FEBS Letters 476 (2000) 68–72 FEBS 23797

Minireview

ATP-dependent chromatin remodeling: going mobile

Craig L. Peterson*

Program in Molecular Medicine and Department of Biochemistry and Molecular Biology, Biotech 2, Suite 301, 373 Plantation St., Worcester, MA 01605, USA

Received 5 May 2000

Edited by Gunnar von Heijne

Abstract Members of the ATP-dependent class of chromatin remodeling enzymes are found in all eukaryotes where they play key roles in many DNA-mediated processes. Each of these enzymes are multi-subunit assembles that hydrolyze ~1000 ATP/min. The energy of ATP hydrolysis is used to disrupt the chromatin structure which can be scored by enhanced factor binding, disruption of the DNase I cleavage pattern of mononucleosomes, formation of dinucleosomes, movements of histone octamers in *cis* and in *trans*, and by generation of nuclease hypersensitive sites. Here the biochemical properties of these enzymes are reviewed and the manner in which ATP-driven nucleosome movements might account for many of these diverse activities is discussed.

Key words: Chromatin remodeling; SWI/SNF; Transcription; Nucleosome mobility

1. Introduction

During interphase of the eukaryotic cell cycle, the bulk of DNA is assembled into highly folded, 100–400 nM nucleoprotein filaments [1]. This is true even for the 'euchromatic' regions of the genome which are actively undergoing RNA transcription, DNA replication, DNA repair or recombination. These DNA-mediated processes can function efficiently in this chromatin environment due to the actions of two classes of highly conserved chromatin remodeling enzymes. The first class includes enzymes that covalently modify the nucleosomal histones (e.g. acetylation, phosphorylation, methylation and ADP-ribosylation; reviewed in [2]) and, at least in the case of histone acetylation, these covalent modifications can destabilize the folding of nucleosomal arrays and promote RNA transcription [3]. The second class of enzymes is composed of multi-subunit complexes that use the energy of ATP hydrolysis to disrupt histone–DNA interactions (reviewed in [4,5]).

Each member of the ATP-dependent family of chromatin remodeling enzymes contains an ATPase subunit that is related to the SWI2/SNF2 subfamily of the DEAD/H superfamily of nucleic acid-stimulated ATPases [6]. Seventeen members of the SWI2/SNF2 family have been identified in the yeast genome [7] and, to date, four of these ATPases have been purified as subunits of distinct chromatin remodeling complexes, ySWI/SNF [8,9], yRSC [10], ISW1 and ISW2 [11]. Additional ATP-dependent remodeling complexes that harbor SWI2/SNF2 family members have been identified in *Drosophila* (dACF [12], dNURF [13], dCHRAC [14], Brahma [15]), human (hSWI/SNF [16], hNURD [17,18] and hRSF [19]), and frog (xMi-2 [20]). Although these complexes have a variable number of subunits (i.e. 3–15), each enzyme hydrolyzes a similar amount of ATP to alter the chromatin structure and to enhance the binding of proteins to nucleosomal DNA binding sites ([4,21]. Furthermore, in the case of the ySWI/SNF, *Drosophila* Brahma, *Drosophila* ISWI and hSWI/SNF complexes, remodeling is required for transcriptional regulation of the target genes in vivo ([22–25]; for review see [5]).

ATP-dependent chromatin remodeling complexes have been further divided into three groups based on whether the sequence of the ATPase subunit is more related to yeast SWI2 (ySWI/SNF, yRSC, Brahma, hSWI/SNF), *Drosophila* ISWI (yISW1, yISW2, dNURF, dCHRAC, dACF, hRSF) or human Mi-2 (hNURD, xMi-2) (reviewed in [5]). Although each of these ATPases share a SWI2/SNF2-like ATPase domain, they harbor additional, unique sequence motifs adjacent to the ATPase domain that are characteristic of each group: the SWI2 group contains a bromodomain, the ISWI group contains a SANT domain and the Mi-2 group contains a chromodomain. Differences among groups are also apparent in the nucleic acid cofactor required for stimulation of ATPase activity. For enzymes that contain a SWI2-like ATPase (ySWI/SNF, yRSC, hSWI/SNF), the ATPase activity is stimulated equally well by 'free' or nucleosomal DNA [8,10,16]. In contrast, the ATPase activity of enzymes that contain an ISWI-like ATPase (yISW1, yISW2, dNURF, dACF) or an Mi-2-like ATPase (xMi-2, hNURD) is optimally stimulated by nucleosomal DNA [11–13,18,20,26]. In the case of ISWI-like ATPases, this requirement for nucleosomal DNA may reflect obligatory interactions with the trypsin-sensitive, histone N-terminal domains [27]. These differences among enzymes may reflect distinct modes of nucleosome remodeling; alternatively, these distinctions may reflect subtle differences in nucleosome recognition or in regulation of the remodeling cycle [28,29].

One of the difficulties in assessing distinctions among ATP-dependent chromatin remodeling enzymes has been that different assays have been used to characterize individual complexes. For instance, the remodeling activities of ySWI/SNF and hSWI/SNF were first described as an ATP-dependent disruption of DNA–histone interactions within a rotationally-phased mononucleosome [8,16]. In contrast, the activities of ISWI-containing complexes (dNURF, dCHRAC, dACF) were initially analyzed by measuring ATP-dependent changes

*Fax: (1)-508-856 4289.
E-mail: craig.peterson@umassmed.edu

PII: S0014-5793(00)01673-2

in the regularity of spacing of nucleosomes within long arrays [12,30,31]. Subsequent studies have defined additional biochemical properties of several ATP-dependent remodeling enzymes and these studies of individual enzymes have led investigators to propose that the SWI/SNF-like enzymes and the ISWI-like enzymes use distinct mechanisms to remodel chromatin structure. Below the biochemical properties of these two groups of enzymes are reviewed and it is then described how subtle differences in their abilities to move histone octamers on short DNA fragments may explain their distinct behaviors in different remodeling assays.

2. Chromatin remodeling by SWI/SNF-like enzymes

The yeast SWI/SNF complex was the first ATP-dependent remodeling enzyme to be purified and, thus, more mechanistic studies have been performed with this complex than with the ISWI-like complexes. SWI/SNF-like complexes (ySWI/SNF, yRSC, hSWI/SNF) hydrolyze ATP in the presence of either DNA or nucleosomes [8,10,16] and the energy of ATP hydrolysis is used to perturb nucleosome structure. Early studies monitored this ATP-dependent 'remodeling' reaction by scoring changes in the DNase I digestion pattern of rotationally-phased mononucleosomes [8,16]. These mononucleosomes are characterized by a 10 bp repeating pattern of DNase I cleavages which reflects the orientation of the DNA minor groove with respect to the histone octamer surface. The addition of ATP and a SWI/SNF-like complex to such phased mononucleosomes leads to a disrupted DNase I digestion pattern that looks like an overlap between the digestion pattern for naked DNA and nucleosomal DNA. This disrupted state is also associated with an enhanced affinity of DNA binding proteins for nucleosomal sites and with an increased accessibility of restriction enzymes [8,32,33]. In the case of the yRSC and hSWI/SNF complexes (but not ySWI/SNF), remodeling of mononucleosomes can also lead to the production of dinucleosome-like particles [34,35]. Surprisingly, all these disrupted features of mononucleosomes persist even in the absence of continued ATP hydrolysis.

The nature of the SWI/SNF-remodeled nucleosome is not yet clear, although several studies have begun to reveal important details of the remodeled state (Table 1). For example, it was originally proposed that SWI/SNF might disrupt nucleosomes by dislodging histone H2A/H2B dimers from nucleosome cores [36]. However, subsequent tests of this model demonstrated that preventing dimer displacement by cross-linking did not prevent disruption [37]. In addition, a more sensitive steady state fluorescence assay indicated that SWI/SNF action does not lead to even a transient removal of the H2A/H2B dimers or to more subtle changes in the histone octamer structure [38]. Moreover, SWI/SNF can disrupt histone–DNA interactions within H3/H4 tetramers alone [38]. Thus, H2A/H2B dimer displacement or their gross rearrangement is not required for SWI/SNF remodeling of mononucleosomes or nucleosomal arrays.

Table 1
Properties of SWI/SNF 'remodeled' nucleosomes

Nucleosomal DNA:
● Disruption of DNase I digestion pattern of mononucleosomes [8,10,16,50]
● Majority of DNA remains on the histone octamer surface [50]
● DNA double helix is not unwound [50]
● Increased accessibility of DNA to DNA binding proteins throughout a mononucleosome [8,16,32,33]
Histone octamer:
● Eviction or gross rearrangement of H2A/H2B dimers is not required [37,38]
● The H2A N-terminal tail is rearranged [51]
● 'Splitting' of H3/H4 tetramer is not required [38]
● Remodeling requires one or both H2A/H2B dimers [38]
Changes in histone–DNA interactions:
● Reduction in the total length of DNA per nucleosome [37]
● Generation of persistent dinucleosome size particles from mononucleosome substrate [34,35]
● Reduction in nucleosome stability at elevated ionic strength [35]
● Increased octamer mobility in *cis* [33,39]
● Increased susceptibility to octamer displacement in *trans* [39,40]

Several recent studies have shown that SWI/SNF-like enzymes can use the energy of ATP hydrolysis to slide nucleosomes on short DNA fragments or in the context of nucleosomal arrays [33,39]. The yRSC and ySWI/SNF complexes have also been reported to transfer histone octamers onto acceptor DNAs in *trans* [39,40]. The ATP-dependent sliding of nucleosomes in *cis* is highly favored over the octamer transfer reaction [39] and, furthermore, octamer transfer cannot be detected in typical mononucleosome or nucleosomal array remodeling assays [8,41]. Thus, it is unclear whether the ATP-dependent transfer of histone octamers in *trans* is mechanistically significant to the remodeling reaction. In contrast, movements of histone octamers in *cis* may explain many of the known properties of SWI/SNF-remodeled nucleosomes. For instance, Jaskelioff et al. [33] have shown that ySWI/SNF can re-distribute the translational positions of nucleosomes within phased 5S nucleosomal arrays, and this mobilization of nucleosomes is responsible for the enhanced rate of restriction enzyme digestion of these remodeled arrays [28,41]. ySWI/SNF can also slide single histone octamers from the middle of short DNA fragments ($\sim$200 bp) to the extreme ends [33]. This mononucleosome sliding reaction generates nucleosome-free DNA which persists in the absence of continued ATP hydrolysis. Furthermore, this ATP-dependent change in nucleosome positioning may also be the source for changes in the DNase I cleavage pattern that are diagnostic of SWI/SNF action on mononucleosome substrates.

In several cases, SWI/SNF remodeling has also been assayed on mononucleosomes assembled onto short DNA fragments (e.g. 154 bp) [33,42]. In these cases, the sliding of histone octamers may be restricted to very short distances (<10 bp) which might seem to be insufficient to generate large increases in DNA accessibility. One possibility is that ATP-dependent remodeling of 154 bp mononucleosome substrates is not due to octamer sliding. Alternatively, Jaskelioff et al. [33] proposed that ySWI/SNF may move histone octamers 'off the end' of DNA fragments such that <147 bp of DNA is associated with the histone octamer. This type of reaction may seem energetically unfavorable, but previous studies have shown that reconstitution of a histone octamer onto a 145 bp DNA fragment can lead to the preferential assembly of only 128 bp of DNA [43]. This model is also consistent with recent electron microscopy studies which indicate that SWI/SNF-remodeled nucleosomes contain only $\sim$100 bp of DNA [37]. This type of reaction may provide an explanation for why remodeled nucleosomes are less stable at elevated ionic strength [35] and for how octamer transfer in *trans* might be initiated (Fig. 1). Furthermore, if SWI/SNF can move octamers off the ends of DNA then the novel dinucleosome-

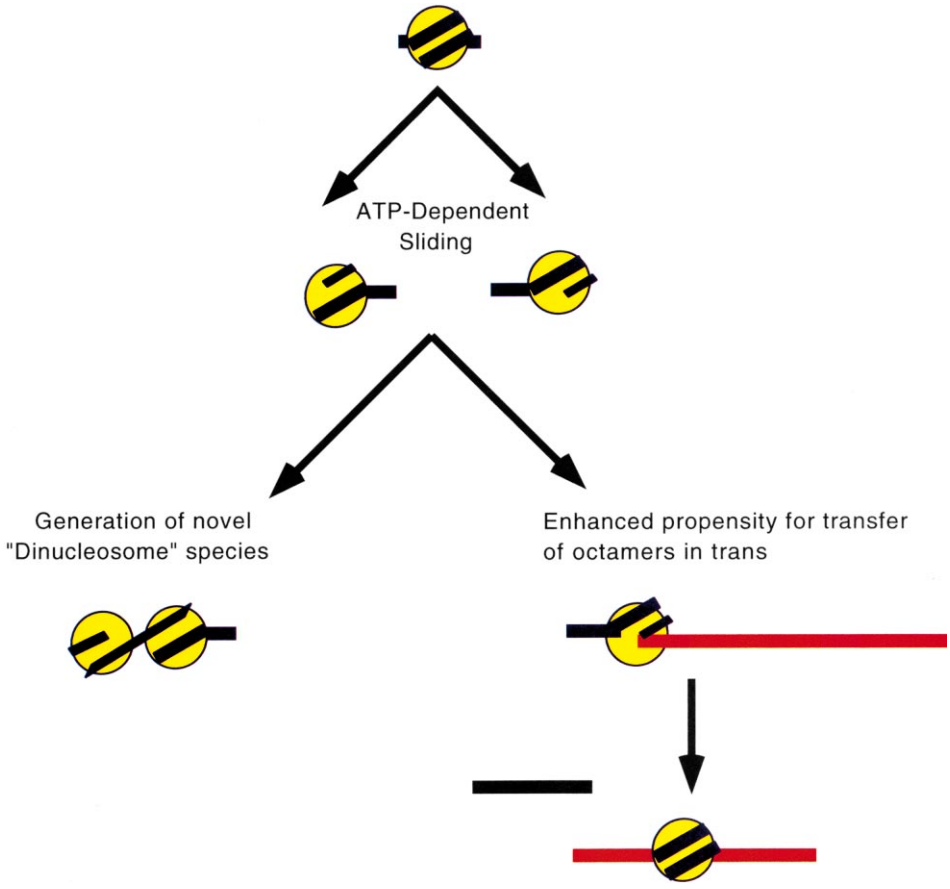

Fig. 1. Possible consequences of ATP-dependent sliding of histone octamers to DNA ends. In one scenario, movement of histone octamers to the DNA ends leads to the formation of dinucleosome-like particles where each nucleosome is bridged by histone–DNA contacts in *trans*. In the second case, movement of a histone octamer to the DNA end enhances the ability of an acceptor DNA (red) to invade a nucleosome in *trans* and lead to octamer transfer.

like species observed in hSWI/SNF and yRSC remodeling reactions may represent two independently remodeled nucleosomes that associate in *trans* via DNA–histone interactions (Fig. 1).

3. Chromatin remodeling by ISWI-like enzymes

There are several distinctions that have been observed between the ISWI (dNURF, dCHRAC, dACF, yISW1, yISW2) and SWI/SNF groups of ATP-dependent remodeling enzymes (Table 2).

1. Although both groups of enzymes hydrolyze very similar amounts of ATP (~1000 ATP/min), the ISWI group of enzymes has optimal ATPase activity only in the presence of nucleosomal DNA [12,13,21,26] (dCHRAC also contains a dispensable subunit, topo II, which has DNA-stimulated ATPase activity; [14,21]). This requirement for nucleosome assembly most likely reflects how these enzymes interact with the nucleosomal substrate rather than pointing to a distinction in how ATP hydrolysis is used for remodeling.
2. Although few mononucleosome experiments have been reported for ISWI-like complexes, this group does not seem as potent at disrupting the DNase I digestion pattern. In one case, the addition of dNURF to a rotationally-phased mononucleosome did lead to changes in the DNase I cleavage pattern [13]. However, in contrast to the disruption of mononucleosomes by SWI/SNF, the enhanced digestion by DNase I due to dNURF action was not associated with an increased accessibility to restriction enzyme digestion. No apyrase studies or mononucleosome gel shift analyses have been reported for ISWI-like enzymes and, thus, it is not known if remodeling by these complexes can lead to dinucleosome-like particles or other types of persistently remodeled species.
3. Like the SWI/SNF group, members of the ISWI group can induce the ATP-dependent sliding of histone octamers on short DNA fragments or on nucleosomal arrays [21,44,45]. Early nucleosomal array disruption assays used MNase or DNase I to monitor the re-distribution of nucleosomes due to a combination of ATP-dependent sliding and the bind-

Table 2
Properties of ISWI 'remodeled' nucleosomes

Nucleosomal DNA:
● Changes in DNase I digestion pattern of mononucleosomes; new protections and enhancements [13]
● Enhanced stability of mononucleosome to MNase digestion [45]
Histone octamer:
● Remodeling requires one or more histone N-terminal tails [27]
● Remodeling requires one or both H2A/H2B dimers [38]
● No eviction of histones [44]
Changes in histone–DNA interactions:
● Increased octamer mobility in *cis* [44,45]

ing of a sequence-specific DNA binding protein, GAGA [30]. Although it was reported that ySWI/SNF does not function in this assay [13], it seems likely that ySWI/SNF was inactivated by the relatively crude sarcosyl-treated *Drosophila* extract assembly system. It is now clear that ySWI/SNF and hSWI/SNF can re-distribute nucleosome positioning within arrays and that this can favor transcription factor binding or restriction enzyme accessibility [33,46]. In other types of assays, some ISWI-like enzymes (dCHRAC, ACF, yISW1, yISW2) have been shown to enhance the regular spacing of nucleosomes within arrays or to facilitate nucleosome assembly [11,12,14]. Other enzymes of the ISWI group (dNURF, rISWI) however, are more like SWI/SNF members, they degrade the regular spacing of nucleosomal arrays [14,26]. Thus, distinct groups of complexes, or different complexes which share the same catalytic subunit (ISWI), show subtle differences in specific assays, but the results are consistent with a similar catalytic mechanism for the remodeling of nucleosomal arrays by both ISWI and SWI/SNF group members.

Different members of the ISWI group also show distinctions in mononucleosome sliding assays [44,45]. For instance, dCHRAC action favors octamer movements from the DNA ends to central positions, whereas dNURF or rISWI can slide a histone octamer from a central position towards the ends. However, in the latter cases these end-directed movements are distinct from those catalyzed by SWI/SNF enzymes, ISWI group members do not appear to move octamers to the extreme ends of DNA fragments. For example, dNURF can slide a histone octamer from the center of a fragment to a position 50 bp from the DNA end, but it does not increase the number of nucleosomes located at the extreme end [44]. Why can't ISWI enzymes move octamers to the DNA ends? A simple model posits that ISWI has a propensity to bind to one or both DNA ends which creates a barrier for the accumulation of octamers. Other subunits of the dCHRAC complex, such as topo II, may also bind to DNA ends which may restrict movements to even more central positions. Binding to DNA ends may also explain why dCHRAC can stabilize mononucleosomes against extensive MNase digestion [45]. Furthermore, the inability to move histone octamers to the very ends of DNA fragments provides a simple explanation for why ISWI-like enzymes are less adept at transferring octamers in *trans* (Fig. 1) and why they are unable to disrupt the DNase I cleavage pattern of a 146 bp mononucleosome [45].

4. How do ATP-dependent remodeling enzymes move histone octamers?

All current data for the SWI/SNF and ISWI groups of enzymes support a simple model in which each of these enzymes uses the energy of ATP hydrolysis to change the path or topology of DNA that is assembled onto the histone octamer. To date, there is no convincing evidence for any ATP-dependent changes in the structure or composition of the histone octamer. In addition, side-by-side comparisons indicate that several members of the ISWI and SWI/SNF groups use nearly identical amounts of ATP hydrolysis to mobilize nucleosomes within linear nucleosomal arrays, which suggests that they use similar catalytic mechanisms to achieve nucleosome disruption or nucleosome movement [21]. We favor models in which the energy of ATP hydrolysis is used to rotate the DNA helix along its long axis relative to the histone octamer. In one such model, the remodeling enzyme would remain at a fixed position relative to the histone octamer, and the DNA helix would be rotated back and forth with each round of ATP hydrolysis. These rotations would translationally diffuse around both wraps of nucleosomal DNA leading to transient disruption of histone–DNA contacts. These disrupted nucleosomes would also be characterized by enhanced mobility. In another similar model, the remodeling enzyme would remain in a fixed position relative to the octamer, but the enzyme and the octamer would not remain in a fixed translational position relative to the DNA. In this model ATP-driven DNA helix rotation would 'screw' the octamer along the DNA helix, changing the translational position of the octamer (analogous to a model proposed by [47]). These types of models are also consistent with current models for how bacterial members of the DEAD/H superfamily of DNA-stimulated ATPases 'roll' the DNA helix during each cycle of ATP binding and hydrolysis [48]. These bacterial enzymes function as monomers and, thus, the ATP-driven helix rotation model may be most relevant to remodeling catalyzed by simple chromatin remodeling enzymes, such as recombinant ISWI [26] or BRG1 [49]. Since all members of the ATP-dependent family of remodeling enzymes function as multi-subunit complexes, we expect that this basic reaction mechanism may be modulated slightly by different, enzyme-associated subunits.

References

[1] Belmont, A.S. and Bruce, K. (1994) J. Cell Biol. 127, 287–302.
[2] Strahl, B.D. and Allis, C.D. (2000) Nature 403, 41–45.
[3] Tse, C., Sera, T., Wolffe, A.P. and Hansen, J.C. (1998) Mol. Cell Biol. 18, 4629–4638.
[4] Kingston, R.E. and Narlikar, G.J. (1999) Genes Dev. 13, 2339–2352.
[5] Muchardt, C. and Yaniv, M. (1999) J. Mol. Biol. 293, 187–198.
[6] Eisen, J.A., Sweder, K.S. and Hanawalt, P.C. (1995) Nucleic Acids Res. 23, 2715–2723.
[7] Pollard, K.J. and Peterson, C.L. (1998) BioEssays 20, 771–780.
[8] Cote, J., Quinn, J., Workman, J.L. and Peterson, C.L. (1994) Science 265, 53–60.
[9] Cairns, B.R., Kim, Y.-J., Sayre, M.H., Laurent, B.C. and Kornberg, R.D. (1994) Proc. Natl. Acad. Sci. USA 91, 1950–1954.
[10] Cairns, B.R. et al. (1996) Cell 87, 1249–1260.
[11] Tsukiyama, T., Palmer, J., Landel, C.C., Shiloach, J. and Wu, C. (1999) Genes Dev. 13, 686–697.
[12] Ito, T., Bulger, M., Pazin, M.J., Kobayashi, R. and Kadonaga, J.T. (1997) Cell 90, 145–155.
[13] Tsukiyama, T. and Wu, C. (1995) Cell 83, 1011–1020.
[14] Varga-Weisz, P.D., Wilm, M., Bonte, E., Dumas, K., Mann, M. and Becker, P.B. (1997) Nature 388, 598–602.
[15] Papoulas, O., Beek, S.J., Moseley, S.L., McCallum, C.M., Sarte, M., Shearn, A. and Tamkun, J.W. (1998) Development 125, 3955–3966.
[16] Kwon, H., Imbalzano, A.N., Khavari, P.A., Kingston, R.E. and Green, M.R. (1994) Nature 370, 477–481.
[17] Tong, J.K., Hassig, C.A., Schnitzler, G.R., Kingston, R.E. and Schreiber, S.L. (1998) Nature 395, 917–921.
[18] Zhang, Y., LeRoy, G., Seelig, H.P., Lane, W.S. and Reinberg, D. (1998) Cell 95, 279–289.
[19] LeRoy, G., Orphanides, G., Lane, W.S. and Reinberg, D. (1998) Science 282, 1900–1904.
[20] Wade, P.A., Jones, P.L., Vermaak, D. and Wolffe, A.P. (1998) Curr. Biol. 8, 843–846.
[21] Boyer, L.A. et al. (2000) J. Biol. Chem., in press.
[22] Elfring, L.K. et al. (1998) Genetics 148, 251–265.

[23] Deuring, R. et al. (2000) Mol. Cell 5, 355–365.
[24] de la Serna, I.L., A., C.K., Hill, D.A., Guidi, C.J., Stephenson, R.O., Sif, S., Kingston, R.E., Imbalzano, A.N. (2000) Mol. Cell Biol. 20, 2839–2851.
[25] Winston, F. and Carlson, M. (1992) Trends Genet. 8, 387–391.
[26] Corona, D.F., Langst, G., Clapier, C.R., Bonte, E.J., Ferrari, S., Tamkun, J.W. and Becker, P.B. (1999) Mol. Cell 3, 239–245.
[27] Georgel, P.T., Tsukiyama, T. and Wu, C. (1997) EMBO J. 16, 4717–4726.
[28] Logie, C., Tse, C., Hansen, J.C. and Peterson, C.L. (1999) Biochemistry 38, 2514–2522.
[29] Peterson, C.L. (1998) Cold Spring Harbor Symposia on Quantitative Biology LXIII, pp. 545–552.
[30] Tsukiyama, T., Becker, P.B. and Wu, C. (1994) Nature 367, 525–532.
[31] Varga-Weisz, P.D., Blank, T.A. and Becker, P.B. (1995) EMBO J. 14, 2209–2216.
[32] Utley, R.T., Cote, J., Owen-Hughes, T. and Workman, J.L. (1997) J. Biol. Chem. 272, 12642–12649.
[33] Jaskelioff, M., Gavin, I., Peterson, C.L. and Logie, C. (2000) Mol. Cell Biol. 20, 3058–3068.
[34] Schnitzler, G., Sif, S. and Kingston, R.E. (1998) Cell 94, 17–27.
[35] Lorch, Y., Cairns, B.R., Zhang, M. and Kornberg, R.D. (1998) Cell 94, 29–34.
[36] Peterson, C.L. and Tamkun, J.W. (1995) Trends Biochem. Sci. 20, 143–146.
[37] Bazett-Jones, D.P., Cote, J., Landel, C.C., Peterson, C.L. and Workman, J.L. (1999) Mol. Cell Biol. 19, 1470–1478.
[38] Boyer, L.A., Shao, X., Ebright, R.H. and Peterson, C.L. (2000) J. Biol. Chem. 275, 11545–11552.
[39] Whitehouse, I., Flaus, A., Cairns, B.R., White, M.F., Workman, J.L. and Owen-Hughes, T. (1999) Nature 400, 784–787.
[40] Lorch, Y., Zhang, M. and Kornberg, R.D. (1999) Cell 96, 389–392.
[41] Logie, C. and Peterson, C.L. (1997) EMBO J. 16, 6772–6782.
[42] Imbalzano, A.N., Schnitzler, G.R. and Kingston, R.E. (1996) J. Biol. Chem. 271, 20726–20733.
[43] Ramsay, N., Felsenfeld, G., Rushton, B.M. and McGhee, J.D. (1984) EMBO J. 3, 2605–2611.
[44] Hamiche, A., Sandaltzopoulos, R., Gdula, D.A. and Wu, C. (1999) Cell 97, 833–842.
[45] Langst, G., Bonte, E.J., Corona, D.F. and Becker, P.B. (1999) Cell 97, 843–852.
[46] Armstrong, J.A., Bieker, J.J. and Emerson, B.M. (1998) Cell 95, 93–104.
[47] Varga-Weisz, P.D. and Becker, P.B. (1995) FEBS Lett. 369, 118–121.
[48] Velankar, S.S., Soultanas, P., Dillingham, M.S., Subramanya, H.S. and Wigley, D.B. (1999) Cell 97, 75–84.
[49] Phelan, M.L., Sif, S., Narlikar, G.J. and Kingston, R.E. (1999) Mol. Cell 3, 247–253.
[50] Cote, J., Peterson, C.L. and Workman, J.L. (1998) Proc. Natl. Acad. Sci. USA 95, 4947–4952.
[51] Lee, K.M., Sif, S., Kingston, R.E. and Hayes, J.J. (1999) Biochemistry 38, 8423–8429.