Quantifying nucleosome dynamics and protein binding with PIE-FCCS and spFRET

Martens, C.L.G.

Citation

Martens, C. L. G. (2023, February 1). *Quantifying nucleosome dynamics and protein binding with PIE-FCCS and spFRET*. *Casimir PhD Series*. Retrieved from https://hdl.handle.net/1887/3514600

Bibliography

[1] Kay, L. E. A book of life?: How the genome became an information system and DNA a language. *Perspectives in biology and medicine* **1998**, 41 (4), 504–528.

[2] Edenberg, E.; Downey, M.; Toczyski, D. Polymerase stalling during replication, transcription and translation. *Current Biology* **2014**, 24 (10), R445–R452.

[3] Annunziato, A. DNA packaging: nucleosomes and chromatin. *Nature Education* **2008**, 1 (1), 26.

[4] Kornberg, R. D. Chromatin Structure: A Repeating Unit of Histones and DNA: Chromatin structure is based on a repeating unit of eight histone molecules and about 200 DNA base pairs. *Science* **1974**, 184 (4139), 868–871.

[5] Woodcock, C.; Safer, J.; Stanchfield, J. Structural repeating units in chromatin: I. Evidence for their general occurrence. *Experimental cell research* **1976**, 97 (1), 101–110.

[6] Owen-Hughes, T.; Workman, J. L. Experimental analysis of chromatin function in transcription control. *Critical reviews in eukaryotic gene expression* **1994**, 4 (4), 403–441.

[7] Van Holde, K. E. Chromatin. Springer Science & Business Media, **2012**.

[8] Olins, D. E.; Olins, A. L. Chromatin history: our view from the bridge. *Nature reviews Molecular cell biology* **2003**, 4 (10), 809–814.

[9] Maeshima, K.; Ide, S.; Hibino, K.; Sasai, M. Liquid-like behavior of chromatin. *Current opinion in genetics & development* **2016**, 37, 36–45.

[10] Everid, A.; Small, J.; Davies, H. Electron-microscope observations on the structure of condensed chromatin: evidence for orderly arrays of

unit threads on the surface of chicken erythrocyte nuclei. *Journal of cell science* **1970**, 7 (1), 35–48.

[11] Oudet, P.; Gross-Bellard, M.; Chambon, P. Electron microscopic and biochemical evidence that chromatin structure is a repeating unit. *Cell* **1975**, 4 (4), 281–300.

[12] Dorigo, B.; Schalch, T.; Kulangara, A.; Duda, S.; Schroeder, R. R.; Richmond, T. J. Nucleosome arrays reveal the two-start organization of the chromatin fiber. *Science* **2004**, 306 (5701), 1571–1573.

[13] Song, F.; Chen, P.; Sun, D.; Wang, M.; Dong, L.; Liang, D.; Xu, R.-M.; Zhu, P.; Li, G. Cryo-EM study of the chromatin fiber reveals a double helix twisted by tetranucleosomal units. *Science* **2014**, 344 (6182), 376–380.

[14] Fazary, A. E.; Ju, Y.-H.; Abd-Rabboh, H. S. How does chromatin package DNA within nucleus and regulate gene expression? *International journal of biological macromolecules* **2017**, 101, 862–881.

[15] Nora, E. P.; Lajoie, B. R.; Schulz, E. G.; Giorgetti, L.; Okamoto, I.; Servant, N.; Piolot, T.; Van Berkum, N. L.; Meisig, J.; Sedat, J.; et al. Spatial partitioning of the regulatory landscape of the X-inactivation centre. *Nature* **2012**, 485 (7398), 381–385.

[16] Babu, A.; Verma, R. S. Chromosome structure: euchromatin and heterochromatin. *International review of cytology* **1987**, 108, 1–60.

[17] Schwartz, U.; Németh, A.; Diermeier, S.; Exler, J. H.; Hansch, S.; Maldonado, R.; Heizinger, L.; Merkl, R.; Längst, G. Characterizing the nuclease accessibility of DNA in human cells to map higher order structures of chromatin. *Nucleic acids research* **2019**, 47 (3), 1239–1254.

[18] Shashikant, T.; Khor, J. M.; Ettensohn, C. A. Global analysis of primary mesenchyme cell cis-regulatory modules by chromatin accessibility profiling. *BMC genomics* **2018**, 19 (1), 1–18.

[19] Mueller, B.; Mieczkowski, J.; Kundu, S.; Wang, P.; Sadreyev, R.; Tolstorukov, M. Y.; Kingston, R. E. Widespread changes in nucleosome accessibility without changes in nucleosome occupancy during a

rapid transcriptional induction. *Genes & development* **2017**, 31 (5), 451–462.

[20] Dixon, J. R.; Selvaraj, S.; Yue, F.; Kim, A.; Li, Y.; Shen, Y.; Hu, M.; Liu, J. S.; Ren, B. Topological domains in mammalian genomes identified by analysis of chromatin interactions. *Nature* **2012**, 485 (7398), 376–380.

[21] Erdel, F.; Rippe, K. Formation of chromatin subcompartments by phase separation. *Biophysical journal* **2018**, 114 (10), 2262–2270.

[22] Strom, A. R.; Emelyanov, A. V.; Mir, M.; Fyodorov, D. V.; Darzacq, X.; Karpen, G. H. Phase separation drives heterochromatin domain formation. *Nature* **2017**, 547 (7662), 241–245.

[23] Wang, N.; Liu, C. Implications of liquid–liquid phase separation in plant chromatin organization and transcriptional control. *Current Opinion in Genetics & Development* **2019**, 55, 59–65.

[24] Peng, L.; Li, E.-M.; Xu, L.-Y. From start to end: Phase separation and transcriptional regulation. *Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms* **2020**, 1863 (12), 194641.

[25] Feric, M.; Misteli, T. Phase separation in genome organization across evolution. *Trends in cell biology* **2021**, 31 (8), 671–685.

[26] Guo, Q.; Shi, X.; Wang, X. RNA and liquid-liquid phase separation. *Non-coding RNA Research* **2021**, 6 (2), 92–99.

[27] Bonner, J.; Ru-chih, C. H. Properties of chromosomal nucleohistone. *Journal of Molecular Biology* **1963**, 6 (3), 169–174.

[28] Beam, S.; Ris, H. On the structure of nucleohistone. *Journal of molecular biology* **1971**, 55 (3), 325–IN2.

[29] Olins, A. L.; Olins, D. E. Spheroid chromatin units (ν bodies). *Science* **1974**, 183 (4122), 330–332.

[30] Lieb, J. D.; Clarke, N. D. Control of transcription through intragenic patterns of nucleosome composition. *Cell* **2005**, 123 (7), 1187–1190.

[31] Huang, R.-c. C.; Bonner, J. Histone, a suppressor of chromosomal RNA synthesis. *Proceedings of the National Academy of Sciences* **1962**, 48 (7), 1216–1222.

[32] Thomas Jr, G.; Prescott, B.; Olins, D. Secondary structure of histones and DNA in chromatin. *Science* **1977**, 197 (4301), 385–388.

[33] Olins, D. E.; Olins, A. L. Nucleosomes: The Structural Quantum in Chromosomes. *American Scientist* **1978**, 66 (6), 704–711.

[34] Luger, K.; Mäder, A. W.; Richmond, R. K.; Sargent, D. F.; Richmond, T. J. Crystal structure of the nucleosome core particle at 2.8 Å resolution. *Nature* **1997**, 389 (6648), 251–260.

[35] Luger, K.; Richmond, T. J. DNA binding within the nucleosome core. *Current Opinion in Structural Biology* **1998**, 8 (1), 33 – 40.

[36] Thåström, A.; Gottesfeld, J.; Luger, K.; Widom, J. Histone- DNA binding free energy cannot be measured in dilution-driven dissociation experiments. *Biochemistry* **2004**, 43 (3), 736–741.

[37] Luger, K. Dynamic nucleosomes. *Chromosome Research* **2006**, 14 (1), 5–16.

[38] Bondarenko, V. A.; Steele, L. M.; Újvári, A.; Gaykalova, D. A.; Kulaeva, O. I.; Polikanov, Y. S.; Luse, D. S.; Studitsky, V. M. Nucleosomes can form a polar barrier to transcript elongation by RNA polymerase II. *Molecular cell* **2006**, 24 (3), 469–479.

[39] Polach, K.; Widom, J. Mechanism of protein access to specific DNA sequences in chromatin: a dynamic equilibrium model for gene regulation. *Journal of molecular biology* **1995**, 254 (2), 130–149.

[40] Lowary, P.; Widom, J. New DNA sequence rules for high affinity binding to histone octamer and sequence-directed nucleosome positioning. *Journal of molecular biology* **1998**, 276 (1), 19–42.

[41] Thåström, A.; Lowary, P.; Widlund, H.; Cao, H.; Kubista, M.; Widom, J. Sequence motifs and free energies of selected natural and non-natural nucleosome positioning DNA sequences. *Journal of molecular biology* **1999**, 288 (2), 213–229.

[42] McGinty, R. K.; Tan, S. Nucleosome structure and function. *Chemical reviews* **2015**, 115 (6), 2255–2273.

[43] Drew, H. R.; Travers, A. A. DNA bending and its relation to nucleosome positioning. *Journal of molecular biology* **1985**, 186 (4), 773–790.

[44] Bolshoy, A.; McNamara, P.; Harrington, R.; Trifonov, E. Curved DNA without AA: experimental estimation of all 16 DNA wedge angles. *Proceedings of the National Academy of Sciences* **1991**, 88 (6), 2312–2316.

[45] Ioshikhes, I.; Bolshoy, A.; Trifonov, E. Preferred positions of AA and TT dinucleotides in aligned nucleosomal DNA sequences. *Journal of Biomolecular Structure and Dynamics* **1992**, 9 (6), 1111–1117.

[46] Morozov, A. V.; Fortney, K.; Gaykalova, D. A.; Studitsky, V. M.; Widom, J.; Siggia, E. D. Using DNA mechanics to predict in vitro nucleosome positions and formation energies. *Nucleic acids research* **2009**, 37 (14), 4707–4722.

[47] Ngo, T. T.; Zhang, Q.; Zhou, R.; Yodh, J. G.; Ha, T. Asymmetric unwrapping of nucleosomes under tension directed by DNA local flexibility. *Cell* **2015**, 160 (6), 1135–1144.

[48] De Bruin, L.; Tompitak, M.; Eslami-Mossallam, B.; Schiessel, H. Why do nucleosomes unwrap asymmetrically? *The Journal of Physical Chemistry B* **2016**, 120 (26), 5855–5863.

[49] Wondergem, J.; Schiessel, H.; Tompitak, M. Performing SELEX experiments in silico. *The Journal of chemical physics* **2017**, 147 (17), 174101.

[50] Li, G.; Widom, J. Nucleosomes facilitate their own invasion. *Nature Structural and Molecular Biology* **2004**, 11 (8), 763–769.

[51] Li, G.; Levitus, M.; Bustamante, C.; Widom, J. Rapid spontaneous accessibility of nucleosomal DNA. *Nature Structural and Molecular Biology* **2005**, 12 (1), 46–53.

[52] Hodges, C.; Bintu, L.; Lubkowska, L.; Kashlev, M.; Bustamante, C. Nucleosomal fluctuations govern the transcription dynamics of RNA polymerase II. *Science* **2009**, 325 (5940), 626–628.

[53] Koopmans, W. J.; Buning, R.; Schmidt, T.; Van Noort, J. spFRET using alternating excitation and FCS reveals progressive DNA unwrapping in nucleosomes. *Biophysical Journal* **2009**, 97 (1), 195–204.

[54] Pennings, S.; Muyldermans, S.; Meersseman, G.; Wyns, L. Formation, stability and core histone positioning of nucleosomes reassembled on bent and other nucleosome-derived DNA. *Journal of molecular biology* **1989**, 207 (1), 183–192.

[55] Teif, V. B.; Rippe, K. Predicting nucleosome positions on the DNA: combining intrinsic sequence preferences and remodeler activities. *Nucleic acids research* **2009**, 37 (17), 5641–5655.

[56] Shogren-Knaak, M.; Ishii, H.; Sun, J.-M.; Pazin, M. J.; Davie, J. R.; Peterson, C. L. Histone H4-K16 acetylation controls chromatin structure and protein interactions. *Science* **2006**, 311 (5762), 844–847.

[57] Erler, J.; Zhang, R.; Petridis, L.; Cheng, X.; Smith, J. C.; Langowski, J. The role of histone tails in the nucleosome: a computational study. *Biophysical journal* **2014**, 107 (12), 2911–2922.

[58] Dorigo, B.; Schalch, T.; Bystricky, K.; Richmond, T. J. Chromatin fiber folding: requirement for the histone H4 N-terminal tail. *Journal of molecular biology* **2003**, 327 (1), 85–96.

[59] Lu, X.; Simon, M. D.; Chodaparambil, J. V.; Hansen, J. C.; Shokat, K. M.; Luger, K. The effect of H3K79 dimethylation and H4K20 trimethylation on nucleosome and chromatin structure. *Nature structural & molecular biology* **2008**, 15 (10), 1122–1124.

[60] Creyghton, M. P.; Cheng, A. W.; Welstead, G. G.; Kooistra, T.; Carey, B. W.; Steine, E. J.; Hanna, J.; Lodato, M. A.; Frampton, G. M.; Sharp, P. A.; et al. Histone H3K27ac separates active from poised enhancers and predicts developmental state. *Proceedings of the National Academy of Sciences* **2010**, 107 (50), 21931–21936.

[61] Koch, C. M.; Andrews, R. M.; Flicek, P.; Dillon, S. C.; Karaöz, U.; Clelland, G. K.; Wilcox, S.; Beare, D. M.; Fowler, J. C.; Couttet, P.; et al. The landscape of histone modifications across 1% of the human genome in five human cell lines. *Genome research* **2007**, 17 (6), 691–707.

[62] Guillemette, B.; Drogaris, P.; Lin, H.-H. S.; Armstrong, H.; Hiragami-Hamada, K.; Imhof, A.; Bonneil, E.; Thibault, P.; Verreault, A.; Festenstein, R. J. H3 lysine 4 is acetylated at active gene promoters and is regulated by H3 lysine 4 methylation. *PLoS genetics* **2011**, 7 (3), e1001354.

[63] Zhiteneva, A.; Bonfiglio, J. J.; Makarov, A.; Colby, T.; Vagnarelli, P.; Schirmer, E. C.; Matic, I.; Earnshaw, W. C. Mitotic post-translational modifications of histones promote chromatin compaction in vitro. *Open biology* **2017**, 7 (9), 170076.

[64] Wang, Q.; Zhang, Y.; Yang, C.; Xiong, H.; Lin, Y.; Yao, J.; Li, H.; Xie, L.; Zhao, W.; Yao, Y.; et al. Acetylation of metabolic enzymes coordinates carbon source utilization and metabolic flux. *Science* **2010**, 327 (5968), 1004–1007.

[65] Zhao, S.; Xu, W.; Jiang, W.; Yu, W.; Lin, Y.; Zhang, T.; Yao, J.; Zhou, L.; Zeng, Y.; Li, H.; et al. Regulation of cellular metabolism by protein lysine acetylation. *Science* **2010**, 327 (5968), 1000–1004.

[66] Barski, A.; Cuddapah, S.; Cui, K.; Roh, T.-Y.; Schones, D. E.; Wang, Z.; Wei, G.; Chepelev, I.; Zhao, K. High-resolution profiling of histone methylations in the human genome. *Cell* **2007**, 129 (4), 823–837.

[67] Yang, K.; Greenberg, M. M. Histone tail sequences balance their role in genetic regulation and the need to protect DNA against destruction in nucleosome core particles containing abasic sites. *ChemBioChem* **2019**, 20 (1), 78–82.

[68] Tsuchiya, M.; Dang, N.; Kerr, E. O.; Hu, D.; Steffen, K. K.; Oakes, J. A.; Kennedy, B. K.; Kaeberlein, M. Sirtuin-independent effects of nicotinamide on lifespan extension from calorie restriction in yeast. *Aging cell* **2006**, 5 (6), 505–514.

[69] Greer, E. L.; Maures, T. J.; Hauswirth, A. G.; Green, E. M.; Leeman, D. S.; Maro, G. S.; Han, S.; Banko, M. R.; Gozani, O.; Brunet, A. Members of the H3K4 trimethylation complex regulate lifespan in a germline-dependent manner in C. elegans. *Nature* **2010**, 466 (7304), 383–387.

[70] Li, F.; Mao, G.; Tong, D.; Huang, J.; Gu, L.; Yang, W.; Li, G.-M. The histone mark H3K36me3 regulates human DNA mismatch repair through its interaction with MutSα. *Cell* **2013**, 153 (3), 590–600.

[71] Pai, C.-C.; Deegan, R. S.; Subramanian, L.; Gal, C.; Sarkar, S.; Blaikley, E. J.; Walker, C.; Hulme, L.; Bernhard, E.; Codlin, S.; et al. A histone H3K36 chromatin switch coordinates DNA double-strand break repair pathway choice. *Nature communications* **2014**, 5 (1), 1–11.

[72] Huang, Y.; Gu, L.; Li, G.-M. H3K36me3-mediated mismatch repair preferentially protects actively transcribed genes from mutation. *Journal of Biological Chemistry* **2018**, 293 (20), 7811–7823.

[73] Supek, F.; Lehner, B. Clustered mutation signatures reveal that error-prone DNA repair targets mutations to active genes. *Cell* **2017**, 170 (3), 534–547.

[74] Chantalat, S.; Depaux, A.; Héry, P.; Barral, S.; Thuret, J.-Y.; Dimitrov, S.; Gérard, M. Histone H3 trimethylation at lysine 36 is associated with constitutive and facultative heterochromatin. *Genome research* **2011**, 21 (9), 1426–1437.

[75] Cherepanov, P.; Sun, Z.-Y. J.; Rahman, S.; Maertens, G.; Wagner, G.; Engelman, A. Solution structure of the HIV-1 integrase-binding domain in LEDGF/p75. *Nature structural & molecular biology* **2005**, 12 (6), 526–532.

[76] Ciuffi, A.; Llano, M.; Poeschla, E.; Hoffmann, C.; Leipzig, J.; Shinn, P.; Ecker, J. R.; Bushman, F. A role for LEDGF/p75 in targeting HIV DNA integration. *Nature medicine* **2005**, 11 (12), 1287–1289.

[77] Shun, M.-C.; Raghavendra, N. K.; Vandegraaff, N.; Daigle, J. E.; Hughes, S.; Kellam, P.; Cherepanov, P.; Engelman, A. LEDGF/p75 functions downstream from preintegration complex formation to

effect gene-specific HIV-1 integration. *Genes & development* **2007**, 21 (14), 1767–1778.

[78] Keys, D. A.; Lee, B.-S.; Dodd, J. A.; Nguyen, T. T.; Vu, L.; Fantino, E.; Burson, L. M.; Nogi, Y.; Nomura, M. Multiprotein transcription factor UAF interacts with the upstream element of the yeast RNA polymerase I promoter and forms a stable preinitiation complex. *Genes & development* **1996**, 10 (7), 887–903.

[79] Kim, H.; Tang, G.-Q.; Patel, S. S.; Ha, T. Opening–closing dynamics of the mitochondrial transcription pre-initiation complex. *Nucleic acids research* **2012**, 40 (1), 371–380.

[80] Robertson, S.; Hapgood, J. P.; Louw, A. Glucocorticoid receptor concentration and the ability to dimerize influence nuclear translocation and distribution. *Steroids* **2013**, 78 (2), 182–194.

[81] Pratt, W. B.; Toft, D. O. Steroid Receptor Interactions with Heat Shock Protein and Immunophilin Chaperones. *Endocrine reviews* **1997**, 18 (3), 306–361.

[82] Pratt, W. B.; Silverstein, A. M.; Galigniana, M. D. A model for the cytoplasmic trafficking of signalling proteins involving the hsp90-binding immunophilins and p50cdc37. *Cellular signalling* **1999**, 11 (12), 839–851.

[83] Petta, I.; Dejager, L.; Ballegeer, M.; Lievens, S.; Tavernier, J.; De Bosscher, K.; Libert, C. The interactome of the glucocorticoid receptor and its influence on the actions of glucocorticoids in combatting inflammatory and infectious diseases. *Microbiology and Molecular Biology Reviews* **2016**, 80 (2), 495–522.

[84] Scheinman, R. I.; Gualberto, A.; Jewell, C. M.; Cidlowski, J. A.; Baldwin Jr, A. S. Characterization of mechanisms involved in transrepression of NF-kappa B by activated glucocorticoid receptors. *Molecular and cellular biology* **1995**, 15 (2), 943–953.

[85] McNally, J. G.; Müller, W. G.; Walker, D.; Wolford, R.; Hager, G. L. The glucocorticoid receptor: rapid exchange with regulatory sites in living cells. *Science* **2000**, 287 (5456), 1262–1265.

[86] Dostert, A.; Heinzel, T. Negative glucocorticoid receptor response elements and their role in glucocorticoid action. *Current pharmaceutical design* **2004**, 10 (23), 2807.

[87] Chen, S.-y.; Wang, J.; Yu, G.-q.; Liu, W.; Pearce, D. Androgen and glucocorticoid receptor heterodimer formation: a possible mechanism for mutual inhibition of transcriptional activity. *Journal of Biological Chemistry* **1997**, 272 (22), 14087–14092.

[88] Savory, J. G.; Préfontaine, G. G.; Lamprecht, C.; Liao, M.; Walther, R. F.; Lefebvre, Y. A.; Haché, R. J. Glucocorticoid receptor homodimers and glucocorticoid-mineralocorticoid receptor heterodimers form in the cytoplasm through alternative dimerization interfaces. *Molecular and cellular biology* **2001**, 21 (3), 781–793.

[89] Garlatti, M.; Daheshia, M.; Slater, E.; Bouguet, J.; Hanoune, J.; Beato, M.; Barouki, R. A functional glucocorticoid-responsive unit composed of two overlapping inactive receptor-binding sites: evidence for formation of a receptor tetramer. *Molecular and cellular biology* **1994**, 14 (12), 8007–8017.

[90] Tsukamoto, T.; Demura, M.; Sudo, Y. Irreversible trimer to monomer transition of thermophilic rhodopsin upon thermal stimulation. *The Journal of Physical Chemistry B* **2014**, 118 (43), 12383–12394.

[91] Perlmann, T.; Wrange, O. Specific glucocorticoid receptor binding to DNA reconstituted in a nucleosome. *The EMBO Journal* **1988**, 7 (10), 3073–3079.

[92] Perlmann, T. Glucocorticoid receptor DNA-binding specificity is increased by the organization of DNA in nucleosomes. *Proceedings of the National Academy of Sciences* **1992**, 89 (9), 3884–3888.

[93] Perlmann, T.; Eriksson, P.; Wrange, O. Quantitative analysis of the glucocorticoid receptor-DNA interaction at the mouse mammary tumor virus glucocorticoid response element. *Journal of Biological Chemistry* **1990**, 265 (28), 17222–17229.

[94] Li, Q.; Wrange, O. Translational positioning of a nucleosomal glucocorticoid response element modulates glucocorticoid receptor affinity. *Genes & development* **1993**, 7 (12a), 2471–2482.

[95] Jin, J.; Lian, T.; Sunney Xie, X.; Su, X.-D. High-accuracy mapping of protein binding stability on nucleosomal DNA using a single-molecule method. *Journal of molecular cell biology* **2014**, 6 (5), 438–440.

[96] Cosgrove, M. S. Histone proteomics and the epigenetic regulation of nucleosome mobility. *Expert review of proteomics* **2007**, 4 (4), 465–478.

[97] Gansen, A.; Valeri, A.; Hauger, F.; Felekyan, S.; Kalinin, S.; Tóth, K.; Langowski, J.; Seidel, C. A. Nucleosome disassembly intermediates characterized by single-molecule FRET. *Proceedings of the National Academy of Sciences of the United States of America* **2009**, 106 (36), 15308–15313.

[98] Poirier, M. G.; Oh, E.; Tims, H. S.; Widom, J. Dynamics and function of compact nucleosome arrays. *Nature Structural and Molecular Biology* **2009**, 16 (9), 938–944.

[99] Grigoryev, S. A. Nucleosome spacing and chromatin higher-order folding. *Nucleus* **2012**, 3 (6), 493–499.

[100] Luo, Y.; North, J. A.; Rose, S. D.; Poirier, M. G. Nucleosomes accelerate transcription factor dissociation. *Nucleic Acids Research* **2014**, 42 (5), 3017–3027.

[101] Paul, M.; Murray, V. Use of an automated capillary DNA sequencer to investigate the interaction of cisplatin with telomeric DNA sequences. *Biomedical Chromatography* **2012**, 26 (3), 350–354.

[102] Abe, K.; Zhao, L.; Periasamy, A.; Intes, X.; Barroso, M. Non-invasive in vivo imaging of near infrared-labeled transferrin in breast cancer cells and tumors using fluorescence lifetime FRET. *PloS one* **2013**, 8 (11), e80269.

[103] Buning, R.; Van Noort, J. Single-pair FRET experiments on nucleosome conformational dynamics. *Enfermedades Infecciosas y Microbiologia Clinica* **2010**, 28 (SUPPL. 3), 1729–1740.

[104] Buning, R.; Kropff, W.; Martens, K.; Van Noort, J. SpFRET reveals changes in nucleosome breathing by neighboring nucleosomes. *Journal of Physics Condensed Matter* **2015**, 27 (6), 64103.

[105] Harriman, O.; Leake, M. Single molecule experimentation in biological physics: exploring the living component of soft condensed matter one molecule at a time. *Journal of Physics: Condensed Matter* **2011**, 23 (50), 503101.

[106] Lenn, T.; Leake, M. C. Experimental approaches for addressing fundamental biological questions in living, functioning cells with single molecule precision. *Open biology* **2012**, 2 (6), 120090.

[107] Leake, M. C. The physics of life: one molecule at a time, **2013**.

[108] Miller, H.; Zhou, Z.; Shepherd, J.; Wollman, A. J.; Leake, M. C. Single-molecule techniques in biophysics: a review of the progress in methods and applications. *Reports on Progress in Physics* **2017**, 81 (2), 024601.

[109] Sheppard, C. J.; Gu, M.; Roy, M. Signal-to-noise ratio in confocal microscope systems. *Journal of Microscopy* **1992**, 168 (3), 209–218.

[110] Oldenbourg, R.; Terada, H.; Tiberio, R.; Inoue, S. Image sharpness and contrast transfer in coherent confocal microscopy. *Journal of microscopy* **1993**, 172 (1), 31–39.

[111] Pawley, J. B. Limitations on optical sectioning in live-cell confocal microscopy. *Scanning: The Journal of Scanning Microscopies* **2002**, 24 (5), 241–246.

[112] Schermelleh, L.; Heintzmann, R.; Leonhardt, H. A guide to super-resolution fluorescence microscopy. *Journal of Cell Biology* **2010**, 190 (2), 165–175.

[113] Leung, B. O.; Chou, K. C. Review of super-resolution fluorescence microscopy for biology. *Applied spectroscopy* **2011**, 65 (9), 967–980.

[114] Beljonne, D.; Curutchet, C.; Scholes, G. D.; Silbey, R. J. Beyond Forster resonance energy transfer in biological and nanoscale systems. *The journal of physical chemistry B* **2009**, 113 (19), 6583–6599.

[115] Clegg, R. M. Förster resonance energy transfer—FRET what is it, why do it, and how it's done. *Laboratory techniques in biochemistry and molecular biology* **2009**, 33, 1–57.

[116] Sahoo, H. Förster resonance energy transfer–A spectroscopic nanoruler: Principle and applications. *Journal of Photochemistry and Photobiology C: Photochemistry Reviews* **2011**, 12 (1), 20–30.

[117] Zauner, T.; Berger-Hoffmann, R.; Müller, K.; Hoffmann, R.; Zuchner, T. Highly adaptable and sensitive protease assay based on fluorescence resonance energy transfer. *Analytical chemistry* **2011**, 83 (19), 7356–7363.

[118] Thompson, N. L. Fluorescence correlation spectroscopy. In Topics in fluorescence spectroscopy, 337–378. Springer, **2002**.

[119] Rigler, R.; Elson, E. S. Fluorescence correlation spectroscopy: theory and applications, volume 65. Springer Science & Business Media, **2012**.

[120] Haustein, E.; Schwille, P. Fluorescence correlation spectroscopy: novel variations of an established technique. *Annu. Rev. Biophys. Biomol. Struct.* **2007**, 36, 151–169.

[121] Hess, S. T.; Huang, S.; Heikal, A. A.; Webb, W. W. Biological and chemical applications of fluorescence correlation spectroscopy: a review. *Biochemistry* **2002**, 41 (3), 697–705.

[122] Elson, E. L. Fluorescence correlation spectroscopy: past, present, future. *Biophysical journal* **2011**, 101 (12), 2855–2870.

[123] Klehs, K.; Spahn, C.; Endesfelder, U.; Lee, S. F.; Fürstenberg, A.; Heilemann, M. Increasing the brightness of cyanine fluorophores for single-molecule and superresolution imaging. *ChemPhysChem* **2014**, 15 (4), 637–641.

[124] Cooper, M.; Ebner, A.; Briggs, M.; Burrows, M.; Gardner, N.; Richardson, R.; West, R. Cy3B™: improving the performance of cyanine dyes. *Journal of fluorescence* **2004**, 14 (2), 145–150.

[125] Ploetz, E.; Lerner, E.; Husada, F.; Roelfs, M.; Chung, S.; Hohlbein, J.; Weiss, S.; Cordes, T. Förster resonance energy transfer and protein-induced fluorescence enhancement as synergetic multi-scale molecular rulers. *Scientific reports* **2016**, 6 (1), 1–18.

[126] Holden, S. J.; Uphoff, S.; Hohlbein, J.; Yadin, D.; Le Reste, L.; Britton, O. J.; Kapanidis, A. N. Defining the limits of single-molecule FRET resolution in TIRF microscopy. *Biophysical journal* **2010**, 99 (9), 3102–3111.

[127] Schwille, P.; Kummer, S.; Heikal, A. A.; Moerner, W.; Webb, W. W. Fluorescence correlation spectroscopy reveals fast optical excitation-driven intramolecular dynamics of yellow fluorescent proteins. *Proceedings of the National Academy of Sciences* **2000**, 97 (1), 151–156.

[128] Kremers, G.-J.; Goedhart, J.; van Munster, E. B.; Gadella, T. W. Cyan and yellow super fluorescent proteins with improved brightness, protein folding, and FRET Förster radius. *Biochemistry* **2006**, 45 (21), 6570–6580.

[129] Kubin, R. F.; Fletcher, A. N. Fluorescence quantum yields of some rhodamine dyes. *Journal of Luminescence* **1982**, 27 (4), 455–462.

[130] Müller, B. K.; Reuter, A.; Simmel, F. C.; Lamb, D. C. Single-pair FRET characterization of DNA tweezers. *Nano letters* **2006**, 6 (12), 2814–2820.

[131] Fields, A. P.; Cohen, A. E. Anti-Brownian traps for studies on single molecules. *Methods in enzymology* **2010**, 475, 149–174.

[132] Prendergast, F. G.; Mann, K. G. Chemical and physical properties of aequorin and the green fluorescent protein isolated from Aequorea forskalea. *Biochemistry* **1978**, 17 (17), 3448–3453.

[133] Ingargiola, A.; Lerner, E.; Chung, S. Y.; Weiss, S.; Michalet, X. FRET-Bursts: An open source toolkit for analysis of freely-diffusing Single-molecule FRET. *PLoS ONE* **2016**, 11 (8).

[134] Laurence, T.; Fore, S.; Huser, T. A fast, flexible algorithm for calculating correlations in Fluorescence Correlation Spectroscopy. *Optics Letters* **2005**, 31 (6).

[135] Chung, H. S.; Louis, J. M.; Eaton, W. A. Distinguishing between protein dynamics and dye photophysics in single-molecule FRET experiments. *Biophysical Journal* **2010**, 98 (4), 696–706.

[136] Stennett, E. M.; Ciuba, M. A.; Levitus, M. Photophysical processes in single molecule organic fluorescent probes. *Chemical Society Reviews* **2014**, 43 (4), 1057–1075.

[137] Müller, B. K.; Zaychikov, E.; Bräuchle, C.; Lamb, D. C. Pulsed interleaved excitation. *Biophysical journal* **2005**, 89 (5), 3508–3522.

[138] Ries, J.; Petráek, Z.; García-Sáez, A. J.; Schwille, P. A comprehensive framework for fluorescence cross-correlation spectroscopy. *New Journal of Physics* **2010**, 12.

[139] Bacia, K.; Petrášek, Z.; Schwille, P. Correcting for spectral cross-talk in dual-color fluorescence cross-correlation spectroscopy. *ChemPhysChem* **2012**, 13 (5), 1221–1231.

[140] Foo, Y. H.; Naredi-Rainer, N.; Lamb, D. C.; Ahmed, S.; Wohland, T. Factors affecting the quantification of biomolecular interactions by fluorescence cross-correlation spectroscopy. *Biophysical journal* **2012**, 102 (5), 1174–1183.

[141] Hendrix, J.; Lamb, D. C. Implementation and application of pulsed interleaved excitation for dual-color FCS and RICS. In Fluorescence Spectroscopy and Microscopy, 653–682. Springer, **2014**.

[142] Schwille, P.; Meyer-Almes, F.-J.; Rigler, R. Dual-color fluorescence cross-correlation spectroscopy for multicomponent diffusional analysis in solution. *Biophysical journal* **1997**, 72 (4), 1878–1886.

[143] Medina, M. A.; Schwille, P. Fluorescence correlation spectroscopy for the detection and study of single molecules in biology. *Bioessays* **2002**, 24 (8), 758–764.

[144] Meseth, U.; Wohland, T.; Rigler, R.; Vogel, H. Resolution of fluorescence correlation measurements. *Biophysical journal* **1999**, 76 (3), 1619–1631.

[145] Magde, D.; Elson, E.; Webb, W. W. Thermodynamic fluctuations in a reacting system—measurement by fluorescence correlation spectroscopy. *Physical review letters* **1972**, 29 (11), 705.

[146] Poirier, M. G.; Bussiek, M.; Langowski, J.; Widom, J. Spontaneous access to DNA target sites in folded chromatin fibers. *Journal of molecular biology* **2008**, 379 (4), 772–786.

[147] Culbertson, M. J.; Burden, D. L. A distributed algorithm for multi-tau autocorrelation. *Review of scientific instruments* **2007**, 78 (4), 044102.

[148] Sint, D.; Raso, L.; Traugott, M. Advances in multiplex PCR: balancing primer efficiencies and improving detection success. *Methods in ecology and evolution* **2012**, 3 (5), 898–905.

[149] Singh, C.; Roy-Chowdhuri, S. Quantitative real-time PCR: recent advances. *Clinical Applications of PCR* **2016**, 161–176.

[150] Zahiri, J.; Hannon Bozorgmehr, J.; Masoudi-Nejad, A. Computational prediction of protein–protein interaction networks: algorithms and resources. *Current genomics* **2013**, 14 (6), 397–414.

[151] Angermueller, C.; Pärnamaa, T.; Parts, L.; Stegle, O. Deep learning for computational biology. *Molecular systems biology* **2016**, 12 (7), 878.

[152] Regmi, R.; Al Balushi, A. A.; Rigneault, H.; Gordon, R.; Wenger, J. Nanoscale volume confinement and fluorescence enhancement with double nanohole aperture. *Scientific reports* **2015**, 5 (1), 1–10.

[153] Kuang, C.; Liu, Y.; Hao, X.; Luo, D.; Liu, X. Creating attoliter detection volume by microsphere photonic nanojet and fluorescence depletion. *Optics Communications* **2012**, 285 (4), 402–406.

[154] Estrada, L. C.; Aramendía, P. F.; Martínez, O. E. 10000 times volume reduction for fluorescence correlation spectroscopy using nano-antennas. *Optics express* **2008**, 16 (25), 20597–20602.

[155] Zheng, Y.; Nguyen, J.; Wei, Y.; Sun, Y. Recent advances in microfluidic techniques for single-cell biophysical characterization. *Lab on a Chip* **2013**, 13 (13), 2464–2483.

[156] Larkin, J. E.; Frank, B. C.; Gavras, H.; Sultana, R.; Quackenbush, J. Independence and reproducibility across microarray platforms. *Nature methods* **2005**, 2 (5), 337–344.

[157] Baker, M. Reproducibility crisis. *Nature* **2016**, 533 (26), 353–66.

[158] Iqbal, S. A.; Wallach, J. D.; Khoury, M. J.; Schully, S. D.; Ioannidis, J. P. Reproducible research practices and transparency across the biomedical literature. *PLoS biology* **2016**, 14 (1), e1002333.

[159] Petersen, E. J.; Hirsch, C.; Elliott, J. T.; Krug, H. F.; Aengenheister, L.; Arif, A. T.; Bogni, A.; Kinsner-Ovaskainen, A.; May, S.; Walser, T.; et al. Cause-and-effect analysis as a tool to improve the reproducibility of nanobioassays: four case studies. *Chemical research in toxicology* **2019**, 33 (5), 1039–1054.

[160] Elofsson, A.; Hess, B.; Lindahl, E.; Onufriev, A.; Van der Spoel, D.; Wallqvist, A. Ten simple rules on how to create open access and reproducible molecular simulations of biological systems, **2019**.

[161] Bustin, S. A.; Wittwer, C. T. MIQE: a step toward more robust and reproducible quantitative PCR. *Clinical chemistry* **2017**, 63 (9), 1537–1538.

[162] De Marco, A. Nanomaterial bio-activation and macromolecules functionalization: the search for reliable protocols. *Protein expression and purification* **2018**, 147, 49–54.

[163] Di Vito, A.; Reitano, E.; Poggi, L.; Iaboni, M. Biotin oligonucleotide labeling reactions: A method to assess their effectiveness and reproducibility. *Analytical biochemistry* **2020**, 593, 113590.

[164] Teixeira da Silva, J. A. Room temperature in scientific protocols and experiments should be defined: a reproducibility issue, **2021**.

[165] Rychlik, W.; Spencer, W.; Rhoads, R. Optimization of the annealing temperature for DNA amplification in vitro. *Nucleic acids research* **1990**, 18 (21), 6409–6412.

[166] Stadhouders, R.; Pas, S. D.; Anber, J.; Voermans, J.; Mes, T. H.; Schutten, M. The effect of primer-template mismatches on the detection and quantification of nucleic acids using the 5ńuclease assay. *The Journal of Molecular Diagnostics* **2010**, 12 (1), 109–117.

[167] Frey, U. H.; Bachmann, H. S.; Peters, J.; Siffert, W. PCR-amplification of GC-rich regions:'slowdown PCR'. *Nature protocols* **2008**, 3 (8), 1312–1317.

[168] Lis, J. T.; Schleif, R. Size fractionation of double-stranded DNA by precipitation with polyethylene glycol. *Nucleic acids research* **1975**, 2 (3), 383–390.

[169] Cheng, C.; Jia, J.-L.; Ran, S.-Y. Polyethylene glycol and divalent salt-induced DNA re-entrant condensation revealed by single molecule measurements. *Soft Matter* **2015**, 11 (19), 3927–3935.

[170] Borah, P. Primer designing for PCR. *Science Vision* **2011**, 11 (3), 134–136.

[171] Kaczmarczyk, A.; Brouwer, T. B.; Pham, C.; Dekker, N. H.; Noort, J. v. Probing chromatin structure with magnetic tweezers. In Nanoscale Imaging, 297–323. Springer, **2018**.

[172] Koopmans, W. J.; Brehm, A.; Logie, C.; Schmidt, T.; Van Noort, J. Single-pair FRET microscopy reveals mononucleosome dynamics. *Journal of Fluorescence* **2007**, 17 (6), 785–795.

[173] Böhm, V.; Hieb, A. R.; Andrews, A. J.; Gansen, A.; Rocker, A.; Tóth, K.; Luger, K.; Langowski, J. Nucleosome accessibility governed by the dimer/tetramer interface. *Nucleic Acids Research* **2011**, 39 (8), 3093–3102.

[174] North, J. A.; Shimko, J. C.; Javaid, S.; Mooney, A. M.; Shoffner, M. A.; Rose, S. D.; Bundschuh, R.; Fishel, R.; Ottesen, J. J.; Poirier, M. G. Regulation of the nucleosome unwrapping rate controls DNA accessibility. *Nucleic Acids Research* **2012**, 40 (20), 10215–10227.

[175] Schiessel, H. The nucleosome: a transparent, slippery, sticky and yet stable DNA-protein complex. *The European Physical Journal E* **2006**, 19 (3), 251–262.

[176] Koopmans, W. J.; Schmidt, T.; van Noort, J. Nucleosome Immobilization Strategies for Single-Pair FRET Microscopy. *ChemPhysChem* **2008**, 9 (14), 2002–2009.

[177] Kelbauskas, L.; Sun, J.; Woodbury, N.; Lohr, D. Nucleosomal stability and dynamics vary significantly when viewed by internal versus terminal labels. *Biochemistry* **2008**, 47 (36), 9627–9635.

[178] Gansen, A.; Tóth, K.; Schwarz, N.; Langowski, J. Structural variability of nucleosomes detected by single-pair förster resonance energy transfer: Histone acetylation, sequence variation, and salt effects. *Journal of Physical Chemistry B* **2009**, 113 (9), 2604–2613.

[179] Van Holde, K.; Zlatanova, A. G., J; Moudrianakis, E. Elements of chromatin structure: histones, nucleosome, and fibres. *Chromatin Structure and Gene Expression* **1995**, 1–26.

[180] Szerlong, H. J.; Hansen, J. C. Nucleosome distribution and linker DNA: Connecting nuclear function to dynamic chromatin structure, **2011**.

[181] Li, Q.; Wrange, O. Accessibility of a glucocorticoid response element in a nucleosome depends on its rotational positioning. *Molecular and Cellular Biology* **1995**, 15 (8), 4375–4384.

[182] Lone, I. N.; Shukla, M. S.; Charles Richard, J. L.; Peshev, Z. Y.; Dimitrov, S.; Angelov, D. Binding of NF-κB to Nucleosomes: Effect of Translational Positioning, Nucleosome Remodeling and Linker Histone H1. *PLoS Genetics* **2013**, 9 (9).

[183] Reul, J.; Kloet, E. D. Two receptor systems for corticosterone in rat brain: microdistribution and differential occupation. *Endocrinology* **1985**, 117 (6), 2505–2511.

[184] Htun, H.; Barsony, J.; Renyi, I.; Gould, D. L.; Hager, G. L. Visualization of glucocorticoid receptor translocation and intranuclear organization in living cells with a green fluorescent protein chimera. *Proceedings of the National Academy of Sciences of the United States of America* **1996**, 93 (10), 4845–4850.

[185] Schiller, B. J.; Chodankar, R.; Watson, L. C.; Stallcup, M. R.; Yamamoto, K. R. Glucocorticoid receptor binds half sites as a monomer and regulates specific target genes. *Genome biology* **2014**, 15 (8), 418.

[186] Schoneveld, O. J.; Gaemers, I. C.; Lamers, W. H. Mechanisms of glucocorticoid signalling. *Biochimica et Biophysica Acta (BBA)-Gene Structure and Expression* **2004**, 1680 (2), 114–128.

[187] Dahlman-Wright, K.; Wright, A.; Gustafsson, J.-A.; Carlstedt-Duke, J. Interaction of the glucocorticoid receptor DNA-binding domain with DNA as a dimer is mediated by a short segment of five amino acids. *Journal of Biological Chemistry* **1991**, 266 (5), 3107–3112.

[188] Datson, N.; Polman, J.; De Jonge, R.; Van Boheemen, P.; Van Maanen, E.; Welten, J.; McEwen, B.; Meiland, H.; Meijer, O. Specific regulatory motifs predict glucocorticoid responsiveness of hippocampal gene expression. *Endocrinology* **2011**, 152 (10), 3749–3757.

[189] Kelbauskas, L.; Chan, N.; Bash, R.; Yodh, J.; Woodbury, N.; Lohr, D. Sequence-dependent nucleosome structure and stability variations detected by Förster resonance energy transfer. *Biochemistry* **2007**, 46 (8), 2239–2248.

[190] Flaus, A.; Richmond, T. J. Positioning and stability of nucleosomes on MMTV 3ĹTR sequences. *Journal of molecular biology* **1998**, 275 (3), 427–441.

[191] Anderson, J.; Widom, J. Sequence and position-dependence of the equilibrium accessibility of nucleosomal DNA target sites. *Journal of molecular biology* **2000**, 296 (4), 979–987.

[192] Sharma, S.; Dokholyan, N. V. DNA sequence mediates nucleosome structure and stability. *Biophysical Journal* **2008**, 94 (1), 1–3.

[193] Jiang, C.; Pugh, B. F. A compiled and systematic reference map of nucleosome positions across the Saccharomyces cerevisiae genome. *Genome Biology* **2009**, 10 (10), 1–11.

[194] MacIsaac, K. D.; Wang, T.; Gordon, D. B.; Gifford, D. K.; Stormo, G. D.; Fraenkel, E. An improved map of conserved regulatory sites for Saccharomyces cerevisiae. *BMC Bioinformatics* **2006**, 7, 1–14.

[195] Lin, Y.-S.; Carey, M. F.; Ptashne, M.; Green, M. R. GAL4 derivatives function alone and synergistically with mammalian activators in vitro. *Cell* **1988**, 54 (5), 659–664.

[196] Record Jr, M. T.; Lohman, T. M.; De Haseth, P. Ion effects on ligand-nucleic acid interactions. *Journal of molecular biology* **1976**, 107 (2), 145–158.

[197] Krichevsky, O.; Bonnet, G. Fluorescence correlation spectroscopy: the technique and its applications. *Reports on Progress in Physics* **2002**, 65 (2), 251.

[198] Torres, T.; Levitus, M. Measuring conformational dynamics: A new FCS-FRET approach. *Journal of Physical Chemistry B* **2007**, 111 (25), 7392–7400.

[199] Tims, H. S.; Gurunathan, K.; Levitus, M.; Widom, J. Dynamics of nucleosome invasion by DNA binding proteins. *Journal of molecular biology* **2011**, 411 (2), 430–448.

[200] Lee, N. K.; Kapanidis, A. N.; Wang, Y.; Michalet, X.; Mukhopadhyay, J.; Ebright, R. H.; Weiss, S. Accurate FRET measurements within single diffusing biomolecules using alternating-laser excitation. *Biophysical journal* **2005**, 88 (4), 2939–2953.

[201] Hazan, N. P.; Tomov, T. E.; Tsukanov, R.; Liber, M.; Berger, Y.; Masoud, R.; Toth, K.; Langowski, J.; Nir, E. Nucleosome core particle disassembly and assembly kinetics studied using single-molecule fluorescence. *Biophysical journal* **2015**, 109 (8), 1676–1685.

[202] Gansen, A.; Felekyan, S.; Kühnemuth, R.; Lehmann, K.; Tóth, K.; Seidel, C. A.; Langowski, J. High precision FRET studies reveal reversible transitions in nucleosomes between microseconds and minutes. *Nature Communications* **2018**, 9 (1), 1–13.

[203] Gibson, M. D.; Gatchalian, J.; Slater, A.; Kutateladze, T. G.; Poirier, M. G. PHF1 Tudor and N-terminal domains synergistically target partially unwrapped nucleosomes to increase DNA accessibility. *Nucleic acids research* **2017**, 45 (7), 3767–3776.

[204] Bowman, G. D.; Poirier, M. G. Post-translational modifications of histones that influence nucleosome dynamics. *Chemical reviews* **2014**, 115 (6), 2274–2295.

[205] Rothbart, S. B.; Strahl, B. D. Interpreting the language of histone and DNA modifications. *Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms* **2014**, 1839 (8), 627–643.

[206] Bannister, A. J.; Kouzarides, T. Regulation of chromatin by histone modifications. *Cell research* **2011**, 21 (3), 381–395.

[207] Cosgrove, M. S.; Boeke, J. D.; Wolberger, C. Regulated nucleosome mobility and the histone code. *Nature structural & molecular biology* **2004**, 11 (11), 1037–1043.

[208] Mersfelder, E. L.; Parthun, M. R. The tale beyond the tail: histone core domain modifications and the regulation of chromatin structure. *Nucleic acids research* **2006**, 34 (9), 2653–2662.

[209] Kingston, R. E.; Narlikar, G. J. ATP-dependent remodeling and acetylation as regulators of chromatin fluidity. *Genes & development* **1999**, 13 (18), 2339–2352.

[210] Saha, A.; Wittmeyer, J.; Cairns, B. R. Chromatin remodelling: the industrial revolution of DNA around histones. *Nature reviews Molecular cell biology* **2006**, 7 (6), 437–447.

[211] Bowerman, S.; Wereszczynski, J. Effects of macroH2A and H2A. Z on nucleosome dynamics as elucidated by molecular dynamics simulations. *Biophysical journal* **2016**, 110 (2), 327–337.

[212] Xiao, X.; Liu, C.; Pei, Y.; Wang, Y.-Z.; Kong, J.; Lu, K.; Ma, L.; Dou, S.-X.; Wang, P.-Y.; Li, G.; et al. Histone H2A ubiquitination reinforces mechanical stability and asymmetry at the single-nucleosome level. *Journal of the American Chemical Society* **2020**, 142 (7), 3340–3345.

[213] Zentner, G. E.; Henikoff, S. Regulation of nucleosome dynamics by histone modifications. *Nature structural & molecular biology* **2013**, 20 (3), 259–266.

[214] Tessarz, P.; Kouzarides, T. Histone core modifications regulating nucleosome structure and dynamics. *Nature reviews Molecular cell biology* **2014**, 15 (11), 703–708.

[215] Mutskov, V.; Gerber, D.; Angelov, D.; Ausio, J.; Workman, J.; Dimitrov, S. Persistent interactions of core histone tails with nucleosomal DNA following acetylation and transcription factor binding. *Molecular and cellular biology* **1998**, 18 (11), 6293–6304.

[216] Polach, K.; Lowary, P.; Widom, J. Effects of core histone tail domains on the equilibrium constants for dynamic DNA site accessibility in nucleosomes. *Journal of molecular biology* **2000**, 298 (2), 211–223.

[217] Neumann, H.; Hancock, S. M.; Buning, R.; Routh, A.; Chapman, L.; Somers, J.; Owen-Hughes, T.; van Noort, J.; Rhodes, D.; Chin, J. W. A method for genetically installing site-specific acetylation in recombinant histones defines the effects of H3 K56 acetylation. *Molecular cell* **2009**, 36 (1), 153–163.

[218] Levenson, J.; Wood, M. 4.42 - Epigenetics – Chromatin Structure and Rett Syndrome. *Learning and Memory: A Comprehensive Reference* **2008**, 859–878.

[219] Sun, Z.; Zhang, Y.; Jia, J.; Fang, Y.; Tang, Y.; Wu, H.; Fang, D. H3K36me3, message from chromatin to DNA damage repair. *Cell & bioscience* **2020**, 10 (1), 1–9.

[220] Tesina, P.; Čermáková, K.; Hořejší, M.; Procházková, K.; Fábry, M.; Sharma, S.; Christ, F.; Demeulemeester, J.; Debyser, Z.; De Rijck, J.; et al. Multiple cellular proteins interact with LEDGF/p75 through a conserved unstructured consensus motif. *Nature communications* **2015**, 6 (1), 1–14.

[221] Eidahl, J. O.; Crowe, B. L.; North, J. A.; McKee, C. J.; Shkriabai, N.; Feng, L.; Plumb, M.; Graham, R. L.; Gorelick, R. J.; Hess, S.; et al. Structural basis for high-affinity binding of LEDGF PWWP to mononucleosomes. *Nucleic acids research* **2013**, 41 (6), 3924–3936.

[222] Turlure, F.; Maertens, G.; Rahman, S.; Cherepanov, P.; Engelman, A. A tripartite DNA-binding element, comprised of the nuclear localization signal and two AT-hook motifs, mediates the association of LEDGF/p75 with chromatin in vivo. *Nucleic acids research* **2006**, 34 (5), 1653–1665.

[223] Llano, M.; Vanegas, M.; Hutchins, N.; Thompson, D.; Delgado, S.; Poeschla, E. M. Identification and characterization of the chromatin-binding domains of the HIV-1 integrase interactor LEDGF/p75. *Journal of molecular biology* **2006**, 360 (4), 760–773.

[224] McNeely, M.; Hendrix, J.; Busschots, K.; Boons, E.; Deleersnijder, A.; Gerard, M.; Christ, F.; Debyser, Z. In vitro DNA tethering of HIV-1 integrase by the transcriptional coactivator LEDGF/p75. *Journal of molecular biology* **2011**, 410 (5), 811–830.

[225] Bartholomeeusen, K.; De Rijck, J.; Busschots, K.; Desender, L.; Gijsbers, R.; Emiliani, S.; Benarous, R.; Debyser, Z.; Christ, F. Differential interaction of HIV-1 integrase and Jpo2 with the C terminus of LEDGF/p75. *Journal of molecular biology* **2007**, 372 (2), 407–421.

[226] Caselli, M.; Latterini, L.; Ponterini, G. Consequences of H-dimerization on the photophysics and photochemistry of oxacarbocyanines. *Physical Chemistry Chemical Physics* **2004**, 6 (14), 3857–3863.

[227] Liu, Y.; Feshitan, J. A.; Wei, M.-Y.; Borden, M. A.; Yuan, B. Ultrasound-modulated fluorescence based on donor-acceptor-labeled microbubbles. *Journal of biomedical optics* **2015**, 20 (3), 036012.

[228] Holzmeister, P.; Wünsch, B.; Gietl, A.; Tinnefeld, P. Single-molecule photophysics of dark quenchers as non-fluorescent FRET acceptors. *Photochemical & Photobiological Sciences* **2014**, 13 (6), 853–858.

[229] Morrison, E. A.; Baweja, L.; Poirier, M. G.; Wereszczynski, J.; Musselman, C. A. Nucleosome composition regulates the histone H3 tail conformational ensemble and accessibility. *Nucleic acids research* **2021**, 49 (8), 4750–4767.

[230] Ghoneim, M.; Fuchs, H. A.; Musselman, C. A. Histone tail conformations: a fuzzy affair with DNA. *Trends in Biochemical Sciences* **2021**.

[231] Pan, Y.; Tsai, C.-J.; Ma, B.; Nussinov, R. Mechanisms of transcription factor selectivity. *Trends in Genetics* **2010**, 26 (2), 75–83.

[232] Zaret, K. S.; Lerner, J.; Iwafuchi-Doi, M. Chromatin scanning by dynamic binding of pioneer factors. *Molecular cell* **2016**, 62 (5), 665–667.

[233] Sung, M.-H.; Guertin, M. J.; Baek, S.; Hager, G. L. DNase footprint signatures are dictated by factor dynamics and DNA sequence. *Molecular cell* **2014**, 56 (2), 275–285.

[234] Groeneweg, F. L.; van Royen, M. E.; Fenz, S.; Keizer, V. I.; Geverts, B.; Prins, J.; de Kloet, E. R.; Houtsmuller, A. B.; Schmidt, T. S.; Schaaf, M. J. Quantitation of glucocorticoid receptor DNA-binding dynamics by single-molecule microscopy and FRAP. *PloS one* **2014**, 9 (3), e90532.

[235] Stormo, G. D.; Zhao, Y. Determining the specificity of protein–DNA interactions. *Nature Reviews Genetics* **2010**, 11 (11), 751–760.

[236] Lin, M.; Guo, J.-t. New insights into protein–DNA binding specificity from hydrogen bond based comparative study. *Nucleic acids research* **2019**, 47 (21), 11103–11113.

[237] Schreiber, G.; Keating, A. E. Protein binding specificity versus promiscuity. *Current opinion in structural biology* **2011**, 21 (1), 50–61.

[238] Greenspan, N. S. Cohen's Conjecture, Howard's Hypothesis, and Ptashne's Ptruth: an exploration of the relationship between affinity and specificity. *Trends in immunology* **2010**, 31 (4), 138–143.

[239] Corona, R. I.; Guo, J.-t. Statistical analysis of structural determinants for protein–DNA-binding specificity. *Proteins: Structure, Function, and Bioinformatics* **2016**, 84 (8), 1147–1161.

[240] Bakiri, L.; Matsuo, K.; Wisniewska, M.; Wagner, E. F.; Yaniv, M. Promoter specificity and biological activity of tethered AP-1 dimers. *Molecular and cellular biology* **2002**, 22 (13), 4952–4964.

[241] Hess, J.; Angel, P.; Schorpp-Kistner, M. AP-1 subunits: quarrel and harmony among siblings. *Journal of cell science* **2004**, 117 (25), 5965–5973.

[242] Bohmann, D.; Bos, T. J.; Admon, A.; Nishimura, T.; Vogt, P. K.; Tjian, R. Human proto-oncogene c-jun encodes a DNA binding protein with structural and functional properties of transcription factor AP-1. *Science* **1987**, 238 (4832), 1386–1392.

[243] Karin, M.; Liu, Z.-g.; Zandi, E. AP-1 function and regulation. *Current opinion in cell biology* **1997**, 9 (2), 240–246.

[244] Biddie, S. C.; John, S.; Sabo, P. J.; Thurman, R. E.; Johnson, T. A.; Schiltz, R. L.; Miranda, T. B.; Sung, M.-H.; Trump, S.; Lightman, S. L.; et al. Transcription factor AP1 potentiates chromatin accessibility and glucocorticoid receptor binding. *Molecular cell* **2011**, 43 (1), 145–155.

[245] Rishi, V.; Bhattacharya, P.; Chatterjee, R.; Rozenberg, J.; Zhao, J.; Glass, K.; Fitzgerald, P.; Vinson, C. CpG methylation of half-CRE sequences creates C/EBPα binding sites that activate some tissue-specific genes. *Proceedings of the National Academy of Sciences* **2010**, 107 (47), 20311–20316.

[246] Gustems, M.; Woellmer, A.; Rothbauer, U.; Eck, S. H.; Wieland, T.; Lutter, D.; Hammerschmidt, W. c-Jun/c-Fos heterodimers regulate cellular genes via a newly identified class of methylated DNA sequence motifs. *Nucleic acids research* **2014**, 42 (5), 3059–3072.

[247] John, M.; Leppik, R.; Busch, S. J.; Granger-Schnarr, M.; Schnarr, M. DNA binding of Jun and Fos bZip domains: homodimers and heterodimers induce a DNA conformational change in solution. *Nucleic acids research* **1996**, 24 (22), 4487–4494.

[248] Abate, C.; Luk, D.; Gentz, R.; Rauscher, F. J.; Curran, T. Expression and purification of the leucine zipper and DNA-binding domains of Fos and Jun: both Fos and Jun contact DNA directly. *Proceedings of the National Academy of Sciences* **1990**, 87 (3), 1032–1036.

[249] Nakabeppu, Y.; Ryder, K.; Nathans, D. DNA binding activities of three murine Jun proteins: stimulation by Fos. *Cell* **1988**, 55 (5), 907–915.

[250] Halazonetis, T. D.; Georgopoulos, K.; Greenberg, M. E.; Leder, P. c-Jun dimerizes with itself and with c-Fos, forming complexes of different DNA binding affinities. *Cell* **1988**, 55 (5), 917–924.

[251] Ryseck, R.-P.; Bravo, R. c-JUN, JUN B, and JUN D differ in their binding affinities to AP-1 and CRE consensus sequences: effect of FOS proteins. *Oncogene* **1991**, 6 (4), 533–542.

[252] Rauscher, F. d.; Voulalas, P. J.; Franza, B.; Curran, T. Fos and Jun bind cooperatively to the AP-1 site: reconstitution in vitro. *Genes & development* **1988**, 2 (12b), 1687–1699.

[253] Eferl, R.; Wagner, E. F. AP-1: a double-edged sword in tumorigenesis. *Nature Reviews Cancer* **2003**, 3 (11), 859–868.

[254] Yoon, H.; Kim, M.; Jang, K.; Shin, M.; Besser, A.; Xiao, X.; Zhao, D.; Wander, S. A.; Briegel, K.; Morey, L.; et al. p27 transcriptionally coregulates cJun to drive programs of tumor progression. *Proceedings of the National Academy of Sciences* **2019**, 116 (14), 7005–7014.

[255] Brennan, A.; Leech, J. T.; Kad, N. M.; Mason, J. M. Selective antagonism of cJun for cancer therapy. *Journal of Experimental & Clinical Cancer Research* **2020**, 39 (1), 1–16.

[256] Risse, G.; Jooss, K.; Neuberg, M.; Brüller, H.; Müller, R. Asymmetrical recognition of the palindromic AP1 binding site (TRE) by Fos protein complexes. *The EMBO journal* **1989**, 8 (12), 3825–3832.

[257] Chinenov, Y.; Kerppola, T. K. Close encounters of many kinds: Fos-Jun interactions that mediate transcription regulatory specificity. *Oncogene* **2001**, 20 (19), 2438–2452.

[258] Schaaf, M. J.; Lewis-Tuffin, L. J.; Cidlowski, J. A. Ligand-selective targeting of the glucocorticoid receptor to nuclear subdomains is associated with decreased receptor mobility. *Molecular Endocrinology* **2005**, 19 (6), 1501–1515.

[259] Picard, D.; Yamamoto, K. R. Two signals mediate hormone-dependent nuclear localization of the glucocorticoid receptor. *The EMBO journal* **1987**, 6 (11), 3333–3340.

[260] Schoenmakers, E.; ALEN, P.; Verrijdt, G.; PEETERS, B.; Verhoeven, G.; Rombauts, W.; Claessens, F. Differential DNA binding by the androgen and glucocorticoid receptors involves the second Zn-finger and a C-terminal extension of the DNA-binding domains. *Biochemical Journal* **1999**, 341 (3), 515–521.

[261] Elbi, C.; Walker, D. A.; Romero, G.; Sullivan, W. P.; Toft, D. O.; Hager, G. L.; DeFranco, D. B. Molecular chaperones function as steroid

receptor nuclear mobility factors. *Proceedings of the National Academy of Sciences* **2004**, 101 (9), 2876–2881.

[262] Ratman, D.; Berghe, W. V.; Dejager, L.; Libert, C.; Tavernier, J.; Beck, I. M.; De Bosscher, K. How glucocorticoid receptors modulate the activity of other transcription factors: a scope beyond tethering. *Molecular and cellular endocrinology* **2013**, 380 (1-2), 41–54.

[263] Voss, T. C.; Schiltz, R. L.; Sung, M.-H.; Yen, P. M.; Stamatoyannopoulos, J. A.; Biddie, S. C.; Johnson, T. A.; Miranda, T. B.; John, S.; Hager, G. L. Dynamic exchange at regulatory elements during chromatin remodeling underlies assisted loading mechanism. *Cell* **2011**, 146 (4), 544–554.

[264] King, H. A.; Trotter, K. W.; Archer, T. K. Chromatin remodeling during glucocorticoid receptor regulated transactivation. *Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms* **2012**, 1819 (7), 716–726.

[265] Keizer, V. I.; Coppola, S.; Houtsmuller, A. B.; Geverts, B.; van Royen, M. E.; Schmidt, T.; Schaaf, M. J. Repetitive switching between DNA-binding modes enables target finding by the glucocorticoid receptor. *Journal of cell science* **2019**, 132 (5).

[266] Chen, C.; Bundschuh, R. Quantitative models for accelerated protein dissociation from nucleosomal DNA. *Nucleic acids research* **2014**, 42 (15), 9753–9760.

[267] Schaaf, M. J.; Cidlowski, J. A. Molecular determinants of glucocorticoid receptor mobility in living cells: the importance of ligand affinity. *Molecular and cellular biology* **2003**, 23 (6), 1922–1934.

[268] Eriksson, P.; Daneholt, B.; Wrange, Ö. The glucocorticoid receptor in homodimeric and monomeric form visualised by electron microscopy. *Journal of structural biology* **1991**, 107 (1), 48–55.

[269] Cairns, W.; Cairns, C.; Pongratz, I.; Poellinger, L.; Okret, S. Assembly of a glucocorticoid receptor complex prior to DNA binding enhances its specific interaction with a glucocorticoid response element. *Journal of Biological Chemistry* **1991**, 266 (17), 11221–11226.

[270] Hu, T.; Grosberg, A. Y.; Shklovskii, B. How proteins search for their specific sites on DNA: the role of DNA conformation. *Biophysical journal* **2006**, 90 (8), 2731–2744.

[271] Eriksson, M.; Härd, T.; Nilsson, L. Molecular dynamics simulations of the glucocorticoid receptor DNA-binding domain in complex with DNA and free in solution. *Biophysical journal* **1995**, 68 (2), 402–426.

[272] Halford, S. E.; Marko, J. F. How do site-specific DNA-binding proteins find their targets? *Nucleic acids research* **2004**, 32 (10), 3040–3052.

[273] Murugan, R. Theory of site-specific DNA-protein interactions in the presence of conformational fluctuations of DNA binding domains. *Biophysical Journal* **2010**, 99 (2), 353–359.

[274] Swinstead, E. E.; Miranda, T. B.; Paakinaho, V.; Baek, S.; Goldstein, I.; Hawkins, M.; Karpova, T. S.; Ball, D.; Mazza, D.; Lavis, L. D.; et al. Steroid receptors reprogram FoxA1 occupancy through dynamic chromatin transitions. *Cell* **2016**, 165 (3), 593–605.

[275] Zhou, H.-X.; Szabo, A. Enhancement of association rates by nonspecific binding to DNA and cell membranes. *Physical review letters* **2004**, 93 (17), 178101.

[276] Klenin, K. V.; Merlitz, H.; Langowski, J.; Wu, C.-X. Facilitated diffusion of DNA-binding proteins. *Physical review letters* **2006**, 96 (1), 018104.

[277] Elcock, A. H. Models of macromolecular crowding effects and the need for quantitative comparisons with experiment. *Current opinion in structural biology* **2010**, 20 (2), 196–206.

[278] Gomez, D.; Klumpp, S. Biochemical reactions in crowded environments: revisiting the effects of volume exclusion with simulations. *Frontiers in Physics* **2015**, 3, 45.

[279] Mirny, L.; Slutsky, M.; Wunderlich, Z.; Tafvizi, A.; Leith, J.; Kosmrlj, A. How a protein searches for its site on DNA: the mechanism of facilitated diffusion. *Journal of Physics A: Mathematical and Theoretical* **2009**, 42 (43), 434013.

[280] Bancaud, A.; Huet, S.; Daigle, N.; Mozziconacci, J.; Beaudouin, J.; Ellenberg, J. Molecular crowding affects diffusion and binding of nuclear proteins in heterochromatin and reveals the fractal organization of chromatin. *The EMBO journal* **2009**, 28 (24), 3785–3798.

[281] Ellis, R. J. Macromolecular crowding: obvious but underappreciated. *Trends in biochemical sciences* **2001**, 26 (10), 597–604.

[282] Richter, K.; Nessling, M.; Lichter, P. Macromolecular crowding and its potential impact on nuclear function. *Biochimica et Biophysica Acta (BBA)-Molecular Cell Research* **2008**, 1783 (11), 2100–2107.

[283] Akabayov, B.; Akabayov, S. R.; Lee, S.-J.; Wagner, G.; Richardson, C. C. Impact of macromolecular crowding on DNA replication. *Nature communications* **2013**, 4 (1), 1–10.