

# BS2520: Protein Structure and Function

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Ajit Varki, Cummings, R.D. and Esko, J.D. (2015) *Essentials of Glycobiology*. Cold Spring Harbor Laboratory Press. Available at: <https://www.ncbi.nlm.nih.gov/books/NBK310274/>.

Anatrace (no date) 'Detergents and Their Uses in Membrane Protein Science'. Available at: <https://www.anatrace.com/Technical-Documentation/Catalogs/Anatrace-Detergents-Booklet-FINAL>.

Bazan, J., Całkosiński, I. and Gamian, A. (2012) 'Phage Display - a Powerful Technique for Immunotherapy', *Human Vaccines & Immunotherapeutics*, 8(12), pp. 1817-1828. Available at: <https://doi.org/10.4161/hv.21703>.

Berg, J.M. et al. (2015a) *Biochemistry*. Eighth edition. New York: W.H. Freeman & Company, a Macmillan Education Imprint.

Berg, J.M. et al. (2015b) *Biochemistry*. Eighth edition. New York: W.H. Freeman & Company, a Macmillan Education Imprint.

Berg, J.M. et al. (2015c) *Biochemistry*. Eighth edition. New York: W.H. Freeman & Company, a Macmillan Education Imprint.

Berg, J.M. et al. (2015d) *Biochemistry*. Eighth edition. New York: W.H. Freeman & Company, a Macmillan Education Imprint.

Berg, J.M. et al. (2015e) *Biochemistry*. Eighth edition. New York: W.H. Freeman & Company, a Macmillan Education Imprint.

Berg, J.M., Tymoczko, J.L. and Stryer, L. (2001) *Biochemistry*. 5th Edition. New York: W. H. Freeman and Co.

Betts, M.J. and Russell, R.B. (2003) 'Amino Acid Properties and Consequences of Substitutions', in *Bioinformatics for Geneticists*. Chichester, West Sussex, England: Wiley, pp. 289-316.

Binz, H.K., Amstutz, P. and Plückthun, A. (2005) 'Engineering Novel Binding Proteins From Nonimmunoglobulin Domains', *Nature Biotechnology*, 23(10), pp. 1257-1268. Available at: <https://doi.org/10.1038/nbt1127>.

'Biological Buffers' (2008). AppliChem. Available at: <https://www.applichem.com/fileadmin/Broschueren/BioBuffer.pdf>.

BLAST (no date). Available at: <http://www.uniprot.org/blast/>.

BLAST: Basic Local Alignment Search Tool (no date a). Available at:  
<http://blast.ncbi.nlm.nih.gov/Blast.cgi>.

BLAST: Basic Local Alignment Search Tool (no date b). Available at:  
<http://blast.ncbi.nlm.nih.gov/Blast.cgi>.

Bordo, D. and Argos, P. (1991) 'Suggestions for "Safe" Residue Substitutions in Site-Directed Mutagenesis', *Journal of Molecular Biology*, 217(4), pp. 721–729. Available at: [https://doi.org/10.1016/0022-2836\(91\)90528-E](https://doi.org/10.1016/0022-2836(91)90528-E).

Buchanan, A. et al. (2012) 'Improved Drug-Like Properties of Therapeutic Proteins by Directed Evolution', *Protein Engineering Design and Selection*, 25(10), pp. 631–638. Available at: <https://doi.org/10.1093/protein/gzs054>.

Cabrita, L.D., Dobson, C.M. and Christodoulou, J. (2010) 'Protein Folding on the Ribosome', *Current Opinion in Structural Biology*, 20(1), pp. 33–45. Available at: <https://doi.org/10.1016/j.sbi.2010.01.005>.

Cohen, B.I., Presnell, S.R. and Cohen, F.E. (1993) 'Origins of Structural Diversity Within Sequentially Identical Hexapeptides', *Protein Science: A Publication Of The Protein Society*, 2(12), pp. 2134–2145. Available at: <https://doi.org/10.1002/pro.5560021213>.

Daugherty, P.S. (2007) 'Protein Engineering With Bacterial Display', *Current Opinion in Structural Biology*, 17(4), pp. 474–480. Available at: <https://doi.org/10.1016/j.sbi.2007.07.004>.

Dobson, C.M. (2001) 'The Structural Basis of Protein Folding and Its Links With Human Disease', *Philosophical Transactions of the Royal Society B: Biological Sciences*, 356(1406), pp. 133–145. Available at: <https://doi.org/10.1098/rstb.2000.0758>.

Eddy, S.R. (2004) 'Where Did The BLOSUM62 Alignment Score Matrix Come From?', *Nature Biotechnology*, 22(8), pp. 1035–1036. Available at: <https://doi.org/10.1038/nbt0804-1035>.

ExpASy BLAST form (no date). Available at: <http://web.expasy.org/blast/>.

ExpASy: SIB Bioinformatics Resource Portal - Resources (no date). Available at: <http://www.expasy.org/resources>.

Fersht, A. (1999) *Structure and Mechanism in Protein Science: A Guide to Enzyme Catalysis and Protein Folding*. New York: W. H. Freeman.

Furukawa, H. et al. (2005) 'Subunit Arrangement and Function in NMDA Receptors', *Nature*, 438(7065), pp. 185–192. Available at: <https://doi.org/10.1038/nature04089>.

Genesilico Metaserver - meta2 (no date). Available at: <https://genesilico.pl/meta2/>.

Gershenson, A. and Gierasch, L.M. (2011) 'Protein Folding in the Cell: Challenges and Progress', *Current Opinion in Structural Biology*, 21(1), pp. 32–41. Available at:

<https://doi.org/10.1016/j.sbi.2010.11.001>.

GlycomeAtlas V5 (no date). Available at:  
<http://rings.t.soka.ac.jp/GlycomeAtlasV5/index.html>.

Griffiths, A.D. (2003) 'Directed Evolution of an Extremely Fast Phosphotriesterase by in Vitro Compartmentalization', *The EMBO Journal*, 22(1), pp. 24–35. Available at:  
<https://doi.org/10.1093/emboj/cdg014>.

Hammer, S.C., Knight, A.M. and Arnold, F.H. (2017) 'Design and Evolution of Enzymes for Non-Natural Chemistry', *Current Opinion in Green and Sustainable Chemistry*, 7, pp. 23–30. Available at: <https://doi.org/10.1016/j.cogsc.2017.06.002>.

Hartl, F.U., Bracher, A. and Hayer-Hartl, M. (2011) 'Molecular Chaperones in Protein Folding and Proteostasis', *Nature*, 475(7356), pp. 324–332. Available at:  
<https://doi.org/10.1038/nature10317>.

Heim, R. and Tsien, R.Y. (1996) 'Engineering Green Fluorescent Protein for Improved Brightness, Longer Wavelengths and Fluorescence Resonance Energy Transfer', *Current Biology*, 6(2), pp. 178–182. Available at: [https://doi.org/10.1016/S0960-9822\(02\)00450-5](https://doi.org/10.1016/S0960-9822(02)00450-5).  
Hellinga, H.W. and Marvin, J.S. (1998) 'Protein Engineering and the Development of Generic Biosensors', *Trends in Biotechnology*, 16(4), pp. 183–189. Available at:  
[https://doi.org/10.1016/S0167-7799\(98\)01174-3](https://doi.org/10.1016/S0167-7799(98)01174-3).

Home - Protein - NCBI (no date). Available at: <http://www.ncbi.nlm.nih.gov/protein>.

Home - PubMed - NCBI (no date). Available at: <http://www.ncbi.nlm.nih.gov/pubmed>.

Hou, J. et al. (2005) 'From the Cover: Global Mapping of the Protein Structure Space and Application in Structure-Based Inference of Protein Function', *Proceedings of the National Academy of Sciences*, 102(10), pp. 3651–3656. Available at:  
<https://doi.org/10.1073/pnas.0409772102>.

Hovmöller, S., Zhou, T. and Ohlson, T. (2002a) 'Conformations of Amino Acids in Proteins', *Acta Crystallographica Section D Biological Crystallography*, 58(5), pp. 768–776. Available at: <https://doi.org/10.1107/S0907444902003359>.

Hovmöller, S., Zhou, T. and Ohlson, T. (2002b) 'Conformations of Amino Acids in Proteins', *Acta Crystallographica Section D Biological Crystallography*, 58(5), pp. 768–776. Available at: <https://doi.org/10.1107/S0907444902003359>.

Jacobson, R.H. et al. (1999) 'Structure of a Stabilizing Disulfide Bridge Mutant That Closes the Active-Site Cleft of T4 Lysozyme', *Protein Science*, 1(1), pp. 46–57. Available at:  
<https://doi.org/10.1002/pro.5560010106>.

Johnson, S. and Scott, J. (2014) *Study and Communication Skills for the Biosciences*. Second edition. Oxford: Oxford University Press.

Jung, H.-I., Cooper, A. and Perham, R.N. (2002) 'Identification of Key Amino Acid Residues in the Assembly of Enzymes into the Pyruvate Dehydrogenase Complex of : A Kinetic and Thermodynamic Analysis', *Biochemistry*, 41(33), pp. 10446–10453.

Available at: <https://doi.org/10.1021/bi020147y>.

Komar, A.A. (2018) 'Unraveling Co-Translational Protein Folding: Concepts and Methods', *Methods*, 137, pp. 71–81. Available at: <https://doi.org/10.1016/j.ymeth.2017.11.007>.

Korczyński, A.D. (no date) 'Chapter 4: Human Prion Diseases'. Available at: <https://moodle.royalholloway.ac.uk/mod/resource/view.php?id=211177>.

Löfblom, J. (2011) 'Bacterial Display in Combinatorial Protein Engineering', *Biotechnology Journal*, 6(9), pp. 1115–1129. Available at: <https://doi.org/10.1002/biot.201100129>.

Madden, D.R. (2002) 'The Structure and Function of Glutamate Receptor Ion Channels', *Nature Reviews Neuroscience*, 3(2), pp. 91–101. Available at: <https://doi.org/10.1038/nrn725>.

Martínez-Maqueda, D. et al. (2013) 'Extraction/Fractionation Techniques for Proteins and Peptides and Protein Digestion', in *Proteomics in Foods: Principles and Applications*. 2013th edn. Springer, pp. 21–50.

Murzin, A.G. et al. (1995) 'SCOP: A Structural Classification of Proteins Database for the Investigation of Sequences and Structures', *Journal of Molecular Biology*, 247(4), pp. 536–540. Available at: [https://doi.org/10.1016/S0022-2836\(05\)80134-2](https://doi.org/10.1016/S0022-2836(05)80134-2).

NCBI Structure Group Home Page (no date). Available at: <http://www.ncbi.nlm.nih.gov/Structure/index.shtml>.

Nilsson, O.B. et al. (2015) 'Cotranslational Protein Folding Inside the Ribosome Exit Tunnel', *Cell Reports*, 12(10), pp. 1533–1540. Available at: <https://doi.org/10.1016/j.celrep.2015.07.065>.

Olson, C.A. et al. (2008) 'mRNA Display Selection of a High-Affinity, Modification-Specific Phospho-I $\kappa$ B $\alpha$ -Binding Fibronectin', *ACS Chemical Biology*, 3(8), pp. 480–485. Available at: <https://doi.org/10.1021/cb800069c>.

Plückthun, A. (2012) 'Ribosome Display: A Perspective', in *Ribosome Display and Related Technologies*. New York: Humana Press, pp. 3–28.

Price, N.C. and Stevens, L. (1999) *Fundamentals of Enzymology: The Cell and Molecular Biology of Catalytic Proteins*. 3rd ed. Oxford: Oxford University Press.

ProZyme - Advancing Glycosciences-index (no date). Available at: <https://prozyme.com/>.

RCSB Protein Data Bank - RCSB PDB (no date). Available at: <http://www.rcsb.org/pdb/home/home.do>.

Ruhaak, L.R. et al. (2018) 'Mass Spectrometry Approaches to Glycomic and Glycoproteomic Analyses', *Chemical Reviews*, 118(17), pp. 7886–7930. Available at: <https://doi.org/10.1021/acs.chemrev.7b00732>.

Sigma Aldrich (no date) 'Detergents Properties and Applications'. Available at: <https://www.sigmaaldrich.com/content/dam/sigma-aldrich/docs/Sigma/Instructions/deterge>

nt\_selection\_table.pdf.

Taylor, M.E. and Drickamer, K. (2011) *Introduction to Glycobiology*. 3rd ed. Oxford: Oxford University Press.

UniProt (no date). Available at: <http://www.uniprot.org/>.

Voet, D. and Voet, J. (2011a) 'Enzymatic Catalysis', in *Biochemistry*. 4th ed. Hoboken, N.J.: John Wiley.

Voet, D. and Voet, J. (2011b) 'Enzymatic Catalysis', in *Biochemistry*. 4th ed. Hoboken, N.J.: John Wiley.

Voet, D. and Voet, J. (2011c) 'Enzymatic Catalysis', in *Biochemistry*. 4th ed. Hoboken, N.J.: John Wiley.

Voet, D. and Voet, J. (2011d) 'Enzymatic Catalysis', in *Biochemistry*. 4th ed. Hoboken, N.J.: John Wiley.

Voet, D. and Voet, J. (2011e) 'Enzymatic Catalysis', in *Biochemistry*. 4th ed. Hoboken, N.J.: John Wiley.

Voet, D. and Voet, J.G. (2011) *Biochemistry*. 4th ed. Hoboken, N.J.: John Wiley.

Voet, D., Voet, J.G. and Pratt, C.W. (2013) *Principles of Biochemistry*. 4th Edition. Hoboken, N.J.: Wiley.

'Web of Science Service for UK Education - Home Page' (no date). Available at: <http://wok.mimas.ac.uk/>.

Wilson, D.S., Keefe, A.D. and Szostak, J.W. (2001) 'The Use of mRNA Display to Select High-Affinity Protein-Binding Peptides', *Proceedings of the National Academy of Sciences of the United States of America*, 98(7). Available at: [https://www.jstor.org/stable/3055315?seq=1#metadata\\_info\\_tab\\_contents](https://www.jstor.org/stable/3055315?seq=1#metadata_info_tab_contents).

Wolfson Institute (no date) 'Technical Resource: Protein Stability and Storage'. Available at: [http://wolfson.huji.ac.il/purification/PDF/StorageProteins/PIERCE\\_ProteinStorage.pdf](http://wolfson.huji.ac.il/purification/PDF/StorageProteins/PIERCE_ProteinStorage.pdf).

Yamakawa, N. et al. (2018) 'Systems Glycomics of Adult Zebrafish Identifies Organ-Specific Sialylation and Glycosylation Patterns', *Nature Communications*, 9(1). Available at: <https://doi.org/10.1038/s41467-018-06950-3>.

Yang, Y., Franc, V. and Heck, A.J.R. (2017) 'Glycoproteomics: A Balance between High-Throughput and In-Depth Analysis', *Trends in Biotechnology*, 35(7), pp. 598–609. Available at: <https://doi.org/10.1016/j.tibtech.2017.04.010>.