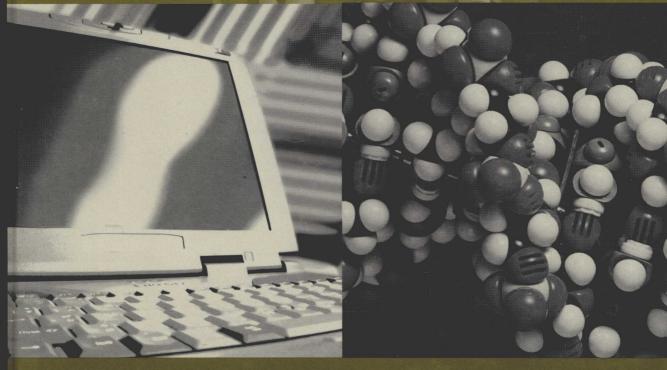


# BIOMACROMOLECULES



Introduction to Structure, Function and Informatics

C. STAN TSAI, Ph.D.

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# Introduction to Structure, Function and Informatics

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# **BIOMACROMOLECULES**



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## **PREFACE**

Biomacromolecules are fundamental structural and functional units of cells and therefore are at the very core of biochemical interest. They have always been the central topics of biochemical texts and literature. Various physicochemical and biochemical investigations greatly improve our knowledge of biomacromolecular structures and dynamics. The computational approach provides a new tool for structural and functional explorations of biomolecules. Sequence analyses and genetic recombination studies have contributed to our understanding of how biomacromolecules function at molecular and genetic levels. Recent years have witnessed an explosion in biological data that are derived primarily from studies of biomacromolecules. An application of information technology to organize, manage, distribute and analyze these biomacromolecular data has ushered in the new discipline of bioinformatics. There is an increased interest and sophistication in the study of biomacromolecules, as genomics and proteomics take central stage of biochemistry, molecular biology and bioinformatics. Slowly though, glycomics has now gained recognition. These developments give rise to a necessity for the comprehensive documentation and unified presentation of the structures, functions and informatics of biomacromolecules, for which this book is proposed to address.

Biomacromolecules, including nucleic acids (polynucleotides), proteins (polypeptides) and glycans (polysaccharides), are either briefly treated in the introductory biochemistry texts or extensively described in the advanced monographs concerning individual classes of compounds. In response to the renewed interest in biomacromolecules among various fields of biomedical sciences, a unified and comprehensive presentation of these topics is needed. The proposed textbook is aimed at bridging the gap between the introductory/elementary biochemistry course and advanced treatises on an individual class of biomacromolecules. The focus is on the integrated presentation of the structural, dynamic and informational biochemistry of nucleic acids, proteins and glycans, not separately, but as combined topics so that their similarities can be identified/acknowledged and differences compared/appreciated. The book intends to meet the demands of students who would like to broaden their biochemical knowledge beyond the introductory level and to prepare those who would like to venture into the advanced field of studies in genomics, proteomics and/or glycomics.

I have been teaching Biomacromolecules ever since the course was introduced into our program in 1968, on-and-off (and mostly on) before and after my retirement. Since the inception, the subject matter has undergone amazing transformations; from generally descriptive to molecular details, from mainly structure/function to informatics. The field has grown to encompass a large volume of information that any attempt to cover even the most superficial aspects of the topics in a single text is practically impossible if not a daunting task.

This book is written for students who have taken elementary/introductory biochemistry and would like to take further courses in biochemistry related to special topics in nucleic acids, proteins, and/or polysaccharides. Thus it is designed for students who are familiar with the general aspects of biochemistry and would like to further their

knowledge or for those who contemplate to pursue the field of studies related to biomacromolecules. It serves as an intermediate textbook in biochemistry, molecular biology and bioinformatics. Its content follows the organization of general/introductory biochemistry so that the continuity of biochemical curriculum is preserved; however the focus is on the macromolecular biochemistry. The book is unique in that it treats nucleic acids, proteins and glycans jointly as biomacromolecules and describes their structures, dynamics and informatics together.

Following introductory topics on biomacromolecules (Chapters 1–3), the elements of biomacromolecular structures (Chapters 4–6) and their studies (Chapters 7–9) are presented. The functions of biomacromolecules are discussed in terms of their interactions (Chapter 10), catalyses (Chapter 11) and metabolisms, including genetic transmission and applications (Chapters 12, 13). Biomacromolecular informatics (Chapter 14), namely genomics (Chapter 15), proteomics (Chapter 16) and glycomics (Chapter 16), are introduced. Chapter 18 describes biomacromolecular evolution. Each chapter presents a proper background in structures, dynamics or informatics of biomacromolecules, providing the context for further studies, which is supplemented by a list of references. In the areas where the speed of change and growth is high, a book cannot be either all-inclusive or entirely current. It is especially difficult for an introductory textbook of this nature to cover the topic materials up-to-date and comprehensively. Students are urged to consult the reference materials (literature cited and Web sites) for further understanding.

Balanced approaches include some general descriptions, which have been treated in general biochemistry texts, otherwise serving as introductory to advanced presentations, but however, not dwelling too deeply on the topics of specialized interest. Some materials that are commonly available in general texts are not repeatedly described here so that others may be considered. For example, discussion on the stereochemistry of monosaccharides (Chapter 3), spectral recordings (Chapter 7) and detailed descriptions on physiological functions or transformations of biomacromolecules, are either omitted or briefly mentioned. However, classical approaches of general interest in the study of biomacromolecules are presented, since they may serve as the background knowledge for advancing current understanding. Solid phase synthesis (Chapter 8) used in the fabrication of biochips (Chapter 14), and chemical modification of enzymes (Chapter 11) applied to the design of affinity/activity-based probes (Chapter 16), are some of examples. The choices of materials presented in this text are derived from many years of the author's teaching experience. The author alone is responsible for inadequate and erroneous presentations that may occur and readers' suggestions are very much appreciated.

I would like to thank all authors whose published works have contributed to a better understanding of biomacromolecular biochemistry and formed the resource materials of this textbook. The public accessibility of all the sequences and three-dimensional structures of biomacromolecules has greatly facilitated the advancement of our knowledge for the structure, function and informatics of biomacromolecules. The efforts of all the developers, contributors and managers of many outstanding Web sites of biomacromolecules are most appreciated. The writing of this text would not have been possible without the contributions and generosity of these investigators, authors and developers. My wife, Alice, has been most instrumental in helping me complete this text, which I would like to present to her as a gift on our tetracontyl anniversary. It is my pleasure to state that the realization of this text goes to former Editor, Luna Han and Editorial program coordinator, Kristin Hauser. They have patiently urged me to initiate the project prior to their departure for their new posts. I am grateful to the John Wiley staffs, Ian Collins, Thomas Moore, Dean Gonzalez, and Danielle Lacourciere for their timely help to assist the transformation of this manuscript to be publishable and to oversee the completion of this project.

Retired politicians and celebrities write personal memoirs. Retired entrepreneurs and investors write financial guides. Retired engineers and professionals write how-to or do-it-yourself manuals. Why cannot retired academics write text or reference books of their specialized fields? After many years of teaching and research experience, we certainly have lots to write about. I have taken up this project after my mandatory retirement, not without skeptics. However, I am relieved that I have made it.

C. Stan Tsai (stan@tsai-info.com) Ottawa, Ontario, Canada

# ABBREVIATIONS IN REPETITIVE USE

Some abbreviations that appear in the literature, but are not repeatedly used in this text, are mentioned but not listed here.

1D one-dimensional 2D two-dimensional

2DE two-dimensional electrophoresis

2D-PAGE two-dimensional polyacrylamide gel electrophoresis

3D three-dimensional
 7TM seven transmembrane
 Ψ(I) hydrophobic (interactions)
 A adenosine/adenylate/adenine

A or Ala alanine A or Gal galactose AA Allo A-H

aa-tRNA 3'-O-aminoacyl-tRNA, aminoacyl-tRNA

AB ab initio prediction
ABP activity-based probe
AC accession number
AC adenylyl cyclase

ACR ancient conserved region
AD transcription activation domain

ADEPT antibody-directed enzyme prodrug therapy

AD(T)P adenosine di(tri)phosphate AFBP affinity-based probe

AGE advanced glycated end-product AIF apoptosis inducing factor

AISMAG An Interactive Server-side Molecular Image Generator

ALU arithmetic logic unit AN or GalNAc N-acetylgalactosamine

ANS 8-anilino-1-naphthalene sulfonate

AP apurinic/apyrimidinic

Apaf apoptotic protease activating factor
APC anaphase-promoting complex
aRS aminoacyl-tRNA synthetase

AS active site/s

ASGPR asialoglycoprotein receptor
BCM Baylor College of Medicine
BD DNA-binding domain
BER base excision repair

BFGF basic fibroblast growth factor bgl blood group locus (loci)

## XVIII ABBREVIATIONS IN REPETITIVE USE

BHA benzyhydrylamine

BIND biomolecular interaction network database

BIOS basic input/output system

BLAST Basic Local Alignment Search Tool

BMCD Biological Macromolecular Crystallization Database

BNL Brookhaven National Laboratories

Boc tert-butoxycarbonyl

bp base pair(s)
Bzl benzyl
C cytosine
C or Cys cysteine

CA correspondence analysis

CAD or CID collisionally-activated dissociation or collisionally-induced

dissociation

cAMP 3',5'-cyclic adenosine monophosphate

CAPRI Critical Assessment of Predicted Interactions

CASP Critical Assessment of Techniques for Protein Structure Prediction
CASPER Computer Aided Spectrum Evaluation of Regular Polysaccharides

CATH Class, Architecture, Topology, Homology

CAZYmes carbohydrate active enzymes
CBP CREB binding protein

CBS Center for Biological Sequence Analysis

cc comment

CCDC Cambridge Crystallographic Data Centre

cccDNA covalently closed circular DNA

ccDNA closed circular DNA

CCSD Complex Carbohydrate Structure Database

CD circular dichroism (spectroscopy)

CD cluster of differentiation Cdb cyclin destruction box

CDG congenital disorders of glycosylation

cDNA complementary DNA

CDR complementarity determining region

CDS, cds coding sequence CE cyanoethyl

CERMAV Centre de Recherches sur les Macromolécules Végétales

CFG Consortium for Functional Glycomics

CG cancer gene/s

cGMP 3',5'-cyclic guanosine monophosphate

CICR Ca<sup>2+</sup>-induced Ca<sup>2+</sup>-release
CID collision-induced dissociation

cM centiMorgan

CM comparative (homology) modeling CMD congenital muscular dystrophy

CMR carbon-13 magnetic resonance (spectroscopy)

CNS central nervous system coagF coagulation factor Con A concanavlin A

COSY J correlated spectroscopy

CP chlorophenyl

CPG controlled pore glass
CPK Corey-Pauling-Koltun

CPS carbamyl phosphate synthetase

CPU central processor unit

CRD carbohydrate-recognition domain

CRE(B) cAMP-response element (binding protein)

CSA Catalytic Site Atlas

CSM common structures of monosaccharides

CSS Carbohydrate Structure Suite

CT carbamoyltransferase CT consensus trees/supertrees

CU control unit
Cyt/cyt cytochrome
D dihydrouridine
D or Asp aspartic acid
Da daltons

(d)A (deoxy)adenosine DAG diacylglycerol DB database

DBMS database management system (d)C (deoxy)cytidine/cytidylate dc distance calculation

DCA discriminant correspondent analysis

DCC dicyclohexyl carbodiimide

DCP dichlorophenyl DD death domain

DDBJ DNA Data Bank of Japan DD-PCR differential display PCR

DE description/s

DED death effector domain (d)G (deoxy)guanosine/guanylate

DH dehydrogenase

DIGE difference in-gel electrophoresis

diS disaccharides

DKFZ German Cancer Research Center

DM distance matrix
DMC dichloromethane
DMTr dimethoxy trityl

DNA deoxyribonucleic acid(s)

DNP dinitrophenyl DNS dansyl

dNTP deoxyribonucleotide-5'-triphosphate

Dol dolichol

dosDNA defined ordered DNA sequences DPO dolichol phosphate-oligosaccharide

DP degree of polymerization
DP dolichol pyrophosphate
DR database cross-reference/S
dsDNA double-stranded DNA

DSS sodium 2,2-methyl-2-silapentane-5-sulfonate

DT date of entry
DTT dithiothreitol
E or Glu glutamic acid
EA enzyme-substrate

EBI European Bioinformatics Institute

EC Enzyme Commission

ECOTL Erythrina corallodendron lectin EDTA ethylenediamine tetraacetate

EF electrofocusing

EFF/FF empirical force field/force field EGF epidermal growth factor

EGFR epidermal growth factor receptor

EGP epidermal growth factor Eif eukaryotic initiation factor

EMBL European Molecular Biology Laboratory
EMBnet European Molecular Biology network

EMin energy minimization
EP enzyme-product
EP eukaryotic primase

EPD eukaryotic promoter database EPL expressed protein ligation ER endoplasmic reticulum

ERK extracellular signal regulated protein kinase

ESI electrospray ionization ESP electrostatic potential EST expressed sequence tag

ExPASy Expert Protein Analysis System

F or Phe phenylalanine

FAB fast atom bombardment
FAD flavin adenine dinucleotide
FaPy formamidopyrimidine
FB(M) fragment-based (method)

FF force field

FG functional genomics
fibF fibrinolytic factor
FID free induction decay
FITC fluorescein isothiocyanate

FMN/FAD flavin mononucleotide/flavin adenine dinucleotide

Fmoc fluorenyl-9-methyloxycarbonyl

FP fingerprint/s
FP fluorescent probe
FR fold recognition

FSSP fold tree, domain dictionary, sequence neighbors, structure

superposition

FT feature/s
FT feature table
FT Fourier transform
FTP file transfer protocol

G general

G guanosine/guanine

G or Glc glucose G or Glv glycine

GA genetic algorithms wheat germ agglutinin GA Gaba γ-aminobutyric acid

**GAP** GTPase activating proteins

glycosidase Gase

**GAT** glutamine amidotransferase

Gbp (giga)-base pairs **GBP** glycan binding proteins GC gas chromatography GD(T)P guanosine di(tri)phosphate

GE gel electrophoresis GE gene expression

**GEF** guanine nucleotide exchange **GIF** graphical interchange format

Gla y-carboxyglutamate

Glc **D-Glucose** 

GlcNacT GlcNAc transferase GN or GlcNAc N-acetylglucosamine

GN gene name GO gene ontology

GOA Gene Ontology Annotation **GOR** Garnier, Osguthorpe and Robson

GP genome project(s)

grid point gp

**GP** glycogen phosphorylase **GPa** phospho-phosphorylase a **GPb** dephospho-phosphorylase b **GPCR** G-protein-coupled receptor **GPI** glycosylphosphotidylinositol

GR glutathine reductase

**GRE** glucocorticoid response element

GSS genome survey sequence GTglycosylation pathways GT glycosyltransferase(s) **GTO** Gaussian type orbitals **GUI** graphical user interface

H or His histidine

HB hydrogen bond(s)

hCG human chorionic gonalotropin

hd helical domain **HDV** hepatitis delta virus

**HEMPAS** hereditary erythroblastic multinuclearity with positive acidified-serum

lysis test

**HGP** Human Genome Project HisF histidine biosynthetic enzyme HIV human immunodeficiency virus

HMhistogram matching **HMM** hidden Markow model

## **XXII** ABBREVIATIONS IN REPETITIVE USE

hnRNA heterogeneous nuclear RNA

hnRNP heterogeneous nuclear ribonucleoprotein

HPLC high performance (high-pressure) chromatography HrPAGE high-resolution polyacrylamide gel electrophoresis

HSE heat shock element HSP heat-shock protein HSP high-scoring pair

HTML HyperText Markup Language

HTPC high-throughput protein crystallography

HTS high-throughput screening

hs heparan sulfate

HTTP HyperText Transfer Protocol

Hyl (Hk) hydroxylysine
Hx hypoxanthine
Hyp (hP) hydroxyproline
I invariant method
I or Ile isoleucine

ICAT isotope-coded affinity tag

ID Identifier

IEF isoelectric focusing
Ig immunoglobulin
IgG immunoglobulin G

IGOT isotope-coded glycosylation-site-specific tagging

IL interleukin

IMAC immobilized metal affinity chromatography

IMP inosine monophosphate
InDel(s) insertion(s) and/or deletion(s)

INSDC International Nucleotide Sequence Database Collaboration

insR insulin receptor
IP Internet Protocol
IP inositol phosphate

IPCR immuno-polymerase chain reaction

**IPG** immobilized pH gradient **IPI** International Protein Index **IPL** intein-mediated protein legation IP<sub>3</sub>R inositol triphosphate receptor IR infrared (spectroscopy) IR instruction register IS insertion sequence **ISOC** Internet society

ISP Internet service provider

ISREC Swiss Institute for Experimental Cancer Research

IUBMB International Union of Biochemistry and Molecular Biology

IUPAC International Union of Pure and Applied Chemistry

IVS intervening sequence(s), intron(s)
JPEG joint photographic experts group

K or Lys lysine

Kb thousand base-pairs Kbp kilo base-pairs

KcaM KEGG Carbohydrate Matcher

kDa Kilo Daltons

KEGG Kyoto Encyclopedia of Genes and Genomes KF-Pol I Klenow fragment of DNA polymerase I

KW keyword L or Leu leucine

LAN local area network
LC liquid chromatography
LCD liquid crystal display
LDH lactate dehydrogenase
LFA Limax flavus agglutinin

LINE long interspersed nuclear element

LINUCS linear notation for unique description of carbohydrate sequence

LOL Lathyrus ochrus lectin

M or Man mannose
M or Met methionine
MA microarray

MAA *Maackia amurensis* agglutinin MAG myelin-associated glycoprotein

MALDI matrix-assisted laser desorption/ionization

MAP mitogen activated protein
MAP-KKK MAP kinase-kinase-kinase
MAR memory address register
MAS maskless array synthesizer

Mb million base-pairs
Mbp (mega)-base pairs
MBP mannose binding protein
MBR memory buffer register
MC Monte Carlo method

MC-SYM macromolecular conformations by symbolic programming

MD mutation data

MEK MAP (mitogen activated protein) kinase-ERK kinase

MeNPOC mehylnitropiperonyloxycarbonyl MHC major histocompatibility complex

MI metastable ion

MIME multipurpose Internet mail extensions
MIP molecularly imprinted polymer

MIPS Munich Info Center for Protein Sequences

miRNA microRNA

ML maximum likelihood MLCK myosin light chain kinase MM molecular mechanics

MMDB molecular modeling database

MMTr monomethoxy trityl
MO molecular orbital(s)
MolD molecular dynamics
momoS monosaccharides

MPB mannose binding protein

MPP mitochondrial processing peptidase

mPu/Py methylpurin/pyrimidine MRE metal response element

## XXIV ABBREVIATIONS IN REPETITIVE USE

mRNA messenger RNA

MRW mean residue weight of monomer

mp matching point
MS mass spectrometry
ms mean-square

MS-MS tandem mass spectrometry
MSP maximal-scoring segment pair/s

m.u. mass unit/s

MW molecular weight m/z mass-to-charge ratio

N or Asn asparagine N or Neu neuramic acid

NAC nascent polypeptide-associated complex NAD(P)<sup>+</sup> nicotinamide adenine dinucleotide (phosphate)

NAD(P)H reduced nicotinamide adenine dinucleotide (phosphate)

NAPPA nucleic acid programmable protein array

NAT natural antisense transcript

NBRF National Biomedical Research Foundation NCBI National Center for Biotechnology Information

NCS noncrystallographic symmetry

ncRNA noncoding RNA
NDB Nucleic Acid Database
NDP nucleoside diphosphates
NER nucleotide excision repair

NeuNAc or Sia N-acetylneuramic acid or sialic acid NGF(R) nerve growth factor (receptor)
NIH National Institute of Health
NJ neighbor joining method

NK natural killer

NLM National Library of Medicine NMD nonsense-mediated mRNA decay

NMR nuclear magnetic resonance (spectroscopy)

NOE nuclear Overhauser effect

NOESY nuclear Overhauser effect and exchange spectroscopy

NOS nitric oxide synthase NPG nucleotide phosphoglycose

NR non-reducing NR non-redundant

nrPTK non-receptor protein tyrosine kinase

nt nucleotide(s)

Nvoc 6-nitroveratryloxycarbonyl

NW network

OC organism classification

oligoS oligosaccharides

ORD optical rotatory dispersion (spectroscopy)

ORF open reading frame

OUT operational taxonomic unit

OS operating system OS organism species

OST oligosaccharyltransferase

XXV

OUT operational taxonomic unit/s

P parsimony P or Pro proline

PABA poly(A) binding protein

PAGE polyacrylamide gel electrophoresis

PAM phenylacetamidomethyl PAM point accepted mutation PC personal computer

PCA principle component analysis PCD programmed cell death

PCNA proliferating cell nuclear antigen PCR polymerase chain reaction

PD pyrimidine dimer PDB Protein Data Bank

PDC pyruvate dehydrogenase complex PDGF platelet derived growth factor

PDP pyruvate dehydrogenase phosphatase

PEG polyethylene glycol

PEP primer extension preamplification

Perl Practical Extraction and Report Language

PEST glutamic acid, serine and threonine

PEG polyethylene glycol

PFGE pulsed field gel electrophoresis
PEP primer extension preamplification

PFK phosphofructokinase

PGGF platelet derived growth factor

PHP Pyrococcus horikoshii

PHYLIP Phylogenetic Inference Package

PIC phenyl isocyanate

PID phosphotyrosine interaction domain PIR Protein Information Resource

PITC phenyl isothiocyanate

pk psudoknot
PKA protein kinase A
PKC protein kinase C
PL phospholipase
PLC phospholipase C
PLD phospholipase D
PLP pyridoxal-5'-phosphate

PMR proton magnetic resonance (spectroscopy)
phosphorus magnetic resonance spectroscopy

PMSF phenylmethylsulfonyl fluoride

PMW position weight matrix PNGF peptide-N-glycosidase F

Pol DNA polymerase poly(DA) poly(deoxyadenylate)

poly(dG-dC) poly(deoxyguanidylate-deoxycytidylate)

poly(U) poly(uridylate)
ppm parts per million
PPP point-to-point protocol