen toxicity: oxygen radical injury in the newborn	55
	Plasma antioxidant status in neonates	
	References	
	econstructed human skin: transplant, graft or iological dressing?	
	Edward J. Wood and Ian R. Harris	
	Introduction	
	The structure of human skin: regeneration and grafting	
	Skin immunology	
	Growing keratinocyte sheets	70
	Is allografting with keratinocyte sheets successful?	72
	Skin banking and the HIV problem	
	Cryopreservation	74
	Dermal equivalents and skin equivalents	
	The future	
	Conclusions	
	References	
C	Opsin genes	
	B. Edward H. Maden	
	Introduction	
	Rhodopsin function and structure in outline	
	Bovine opsin cDNA	
	Bovine and human opsin genes	
	Human colour vision	
	Red and green abnormalities and the absolute red-green map	
	Drosophila opsins and opsin phylogeny	
	The seven transmembrane believe superfamily of recentors	10

	Exploring the details of structure and function of opsins	101
	Concluding comments	108
	References	108
Z	The roles of molecular chaperones in vivo	
U	Peter A. Lund	
	Introduction	
	The hsp70 proteins: multi-functional and ubiquitous chaperones	114
	The hsp60 proteins: archetypal molecular chaperones	116
	The cytosolic TCPI-like proteins	118
	Other molecular chaperones: probable and possible	118
	Summary	119
	References	122
7	Molecular chaperones: physical and mechanistic propert	ies
	Steven G. Burston and Anthony R. Clarke	
	Introduction	125
	The hsp70 molecular chaperone	126
	Hsp70 as part of a larger molecular chaperone complex	128
	The role of hsp70 in maintaining a translocation-competent	
	protein conformation	128
	The actions of chaperonins in assisted protein folding	129
	TCPI ring complex: a eukaryotic chaperone in the cytosol	133
	Hsp90: molecular chaperone or protein regulator?	134
	Summary	134
	References	135
0	Affinity precipitation: a novel approach to protein purific	ation
0	Jane A. Irwin and Keith F. Tipton	
	Introduction	137
	Affinity precipitation with bis-ligands	
	Affinity precipitation with heterobifunctional ligands	
	Conclusion	
	References	
0	Molecular pathology of prion diseases	
7	Corinne Smith and John Collinge	
	Introduction	157

	Molecular genetics of the human prion diseases	159
	A model of prion propagation	165
	Effect of disruption of PrP gene in mice	166
	Analysis of prion structural elements	167
	Summary of theories of prion propagation	170
	Conclusions	171
	Further reading	172
	References	172
IO Rib	pozymes	
U	Helen A. James and Philip C. Turner	
	Introduction	175
	RNA catalysis	175
	Self-splicing RNAs	177
	Ribonuclease P	180
	Self-cleaving RNAs	181
	Hammerhead ribozymes	182
	Hairpin ribozymes	187
	Hepatitis delta virus	188
	Neurospora mitochondrial VS RNA	
	Ribozyme delivery	
	Suggestions for further reading	
	References	
Pr	otein stability at high temperatures	
	D.A. Cowan	
	Introduction	193
	Thermophilic organisms	194
	Thermostable proteins	195
	Mechanisms of protein thermostability	200
	Inactivation at high temperatures	201
	Consequences of hyperstability	201
	Protein engineering for thermostability	204
	Biotechnological implications	204
	Future applications	205
	Summary	206
	References	206
Su	bject index2	207

# **Bacterial DD-transpeptidases** and penicillin

## Marc Jamin, Jean-Marc Wilkin and Jean-Marie Frère\*

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## Introduction: the bacterial DD-transpeptidases and the peptidoglycan

D-Alanyl-D-alanine peptidases (DD-peptidases) are membrane-bound enzymes involved in the synthesis and remodelling of the peptidoglycan (or murein), a macromolecular sacculus composed of linear glycan chains cross-linked by short peptides (Figure 1), which completely surrounds the cytoplasmic membrane of bacterial cells and is responsible for their shape and mechanical resistance to their own osmotic pressure<sup>1</sup>.

The peptidoglycan is a dynamic structure that is continuously remodelled during the cell cycle under the regulated control of two conflicting synthetic (transpeptidase and transglycosylase activities) and hydrolytic (endopeptidase, carboxypeptidase and glycosidase activities) machineries. While the external face of the murein shell is eroded by these autolytic enzymes, disaccharide—peptide precursors linked to an isoprenoid lipid carrier are formed in the cytoplasm, either by *de novo* synthesis or by recycling the liberated peptides. These building blocks are translocated across the cell membrane and incorporated into the peptidoglycan by reactions which occur in the extracellular compartment; disaccharide—peptide units are added to the growing glycan chains and the peptide bridges are subsequently formed by transpeptidation between the peptide chains of adjacent strands. The R-D-alanyl group

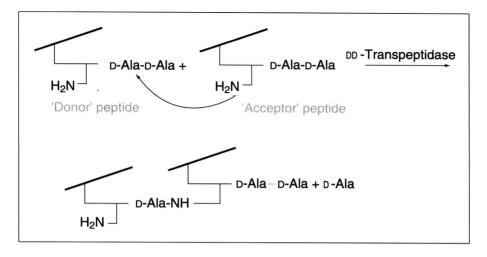


Figure 1. Formation of the peptide bridge in peptidoglycan synthesis

The heavy lines represent the glycan chains composed of alternating N-acetylglucosaminyl and N-acetylmuramyl residues. The peptide moiety attached to the lactyl side-chain of the latter exhibits specific variations in the different bacterial genera. In Gram-negative bacteria, a

sequence is found, where the free 'acceptor' amino group is on the D centre of meso-diaminopimelic acid (m- $A_2$ pm; a detailed structure of the C-terminal tetrapeptide can be found in Figure 3b). For more details, see references I and 2 and references therein.

The reaction can also be represented by the simple scheme:

$$R_1$$
-D-Ala-D-Ala +  $R_2$ -NH<sub>2</sub> $\rightarrow R_1$ -D-Ala-NH- $R_2$ + D-Ala

where  $R_1$ -D-Ala-D-Ala and  $R_2$ -NH<sub>2</sub> are the donor and acceptor peptides, respectively.

of a D-alanyl-D-alanine-terminated 'donor' precursor is transferred to the amino-group of a neighbouring 'acceptor' peptide and the C-terminal D-alanine of the former is released (Figure 1). The equilibrium of that reaction is displaced to the formation of the murein by the insolubilization of the polymer and the diffusion of D-alanine away from the reaction site<sup>2</sup>.

#### How penicillin kills bacteria

All DD-transpeptidases discovered so far are active-site serine enzymes whose catalytic pathways involve transient acylenzyme adducts (Figure 2a) where the penultimate D-alanine residue of the 'donor' substrate is ester-linked to the active-site serine side-chain.

Penicillins, cephalosporins (Figure 2b) and other  $\beta$ -lactam antibiotics inhibit peptidoglycan biosynthesis by inactivating the DD-transpeptidases; they

form a covalent, stable acylenzyme with the same residue (Figure 2), thus blocking the bacterial growth and division<sup>3,4</sup>. Uncross-linked peptidoglycan is unable to resist the cell osmotic pressure and lysis most often occurs, but a triggering of the bacterial autolytic system also appears to play an important role in this phenomenon, at least in some species. The specificity of  $\beta$ -lactams as antibacterial agents results from the fact that the peptide moiety of peptidoglycan is unique to the bacterial world, and that no similar transpeptidation reaction involving D-alanyl-D-alanine-terminated peptides exists in eukaryotic organisms.

Figure 2. Catalytic pathway of DD-transpeptidases (E-OH) and inactivation by penicillins (a) and structures of penicillins and cephalosporins (b)

(a) Hydrolysis or aminolysis of the penicilloyl-enzyme is so slow that this reaction is generally devoid of physiological importance. It can also involve an additional breakdown of the penicilloyl moiety. (b) The structures of penicillins and cephalosporins are shown in detail. The  $\beta$ -lactam ring is shown in blue. Typical examples are (c) benzylpenicillin and (d) cephalosporin C. In 6-amino-penicillanate, the amino group of the side-chain is unsubstituted ( $R_3$ -CO- is replaced by H).

(a)
$$R_{3} \cdot CO_{N/N} = E \cdot O - D \cdot Ala \cdot R_{1} + D \cdot Ala \cdot R_{1} + D \cdot Ala \cdot R_{2} + E \cdot OH$$

$$R_{3} \cdot CO_{N/N} = E \cdot O - D \cdot Ala \cdot R_{1} + D \cdot Ala \cdot R_{2} + E \cdot OH$$

$$R_{3} \cdot CO_{N/N} = E \cdot O - C \cdot CO_{1} \cdot CO_{2} \cdot CO$$

(c) 
$$R_{3} = C_{6}H_{5}-CH_{2}$$
 
$$R_{4} = \frac{-OOC}{+H_{3}N} CH - (CH_{2})_{3}$$

#### The physiological DD-transpeptidases

The physiologically important DD-transpeptidases are membrane-bound proteins which can be labelled with radioactive or fluorescent penicillins and separated by SDS/PAGE. These techniques reveal the presence of several 'penicillin-binding proteins' (PBPs) in the membrane of all eubacteria<sup>5</sup>. The role of these various enzymes in peptidoglycan synthesis and cell division is presently best understood in Escherichia coli (Table 1). The position of the active-site serine in the sequence allowed the PBPs to be divided into low- and high-molecular-mass enzymes. The low-molecular-mass PBPs (LMM-PBPs) exhibit carboxypeptidase (PBPs 4, 5 and 6) activities which seem to be dispensable to the survival of the bacteria but which take part in the regulation of the cell cycle. The high-molecular-mass PBPs (HMM-PBPs) are two-domain proteins with a C-terminal, penicillin-binding domain responsible for the transpeptidase activity. Genetic and morphological approaches highlighted the roles of the HMM-PBPs, and of the products of additional genes, in cell wall elongation, septum formation during the cell division and in shape determination<sup>2,5-7</sup>. Intimately associated with the autolysins in the regulation of the cell cycle, the different DD-transpeptidases undergo activation and deactivation in the different steps of this cycle8. However, the catalytic and regulation mechanisms of these enzymes remain poorly understood, since large quantities of purified proteins have never been available.

The cloning and sequencing of the genes coding for various PBPs of several species have supplied detailed information on the primary structures of the corresponding proteins and, more recently, the elimination of the DNA region coding for the membrane-anchoring peptide has allowed the production of some apparently functional, soluble penicillin-binding domains of these enzymes. Nevertheless, most of the information which has been accumulated on the catalytic properties of penicillin-sensitive DD-transpeptidases, and on their interactions with  $\beta$ -lactams, has been obtained with soluble DD-peptidases synthesized by some members of the Actinomycetales order.

### The DD-peptidases of Streptomyces R61, Streptomyces K15 and Actinomadura R39<sup>2</sup>

The DD-peptidases of Streptomyces R61 and Actinomadura R39 are secreted in the extracellular medium as soluble proteins, and that of Streptomyces K15 is loosely bound to the cytoplasmic membrane and can be solubilized in the presence of 0.5 M NaCl. The purified proteins catalyse the cleavage of the C-terminal D-alanine of simple synthetic peptides, such as  $N^{\alpha}$ ,  $N^{\epsilon}$ -diacetyl-L-lysyl-D-alanyl-D-alanine (Ac<sub>2</sub>KAA) and  $N^{\alpha}$ -acetyl-L-lysyl-D-alanyl-D-alanine (AcKAA). In the presence of acceptor compounds exhibiting a suitably located amino group, they also perform transpeptidation reactions according to the scheme depicted in the legend of Figure 1. The Streptomyces K15 enzyme is so efficient as a transpeptidase that it only hydrolyses a minor proportion of the