

# DNA Option Course 2018 - 2019

Reading List for the Level 4 DNA option - Semester 1  
2018/19

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[1]

H. F. Lodish, Molecular cell biology, 7th ed., International ed. New York: W.H. Freeman and Company, 2013.

[2]

B. Alberts, Molecular biology of the cell, Sixth edition. New York, NY: Garland Science, Taylor and Francis Group, 2015.

[3]

J. E. Krebs, E. S. Goldstein, and S. T. Kilpatrick, Lewin's genes XII, 12th ed. Burlington, Mass: Jones & Bartlett Learning, 2018.

[4]

C. R. Calladine, 1. Understanding DNA: the molecule & how it works, 3rd ed. San Diego, Calif: Academic, 2004.

[5]

J. D. Watson and F. H. C. Crick, '2. A Structure for Deoxyribose Nucleic Acid', 1953 [Online]. Available:  
<https://ezproxy.lib.gla.ac.uk/login?url=https://www.nature.com/articles/171737a0.pdf>

[6]

H. C. M. Nelson, J. T. Finch, B. F. Luisi, and A. Klug, '3. The structure of an

oligo(dA)-oligo(dT) tract and its biological implications', *Nature*, vol. 330, no. 6145, pp. 221–226, Nov. 1987 [Online]. Available: <http://ezproxy.lib.gla.ac.uk/login?url=https://www.nature.com/nature/journal/v330/n6145/abs/330221a0.html>

[7]

R. Hänsel-Hertsch, M. Di Antonio, and S. Balasubramanian, '4. DNA G-quadruplexes in the human genome: detection, functions and therapeutic potential', *Nature Reviews Molecular Cell Biology*, vol. 18, no. 5, pp. 279–284, Feb. 2017, doi: 10.1038/nrm.2017.3.

[8]

A. R. Chandrasekaran, N. Anderson, M. Kizer, K. Halvorsen, and X. Wang, '5. Beyond the Fold: Emerging Biological Applications of DNA Origami', *ChemBioChem*, vol. 17, no. 12, pp. 1081–1089, Jun. 2016, doi: 10.1002/cbic.201600038.

[9]

R. Rohs, X. Jin, S. M. West, R. Joshi, B. Honig, and R. S. Mann, '6. Origins of Specificity in Protein-DNA Recognition', *Annual Review of Biochemistry*, vol. 79, no. 1, pp. 233–269, Jun. 2010, doi: 10.1146/annurev-biochem-060408-091030.

[10]

P. A. Rice, S. Yang, K. Mizuuchi, and H. A. Nash, '7. Crystal Structure of an IHF-DNA Complex: A Protein-Induced DNA U-Turn', *Cell*, vol. 87, no. 7, pp. 1295–1306, Dec. 1996, doi: 10.1016/S0092-8674(00)81824-3.

[11]

A. J. Bogdanove, A. Bohm, J. C. Miller, R. D. Morgan, and B. L. Stoddard, 'Engineering altered protein-DNA recognition specificity', *Nucleic Acids Research*, vol. 46, no. 10, pp. 4845–4871, Jun. 2018, doi: 10.1093/nar/gky289.

[12]

F. Hille, H. Richter, S. P. Wong, M. Bratovič, S. Ressel, and E. Charpentier, 'The Biology of CRISPR-Cas: Backward and Forward', *Cell*, vol. 172, no. 6, pp. 1239–1259, Mar. 2018, doi: 10.1016/j.cell.2017.11.032.

[13]

N. Gilbert and J. Allan, 'Supercoiling in DNA and chromatin', *Current Opinion in Genetics & Development*, vol. 25, pp. 15–21, Apr. 2014, doi: 10.1016/j.gde.2013.10.013.

[14]

A. J. Schoeffler and J. M. Berger, '11. DNA topoisomerases: harnessing and constraining energy to govern chromosome topology', *Quarterly Reviews of Biophysics*, vol. 41, no. 01, Feb. 2008, doi: 10.1017/S003358350800468X.

[15]

E. Nogales, R. K. Louder, and Y. He, '12. Structural Insights into the Eukaryotic Transcription Initiation Machinery', *Annual Review of Biophysics*, vol. 46, no. 1, pp. 59–83, May 2017, doi: 10.1146/annurev-biophys-070816-033751.

[16]

E. Nudler, '13. RNA Polymerase Active Center: The Molecular Engine of Transcription', *Annual Review of Biochemistry*, vol. 78, no. 1, pp. 335–361, Jun. 2009, doi: 10.1146/annurev.biochem.76.052705.164655.

[17]

K. M. Lelli, M. Slattery, and R. S. Mann, '14. Disentangling the Many Layers of Eukaryotic Transcriptional Regulation', *Annual Review of Genetics*, vol. 46, no. 1, pp. 43–68, Dec. 2012, doi: 10.1146/annurev-genet-110711-155437.

[18]

M. J. Rowley and V. G. Corces, 'Organizational principles of 3D genome architecture', *Nature Reviews Genetics*, vol. 19, no. 12, pp. 789–800, Dec. 2018, doi: 10.1038/s41576-018-0060-8.

[19]

C. R. Clapier, J. Iwasa, B. R. Cairns, and C. L. Peterson, '16. Mechanisms of action and

regulation of ATP-dependent chromatin-remodelling complexes', *Nature Reviews Molecular Cell Biology*, vol. 18, no. 7, pp. 407–422, May 2017, doi: 10.1038/nrm.2017.26.

[20]

F. Uhlmann, '17. SMC complexes: from DNA to chromosomes', *Nature Reviews Molecular Cell Biology*, vol. 17, no. 7, pp. 399–412, Apr. 2016, doi: 10.1038/nrm.2016.30.

[21]

R. T. Pomerantz and M. O'Donnell, '18. Replisome mechanics: insights into a twin DNA polymerase machine', *Trends in Microbiology*, vol. 15, no. 4, pp. 156–164, Apr. 2007, doi: 10.1016/j.tim.2007.02.007.

[22]

J. Renkawitz, C. A. Lademann, and S. Jentsch, '19. Mechanisms and principles of homology search during recombination', *Nature Reviews Molecular Cell Biology*, vol. 15, no. 6, pp. 369–383, May 2014, doi: 10.1038/nrm3805.

[23]

K. Kaniecki, L. De Tullio, and E. C. Greene, 'A change of view: homologous recombination at single-molecule resolution', *Nature Reviews Genetics*, vol. 19, no. 4, pp. 191–207, Dec. 2017, doi: 10.1038/nrg.2017.92.

[24]

D. B. Wigley, '21. Bacterial DNA repair: recent insights into the mechanism of RecBCD, AddAB and AdnAB', *Nature Reviews Microbiology*, vol. 11, no. 1, pp. 9–13, Dec. 2012, doi: 10.1038/nrmicro2917.

[25]

P. Lesbats, A. N. Engelman, and P. Cherepanov, '23. Retroviral DNA Integration', *Chemical Reviews*, vol. 116, no. 20, pp. 12730–12757, Oct. 2016, doi: 10.1021/acs.chemrev.6b00125.

[26]

D. Liu, G. Keijzers, and L. J. Rasmussen, '24. DNA mismatch repair and its many roles in eukaryotic cells', *Mutation Research/Reviews in Mutation Research*, vol. 773, pp. 174–187, Jul. 2017, doi: 10.1016/j.mrrev.2017.07.001.

[27]

A. A. Goodarzi and P. A. Jeggo, '25. The Repair and Signaling Responses to DNA Double-Strand Breaks', *Adv Genet*, vol. 82, pp. 1–45, 2013, doi: 10.1016/B978-0-12-407676-1.00001-9. [Online]. Available: <http://ezproxy.lib.gla.ac.uk/login?url=http://linkinghub.elsevier.com/retrieve/pii/B9780124076761000019>

[28]

J. A. Marteijn, H. Lans, W. Vermeulen, and J. H. J. Hoeijmakers, '26. Understanding nucleotide excision repair and its roles in cancer and ageing', *Nature Reviews Molecular Cell Biology*, vol. 15, no. 7, pp. 465–481, Jun. 2014, doi: 10.1038/nrm3822.

[29]

E. Pennisi, 'DNA's Cast of Thousands', *Science*, vol. 300, no. 5617, pp. 282–285, Apr. 2003, doi: 10.1126/science.300.5617.282.

[30]

N. Abe et al., 'Deconvolving the Recognition of DNA Shape from Sequence', *Cell*, vol. 161, no. 2, pp. 307–318, Apr. 2015, doi: 10.1016/j.cell.2015.02.008.

[31]

K. K. Swinger and P. A. Rice, 'IHF and HU: flexible architects of bent DNA', *Current Opinion in Structural Biology*, vol. 14, no. 1, pp. 28–35, Feb. 2004, doi: 10.1016/j.sbi.2003.12.003.

[32]

H. Ledford, 'Five big mysteries about CRISPR's origins', *Nature*, vol. 541, no. 7637, pp. 280–282, Jan. 2017, doi: 10.1038/541280a.

[33]

M. Adli, 'The CRISPR tool kit for genome editing and beyond', *Nature Communications*, vol. 9, no. 1, Dec. 2018, doi: 10.1038/s41467-018-04252-2.

[34]

S. H. Chen, N.-L. Chan, and T. Hsieh, 'New Mechanistic and Functional Insights into DNA Topoisomerases', *Annual Review of Biochemistry*, vol. 82, no. 1, pp. 139–170, Jun. 2013, doi: 10.1146/annurev-biochem-061809-100002.

[35]

P. Tessarz and T. Kouzarides, 'Histone core modifications regulating nucleosome structure and dynamics', *Nature Reviews Molecular Cell Biology*, vol. 15, no. 11, pp. 703–708, Oct. 2014, doi: 10.1038/nrm3890.

[36]

S. Doublia and K. E. Zahn, 'Structural insights into eukaryotic DNA replication', *Frontiers in Microbiology*, vol. 5, Aug. 2014, doi: 10.3389/fmicb.2014.00444.

[37]

S. C. West, 'The search for a human Holliday junction resolvase', *Biochemical Society Transactions*, vol. 37, no. 3, pp. 519–526, Jun. 2009, doi: 10.1042/BST0370519.

[38]

S. P. Montaña and P. A. Rice, 'Moving DNA around: DNA transposition and retroviral integration', *Current Opinion in Structural Biology*, vol. 21, no. 3, pp. 370–378, Jun. 2011, doi: 10.1016/j.sbi.2011.03.004.

[39]

P. Modrich, 'Mechanisms in *Escherichia coli* and Human Mismatch Repair (Nobel Lecture)', *Angewandte Chemie International Edition*, vol. 55, no. 30, pp. 8490–8501, Jul. 2016, doi: 10.1002/anie.201601412.

[40]

S. Deindl et al., 'ISWI Remodelers Slide Nucleosomes with Coordinated Multi-Base-Pair Entry Steps and Single-Base-Pair Exit Steps', *Cell*, vol. 152, no. 3, pp. 442–452, Jan. 2013, doi: 10.1016/j.cell.2012.12.040.

[41]

J. E. Graham, K. J. Mariani, and S. C. Kowalczykowski, 'Independent and Stochastic Action of DNA Polymerases in the Replisome', *Cell*, vol. 169, no. 7, pp. 1201–1213.e17, Jun. 2017, doi: 10.1016/j.cell.2017.05.041.

[42]

T. Terakawa, S. Bisht, J. M. Eeftens, C. Dekker, C. H. Haering, and E. C. Greene, 'The condensin complex is a mechanochemical motor that translocates along DNA', *Science*, vol. 358, no. 6363, pp. 672–676, Nov. 2017, doi: 10.1126/science.aan6516.

[43]

R. Jia, P. Chai, H. Zhang, and X. Fan, 'Novel insights into chromosomal conformations in cancer', *Molecular Cancer*, vol. 16, no. 1, Dec. 2017, doi: 10.1186/s12943-017-0741-5.

[44]

M Ryan Corces et al., 'The chromatin accessibility landscape of primary human cancers', *Science*, 2018 [Online]. Available: <http://science.sciencemag.org/content/362/6413/eaav1898.long>

[45]

A. V. Wright, J.-J. Liu, G. J. Knott, K. W. Doxzen, E. Nogales, and J. A. Doudna, 'Structures of the CRISPR genome integration complex', *Science*, vol. 357, no. 6356, pp. 1113–1118, Sep. 2017, doi: 10.1126/science.aao0679.

[46]

Ludmil B Alexandrov et al., 'Mutational signatures associated with tobacco smoking in human cancer', *Mutational signatures associated with tobacco smoking in human cancer*,

2016 [Online]. Available:

<http://ezproxy.lib.gla.ac.uk/login?url=http://science.sciencemag.org/content/354/6312/618.long>

[47]

Ludmil B Alexandrov, 'Understanding the origins of human cancer', *Science*, 2018 [Online]. Available: <http://science.sciencemag.org/content/350/6265/1175.1.long>

[48]

W. Zhao et al., 'BRCA1–BARD1 promotes RAD51-mediated homologous DNA pairing', *Nature*, vol. 550, no. 7676, pp. 360–365, Oct. 2017, doi: 10.1038/nature24060.

[49]

P. Cejka, 'Biochemistry: Complex assistance for DNA invasion', *Nature*, Oct. 2017, doi: 10.1038/nature24149.