

# DNA Option Course 2018 - 2019

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

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Abe, N., Dror, I., Yang, L., Slattery, M., Zhou, T., Bussemaker, H. J., Rohs, R., & Mann, R. S. (2015). Deconvolving the Recognition of DNA Shape from Sequence. *Cell*, 161(2), 307–318. <https://doi.org/10.1016/j.cell.2015.02.008>

Adli, M. (2018). The CRISPR tool kit for genome editing and beyond. *Nature Communications*, 9(1). <https://doi.org/10.1038/s41467-018-04252-2>

Alberts, B. (2015). *Molecular biology of the cell* (Sixth edition). Garland Science, Taylor and Francis Group.

Bogdanove, A. J., Bohm, A., Miller, J. C., Morgan, R. D., & Stoddard, B. L. (2018). Engineering altered protein–DNA recognition specificity. *Nucleic Acids Research*, 46(10), 4845–4871. <https://doi.org/10.1093/nar/gky289>

Calladine, C. R. (2004). 1. *Understanding DNA: the molecule & how it works* (3rd ed). Academic.

Cejka, P. (2017). Biochemistry: Complex assistance for DNA invasion. *Nature*. <https://doi.org/10.1038/nature24149>

Chandrasekaran, A. R., Anderson, N., Kizer, M., Halvorsen, K., & Wang, X. (2016). 5. Beyond the Fold: Emerging Biological Applications of DNA Origami. *ChemBioChem*, 17(12), 1081–1089. <https://doi.org/10.1002/cbic.201600038>

Chen, S. H., Chan, N.-L., & Hsieh, T. (2013). New Mechanistic and Functional Insights into DNA Topoisomerases. *Annual Review of Biochemistry*, 82(1), 139–170. <https://doi.org/10.1146/annurev-biochem-061809-100002>

Clapier, C. R., Iwasa, J., Cairns, B. R., & Peterson, C. L. (2017). 16. Mechanisms of action and regulation of ATP-dependent chromatin-remodelling complexes. *Nature Reviews Molecular Cell Biology*, 18(7), 407–422. <https://doi.org/10.1038/nrm.2017.26>

Deindl, S., Hwang, W. L., Hota, S. K., Blosser, T. R., Prasad, P., Bartholomew, B., & Zhuang, X. (2013). ISWI Remodelers Slide Nucleosomes with Coordinated Multi-Base-Pair Entry Steps and Single-Base-Pair Exit Steps. *Cell*, 152(3), 442–452. <https://doi.org/10.1016/j.cell.2012.12.040>

Doublie, S., & Zahn, K. E. (2014). Structural insights into eukaryotic DNA replication. *Frontiers in Microbiology*, 5. <https://doi.org/10.3389/fmicb.2014.00444>

Gilbert, N., & Allan, J. (2014). Supercoiling in DNA and chromatin. *Current Opinion in*

Genetics & Development, 25, 15–21. <https://doi.org/10.1016/j.gde.2013.10.013>

Goodarzi, A. A., & Jeggo, P. A. (2013). 25. The Repair and Signaling Responses to DNA Double-Strand Breaks. *Adv Genet*, 82, 1–45.  
<https://doi.org/10.1016/B978-0-12-407676-1.00001-9>

Graham, J. E., Marians, K. J., & Kowalczykowski, S. C. (2017). Independent and Stochastic Action of DNA Polymerases in the Replisome. *Cell*, 169(7), 1201–1213.e17.  
<https://doi.org/10.1016/j.cell.2017.05.041>

Hänsel-Hertsch, R., Di Antonio, M., & Balasubramanian, S. (2017). 4. DNA G-quadruplexes in the human genome: detection, functions and therapeutic potential. *Nature Reviews Molecular Cell Biology*, 18(5), 279–284. <https://doi.org/10.1038/nrm.2017.3>

Hille, F., Richter, H., Wong, S. P., Bratovič, M., Ressel, S., & Charpentier, E. (2018). The Biology of CRISPR-Cas: Backward and Forward. *Cell*, 172(6), 1239–1259.  
<https://doi.org/10.1016/j.cell.2017.11.032>

Jia, R., Chai, P., Zhang, H., & Fan, X. (2017). Novel insights into chromosomal conformations in cancer. *Molecular Cancer*, 16(1).  
<https://doi.org/10.1186/s12943-017-0741-5>

Kaniecki, K., De Tullio, L., & Greene, E. C. (2017). A change of view: homologous recombination at single-molecule resolution. *Nature Reviews Genetics*, 19(4), 191–207.  
<https://doi.org/10.1038/nrg.2017.92>

Krebs, J. E., Goldstein, E. S., & Kilpatrick, S. T. (2018). *Lewin's genes XII* (12th ed). Jones & Bartlett Learning.

Ledford, H. (2017). Five big mysteries about CRISPR's origins. *Nature*, 541(7637), 280–282.  
<https://doi.org/10.1038/541280a>

Lelli, K. M., Slattery, M., & Mann, R. S. (2012). 14. Disentangling the Many Layers of Eukaryotic Transcriptional Regulation. *Annual Review of Genetics*, 46(1), 43–68.  
<https://doi.org/10.1146/annurev-genet-110711-155437>

Lesbats, P., Engelman, A. N., & Cherepanov, P. (2016). 23. Retroviral DNA Integration. *Chemical Reviews*, 116(20), 12730–12757. <https://doi.org/10.1021/acs.chemrev.6b00125>  
Liu, D., Keijzers, G., & Rasmussen, L. J. (2017). 24. DNA mismatch repair and its many roles in eukaryotic cells. *Mutation Research/Reviews in Mutation Research*, 773, 174–187.  
<https://doi.org/10.1016/j.mrrev.2017.07.001>

Lodish, H. F. (2013). *Molecular cell biology* (7th ed., international ed). W.H. Freeman and Company.

Ludmil B Alexandrov. (2018a). Understanding the origins of human cancer. *Science*.  
<http://science.sciencemag.org/content/350/6265/1175.1.long>

Ludmil B Alexandrov et al. (2016). Mutational signatures associated with tobacco smoking in human cancer. *Mutational Signatures Associated with Tobacco Smoking in Human Cancer*.  
<http://ezproxy.lib.gla.ac.uk/login?url=http://science.sciencemag.org/content/354/6312/618>.

long

M Ryan Corces et al. (2018b). The chromatin accessibility landscape of primary human cancers. *Science*. <http://science.sciencemag.org/content/362/6413/eaav1898.long>

Marteijn, J. A., Lans, H., Vermeulen, W., & Hoeijmakers, J. H. J. (2014). 26. Understanding nucleotide excision repair and its roles in cancer and ageing. *Nature Reviews Molecular Cell Biology*, 15(7), 465–481. <https://doi.org/10.1038/nrm3822>

Modrich, P. (2016). Mechanisms in *Prokaryotic and Human Mismatch Repair* (Nobel Lecture). *Angewandte Chemie International Edition*, 55(30), 8490–8501. <https://doi.org/10.1002/anie.201601412>

Montaño, S. P., & Rice, P. A. (2011). Moving DNA around: DNA transposition and retroviral integration. *Current Opinion in Structural Biology*, 21(3), 370–378. <https://doi.org/10.1016/j.sbi.2011.03.004>

Nelson, H. C. M., Finch, J. T., Luisi, B. F., & Klug, A. (1987). 3. The structure of an oligo(dA)-oligo(dT) tract and its biological implications. *Nature*, 330(6145), 221–226. <http://ezproxy.lib.gla.ac.uk/login?url=https://www.nature.com/nature/journal/v330/n6145/a bs/330221a0.html>

Nogales, E., Louder, R. K., & He, Y. (2017). 12. Structural Insights into the Eukaryotic Transcription Initiation Machinery. *Annual Review of Biophysics*, 46(1), 59–83. <https://doi.org/10.1146/annurev-biophys-070816-033751>

Nudler, E. (2009). 13. RNA Polymerase Active Center: The Molecular Engine of Transcription. *Annual Review of Biochemistry*, 78(1), 335–361. <https://doi.org/10.1146/annurev.biochem.76.052705.164655>

Pennisi, E. (2003). DNA's Cast of Thousands. *Science*, 300(5617), 282–285. <https://doi.org/10.1126/science.300.5617.282>

Pomerantz, R. T., & O'Donnell, M. (2007). 18. Replisome mechanics: insights into a twin DNA polymerase machine. *Trends in Microbiology*, 15(4), 156–164. <https://doi.org/10.1016/j.tim.2007.02.007>

Renkawitz, J., Lademann, C. A., & Jentsch, S. (2014). 19. Mechanisms and principles of homology search during recombination. *Nature Reviews Molecular Cell Biology*, 15(6), 369–383. <https://doi.org/10.1038/nrm3805>

Rice, P. A., Yang, S., Mizuuchi, K., & Nash, H. A. (1996). 7. Crystal Structure of an IHF-DNA Complex: A Protein-Induced DNA U-Turn. *Cell*, 87(7), 1295–1306. [https://doi.org/10.1016/S0092-8674\(00\)81824-3](https://doi.org/10.1016/S0092-8674(00)81824-3)

Rohs, R., Jin, X., West, S. M., Joshi, R., Honig, B., & Mann, R. S. (2010). 6. Origins of Specificity in Protein-DNA Recognition. *Annual Review of Biochemistry*, 79(1), 233–269. <https://doi.org/10.1146/annurev-biochem-060408-091030>

Rowley, M. J., & Corces, V. G. (2018). Organizational principles of 3D genome architecture. *Nature Reviews Genetics*, 19(12), 789–800. <https://doi.org/10.1038/s41576-018-0060-8>

- Schoeffler, A. J., & Berger, J. M. (2008). 11. DNA topoisomerases: harnessing and constraining energy to govern chromosome topology. *Quarterly Reviews of Biophysics*, 41(01). <https://doi.org/10.1017/S003358350800468X>
- Swinger, K. K., & Rice, P. A. (2004). IHF and HU: flexible architects of bent DNA. *Current Opinion in Structural Biology*, 14(1), 28–35. <https://doi.org/10.1016/j.sbi.2003.12.003>
- Terakawa, T., Bisht, S., Eeftens, J. M., Dekker, C., Haering, C. H., & Greene, E. C. (2017). The condensin complex is a mechanochemical motor that translocates along DNA. *Science*, 358(6363), 672–676. <https://doi.org/10.1126/science.aan6516>
- Tessarz, P., & Kouzarides, T. (2014). Histone core modifications regulating nucleosome structure and dynamics. *Nature Reviews Molecular Cell Biology*, 15(11), 703–708. <https://doi.org/10.1038/nrm3890>
- Uhlmann, F. (2016). 17. SMC complexes: from DNA to chromosomes. *Nature Reviews Molecular Cell Biology*, 17(7), 399–412. <https://doi.org/10.1038/nrm.2016.30>
- Watson, J. D., & Crick, F. H. C. (1953). 2. A Structure for Deoxyribose Nucleic Acid. <https://ezproxy.lib.gla.ac.uk/login?url=https://www.nature.com/articles/171737a0.pdf>
- West, S. C. (2009). The search for a human Holliday junction resolvase. *Biochemical Society Transactions*, 37(3), 519–526. <https://doi.org/10.1042/BST0370519>
- Wigley, D. B. (2012). 21. Bacterial DNA repair: recent insights into the mechanism of RecBCD, AddAB and AdnAB. *Nature Reviews Microbiology*, 11(1), 9–13. <https://doi.org/10.1038/nrmicro2917>
- Wright, A. V., Liu, J.-J., Knott, G. J., Doxzen, K. W., Nogales, E., & Doudna, J. A. (2017). Structures of the CRISPR genome integration complex. *Science*, 357(6356), 1113–1118. <https://doi.org/10.1126/science.aao0679>
- Zhao, W., Steinfeld, J. B., Liang, F., Chen, X., Maranon, D. G., Jian Ma, C., Kwon, Y., Rao, T., Wang, W., Sheng, C., Song, X., Deng, Y., Jimenez-Sainz, J., Lu, L., Jensen, R. B., Xiong, Y., Kupfer, G. M., Wiese, C., Greene, E. C., & Sung, P. (2017). BRCA1–BARD1 promotes RAD51-mediated homologous DNA pairing. *Nature*, 550(7676), 360–365. <https://doi.org/10.1038/nature24060>