

Advances in Structural Biology

Applications in Protein Structure, Function, and Disease

EDITED BY **Anas Shamsi • Imtaiyaz Hassan • Moyad Shahwan • Belgin Sever**



Advances in Structural Biology

This page intentionally left blank

Advances in Structural Biology

Applications in Protein Structure,
Function, and Disease

Edited by

ANAS SHAMSI

Centre of Medical and Bio-allied Health Sciences Research,
Ajman University, Ajman, United Arab Emirates

IMTAIYAZ HASSAN

Center for Interdisciplinary Research in Basic Sciences, Jamia Millia
Islamia, New Delhi, India

MOYAD SHAHWAN

College of Pharmacy and Health Sciences, Ajman University,
Ajman, United Arab Emirates

BELGIN SEVER

Department of Pharmaceutical Chemistry, Anadolu University,
Eskişehir, Türkiye



ACADEMIC PRESS

An imprint of Elsevier

Academic Press is an imprint of Elsevier
125 London Wall, London EC2Y 5AS, United Kingdom
50 Hampshire Street, 5th Floor, Cambridge, MA 02139, United States

Copyright © 2027 Elsevier Inc. All rights are reserved, including those for text and data mining, AI training, and similar technologies.

For accessibility purposes, images in electronic versions of this book are accompanied by alt text descriptions independently provided by Elsevier, generated with the aid of AI. For more information, see <https://www.elsevier.com/about/accessibility> or Radarweg 29, 1043 NX Amsterdam, Netherlands.

Books and Journals published by Elsevier comply with applicable product safety requirements. For any product safety concerns or queries, please contact our authorised representative, Elsevier B.V., at productsafety@elsevier.com.

Publisher's note: Elsevier takes a neutral position with respect to territorial disputes or jurisdictional claims in its published content, including in maps and institutional affiliations.

No part of this publication may be reproduced or transmitted in any form or by any means, electronic or mechanical, including photocopying, recording, or any information storage and retrieval system, without permission in writing from the publisher. Details on how to seek permission, further information about the Publisher's permissions policies and our arrangements with organizations such as the Copyright Clearance Center and the Copyright Licensing Agency, can be found at our website: www.elsevier.com/permissions.

This book and the individual contributions contained in it are protected under copyright by the Publisher (other than as may be noted herein).

Notices

Knowledge and best practice in this field are constantly changing. As new research and experience broaden our understanding, changes in research methods, professional practices, or medical treatment may become necessary.

Practitioners and researchers must always rely on their own experience and knowledge in evaluating and using any information, methods, compounds, or experiments described herein. In using such information or methods they should be mindful of their own safety and the safety of others, including parties for whom they have a professional responsibility.

To the fullest extent of the law, neither the Publisher nor the authors, contributors, or editors, assume any liability for any injury and/or damage to persons or property as a matter of products liability, negligence or otherwise, or from any use or operation of any methods, products, instructions, or ideas contained in the material herein.

ISBN: 978-0-443-44988-8

For Information on all Academic Press publications
visit our website at <https://www.elsevier.com/books-and-journals>

Publisher: Megan Ball
Acquisitions Editor: Michelle Fisher
Editorial Project Manager: Harshita Bathla
Production Project Manager: Vijayaraj Purushothaman
Cover Designer: Mark Rogers

Printed in England by CPI Group (UK) Ltd
Croydon CR0 4YY
United Kingdom

Typeset by MPS Limited, Chennai, India



Contents

<i>List of contributors</i>	xv
<i>About the editors</i>	xxi
<i>Acknowledgments</i>	xxiii

Section I Foundations: computational and conceptual

1. Unraveling protein function with structural biology approaches	3
Sana Qausain, Mohd Basheeruddin, Ashish Anjankar, Md. Khurshid A. Khan, Faez Iqbal Khan, Archana Dhok, Mohammad Affan Kareem and Netri Upadhyay	
1.1 Introduction	3
1.2 Protein structure as a dynamic hierarchy	5
1.3 Experimental approaches in structural biology	6
1.4 Computational and integrative approaches	10
1.5 Structural insights into protein function	13
1.6 Emerging paradigms and limitations of structure-function relationships	16
1.7 Translational applications of structural biology	20
1.8 Recent advances and future perspectives in structural biology	22
1.9 Conclusion	24
References	26
2. Bioinformatics tools for protein modeling in neurodegenerative diseases	31
Shubhi Singh, Rudrani Rath, Sushma Jeyaraj, Aysha Afreen Rafeek and Priya Swaminathan	
2.1 Introduction	31
2.2 Protein modelling approaches: foundations and methodologies	32
2.3 Computational tools for protein modelling	37
2.4 Tool selection criteria for neurodegenerative disease research	41
2.5 Case studies: protein modelling in specific neurodegenerative diseases	41
2.6 Molecular docking and dynamics	44
2.7 Protein structure refinement	49
2.8 Challenges and limitations	52
2.9 Future perspectives and emerging technologies	53
2.10 Conclusion	54
References	55

3. Bioinformatics tools for protein modeling in cancer	59
Alpana Srishti Rai, Seneha Santoshi and Shazia Rashid	
3.1 Introduction	59
3.2 The evolving landscape of protein structure prediction	60
3.3 Bioinformatics tools for protein modeling	67
3.4 Key applications in cancer biology and therapeutics	78
3.5 Current challenges and methodological limitations	80
3.6 Future research outlook	81
3.7 Conclusion	82
References	82
4. Unraveling protein folding and structural dynamics	85
Faiza Iram, Ayesha Aiman, Luqman Ahmad Khan and Asimul Islam	
4.1 Introduction	85
4.2 Protein folding problem	87
4.3 Thermodynamics and kinetics of protein folding	88
4.4 The energy landscape of protein folding	90
4.5 Protein dynamics: motion and function	93
4.6 Experimental and computational approaches to study protein folding and dynamics	93
4.7 Protein misfolding, aggregation, and disease	100
4.8 Conclusion and future perspectives	100
References	101
 Section II Methodologies: experimental and integrative techniques	
5. Cryo-electron microscopy in membrane protein structural biology	113
Tofayel Ahmed, Antara Saha and Debalaya Mukherjee	
5.1 Introduction	113
5.2 Transient receptor potential channels	116
5.3 Potassium (K^+) channels	118
5.4 Gamma-aminobutyric acid type A receptors, 5-HT _{3A} , and glycine receptors	122
5.5 Ion channel complexes from a native source	124
5.6 G-protein coupled receptors	125
5.7 Bacterial secretion systems	128
5.8 NADH:ubiquinone oxidoreductase (complex I)	130
5.9 ATP synthase	132
5.10 Conclusion	134

Acknowledgements	135
Conflict of interests	135
References	135
6. Computational and artificial intelligence methodologies for big data analytics in structural biology	145
Mohammad Kalim Ahmad Khan, Umme Aiman and Salman Akhtar	
6.1 Introduction	145
6.2 Sources and types of biological big data	149
6.3 Characteristics of biological big data	156
6.4 Computational methodologies for big data analytics	159
6.5 Applications in structural biology and bioinformatics	163
6.6 Case studies	174
6.7 Future directions and emerging trends in integrative drug discovery	179
6.8 Future directions	182
6.9 Conclusion	185
Acknowledgments	185
References	185
7. Big data enabled discovery in bioinformatics and structural biology	193
Jaoud Ansari, Shabana Khatoon, MD Kaif, Gourav Choudhir, Naseem Gaur and Asimul Islam	
List of abbreviations	193
7.1 Introduction	194
7.2 Types of big data in structural biology and bioinformatics	195
7.3 Challenges in big data analytics	199
7.4 Analytical techniques and tools for structural biology big data	203
7.5 Machine learning and artificial intelligence	211
7.6 Applications of big data analytics	216
7.7 Conclusions	218
References	218
8. AI and machine learning in structural biology	229
Sanjay Kumar	
8.1 Introduction	229
8.2 Fundamentals of artificial intelligence in structural biology	231
8.3 How artificial intelligence works	235
8.4 How to create an artificial intelligence model?	237
8.5 Landmark breakthroughs	238

8.6	Artificial intelligence applications in structural biology	244
8.7	Challenges and limitations	247
8.8	Future directions	248
8.9	Conclusion	248
	References	249
9.	Integrating structural and omics data for drug discovery	253
	Neha and Khushi Raza	
	List of abbreviations	253
9.1	Introduction	253
9.2	Structural biology technologies and their applications	259
9.3	Omics technologies: comprehensive molecular profiling through integrated data layers	261
9.4	Computational frameworks for data integration	265
9.5	Network-guided target selection and iterative lead optimization	268
9.6	Personalized medicine and precision drug discovery: from population-level therapeutics to patient-specific treatment	271
9.7	Technical challenges and limitations	273
9.8	Conclusion and future directions	275
	Acknowledgment	276
	Conflict of interest	276
	Compliance with ethical standards	276
	References	276
Section III	Applications	
10.	Applications of structural biology in drug discovery	287
	Saira Hamid, Sarah Siddiquah, Hanzla Shaz and Imtaiyaz Hassan	
10.1	Introduction	287
10.2	Fundamental techniques of structural biology used in drug discovery	288
10.3	Role of structural biology across drug design	294
10.4	Understanding drug-target interactions	298
10.5	Structural biology in studying drug resistance	301
10.6	Applications in biologics and macromolecular drugs	303
10.7	Integration with computational and AI-based approaches	305
10.8	Case studies in structure-guided drug discovery	307
10.9	Challenges and limitations	310
10.10	Future perspectives	311
	AI disclosure	311
	References	311

11. Structural biology approaches in vaccine development 319**Aaliya Taiyab and Imtaiyaz Hassan**

11.1	Introduction	319
11.2	Structural biology tools used in vaccine development	322
11.3	Structural biology in identifying vaccine targets	326
11.4	Structure-based antigen design/reverse vaccinology 2.0	328
11.5	Epitope-focused vaccine design	330
11.6	Nanoparticle-based vaccines designed using structural biology	332
11.7	Computational integration in structural vaccine design	334
11.8	Challenges and future perspectives	336
11.9	Conclusions	338
	References	338

12. Structural biology in antiviral drug design 343**Sana Tanweer, Sanchit Varma and Malika Adam Abeeda**

12.1	Introduction	343
12.2	Fundamentals of structural biology in drug design	344
12.3	Viral entry and immune response	345
12.4	Immune evasion by viruses	347
12.5	Antiviral drugs and their classification	348
12.6	Antiviral drug development and target identification	348
12.7	Antiviral drug targets	348
12.8	Target identification and selection	353
12.9	In silico techniques for synthesis of candidate drugs	354
12.10	Computer aided structure based drug design	355
12.11	Structural mapping methods	359
12.12	X-ray crystallography	359
12.13	Nuclear magnetic resonance Spectroscopy	361
12.14	Cryo-electron microscopy	364
12.15	Drugs developed by structure-based drug design	366
12.16	Structure-based drug design for antivirals against HIV	366
12.17	Structure-based drug design for antivirals against hepatitis B	366
12.18	Structure-based drug design for antivirals against influenza	368
12.19	Structure-based drug design for SARS-CoV-2 antivirals	368
12.20	Advantages of structural-based drug design	369
12.21	Disadvantages of structural-based drug design	369
12.22	Challenges and limitations	370
12.23	Prospects for the future and global health readiness	371

12.24	Conclusion	371
	References	372
13.	Structural bioinformatics in personalized medicine	381
	Sarika Bano, Aaliya Javed, Anas Shamsi and Asimul Islam	
13.1	Introduction	381
13.2	Personalized medicine and structural medicine: introduction	382
13.3	Significance of structural bioinformatics and PM	383
13.4	Bioinformatics steps in genomic data processing for PM	384
13.5	Application of structural bioinformatics in PM and vaccine development	386
13.6	Genomic analysis in PM	387
13.7	Challenges in incorporating structural bioinformatics into PM design	388
13.8	Advantages and disadvantages of PM	389
13.9	Advancement in methods for PM development	390
13.10	Future perspective	391
13.11	Conclusion	392
	References	392
14.	Structural biology in understanding bacterial resistance	397
	Deepali Gupta, Mukesh Kumar, Dominic Skaria Mathew, Ishaan Bhardwaj, Shivani Dixit and Punit Kaur	
14.1	Introduction	397
14.2	Molecular mechanism underlying antimicrobial resistance	398
14.3	Structure biology approaches to study antimicrobial resistance	400
14.4	Structural basis of major antimicrobial resistance mechanism	400
14.5	Advanced structural and computational approaches for understanding antimicrobial resistance	413
14.6	Future perspectives	416
14.7	Conclusion	416
	AI disclosure	417
	References	417
15.	Structural biology approaches in neurodegeneration and aging	423
	Minhal Abidi, Sana Iram, Jamal-E -Fatima, Hamda Khan, Shaheda Perween, Safia Habib and Moinuddin	
15.1	Introduction: aging and neurodegeneration—a structural view	423
15.2	Molecular pathways of protein misfolding and aggregation during aging of the brain	426

15.3	Mitochondrial dysfunction and oxidative stress structural biology	431
15.4	Cell and structural mechanisms of synaptic degeneration	436
15.5	Role of posttranslational modifications in structural alterations	441
15.6	Interplay of proteostasis, autophagy, and neuroinflammation	446
15.7	Computational approaches and integrative structural biology	449
15.8	Translational implications: structural insights to therapeutic development	452
15.9	Novel horizons: structural biomarkers and interventions to aging	455
15.10	Conclusions and perspectives	457
	References	458

16. Structural biology of protein misfolding and aggregation: from disease to therapeutic innovations 471

Neha Kausar Ansari and Aabgeena Naeem

16.1	Introduction	471
16.2	Structural determinants of protein misfolding and aggregation	472
16.3	Mechanism of misfolding and aggregation	475
16.4	Molecular and cellular consequences	481
16.5	Structural themes for protein aggregation diseases	487
16.6	Disease-specific structural themes	489
16.7	Therapeutic and structural modulation strategies	494
16.8	Conclusions	497
	Acknowledgments	497
	Conflict of interest	498
	References	498

17. Integrated structural approaches in immunotherapy 513

Hamda Khan, Minhal Abidi, Safia Habib, Arbab Husain, Afreen Khanam, Rizwan Ahmad, Mohd Mustafa and Moinuddin

17.1	Immunotherapy	513
17.2	Mechanism of cancer immunotherapy	514
17.3	Immune checkpoint inhibitors	515
17.4	Monoclonal antibodies and cancer therapy	518
17.5	Chimeric antigen receptor T cell in cancer therapy	520
17.6	Viro immunotherapy in cancer therapy	522
17.7	Cytokines and immune modulators in cancer therapy	523
17.8	Cancer Immunotherapy targeting glycation	524
17.9	Glycosylation and cancer immunotherapy	526
17.10	Conclusion	527
	References	527

Section IV Translational biology

18. Structural and systems biology in cancer therapy 535

Mohd Basheeruddin, Sana Qausain, Ashish Anjankar, Faez Iqbal Khan,
Samarth Shukla, Shazia Jamal, Neesar Ahmed, Vaibhav Anjankar,
Zahoor Ahmad Parray and Netri Upadhyay

18.1	Introduction	535
18.2	Foundations of structural biology in cancer research	542
18.3	Omics integration	550
18.4	Computational modeling and dynamic simulations	558
18.5	Convergence of structural and systems biology	560
18.6	Structural systems pharmacology	562
18.7	Illustrative examples	565
18.8	Applications in cancer therapy	567
18.9	Future direction and potential role of artificial intelligence	573
18.10	Conclusion	574
	References	575

19. Protein structural biology in precision medicine and clinical translation 583

Maryam Khan, Minal Richi and Sara Othman

	List of abbreviations	583
19.1	Introduction	583
19.2	Structural basis of protein dysfunction in disease	589
19.3	Protein structure-guided drug discovery	592
19.4	Translational and clinical applications	595
19.5	Conclusion and future direction	602
	Contributions	603
	Conflict of Interest	603
	References	603

20. Future trends in structural biology 613

Saleha Anwar, Sumaiya Khan, Sahar Afzal Khan, Khuzin Dinislam, Suhel Parvez and Anas Shamsi

20.1	Introduction	613
20.2	Advancements in hybrid and integrative structural biology	615
20.3	Mass spectrometry	624
20.4	Structural biology as a foundation for translational research	627
20.5	Structure-guided therapeutics and drug discovery	631
20.6	New paradigms in fragment-based and allosteric drug discovery	635

20.7	Structural biology in vaccine and antiviral design	637
20.8	Structural systems biology and network modeling	637
20.9	Conclusions	640
	Acknowledgement	641
	References	641

<i>Index</i>	<i>651</i>
--------------	------------

CHAPTER 6

Computational and artificial intelligence methodologies for big data analytics in structural biology

Mohammad Kalim Ahmad Khan, Umme Aiman, and Salman Akhtar

Department of Bioengineering, Integral University, Lucknow, Uttar Pradesh, India

6.1 Introduction

The explosive growth of high-throughput biological technologies has deeply impacted the life sciences world, making it a data-intensive field. Modern platforms such as next-generation sequencing (NGS), cryo-electron microscopy (cryo-EM), high-resolution mass spectrometry (MS), and large-scale interactomes have been capable of generating enormous genomic, transcriptomic, proteomic, structural, and imaging datasets at extremely high speeds and scales (Park et al., 2021). As a result, there have been major analytical and computational challenges, primarily in the domain of structural biology and bioinformatics, where comprehending the functional, structural, and evolutionary impact of these data requires the use of advanced computational methods. The biological data have several core features, such as their massive scale, high throughput, natural heterogeneity, a high degree of uncertainty, and the need for biological significance. These features call for the creation of strong analytical frameworks that can connect different types of data, reduce noise, guarantee reproducibility, and yield biologically meaningful results (Auslander et al., 2021).

Biomedical major repositories are a good example of exponential data growth due to multimodality and strong dependence on biological context. Protein sequences, three-dimensional structures, and multiomics profiles ought to be processed using computational strategies that handle the noise and enable reproducible inference. The enormous growth of protein sequences illustrated in Figs. 6.1, 6.2, and 6.3 demonstrates that current sequencing technologies consistently outperform traditional computational pipelines.

Conventional computer-based methods or heuristic computational approaches have had a hard time trying to address these challenges at scale. To address this gap, machine learning (ML), deep learning (DL), and advanced statistical modeling frameworks have gradually become the main tools and emerged as central pillars of modern structural biology. DL has brought about a significant change in structural biology (Cui et al.,