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Three-dimensional structure of human chromatin accessibility complex hCHRAC by electron microscopy

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Abstract

ATP-dependent chromatin remodeling complexes modulate the dynamic assembly and remodeling of chromatin involved in DNA transcription, replication, and repair. There is little structural detail known about these important multiple-subunit enzymes that catalyze chromatin remodeling processes. Here we report a three-dimensional structure of the human chromatin accessibility complex, hCHRAC, using single particle reconstruction by negative stain electron microscopy. This structure shows an asymmetric 15×10×12 nm disk shape with several lobes protruding out of its surfaces. Based on the factors of larger contact area, smaller steric hindrance, and direct involvement of hCHRAC in interactions with the nucleosome, we propose that four lobes on one side form a multiple-site contact surface 10 nm in diameter for nucleosome binding. This work provides the first determination of the three-dimensional structure of the ISWI family of chromatin remodeling complexes.

Keywords

hCHRAC; nucleosome; three-dimensional structure; electron microscopy; chromatin remodeling

1. Introduction

Compaction of eukaryotic genomes into condensed chromatin fibers is required to fit over a meter of DNA within the limited volume of the nucleus (Horn and Peterson, 2002). The dynamic assembly and remodeling of chromatin involved in DNA transcription, replication, and repair is modulated by activities of remodeling complexes in living cells (Saha et al., 2006). These complexes are classified into several families, ISWI, RAD54, SWI/SNF, RSC, CHD, and INO80 (Eberhardter and Becker, 2004; Lall, 2007; Lusser and Kadonaga, 2003). They share the presence of a motor subunit that belongs to the SWI2/SNF2 type of ATPase. The imitation-switch (ISWI) family of chromatin remodeling complexes also contains a non-catalytic binding protein from the BAZ/WAL family, and occasionally some other regulatory subunits. These ISWI-family chromatin remodeling complexes, such as the chromatin accessibility complex (CHRAC), the ATP-dependent chromatin assembly and remodeling factor (ACF), the nucleosome remodeling factor (NURF), and the remodeling and spacing factor (RSF), have been identified in *Drosophila* (Ito et al., 1997; Tsukiyama et al., 1995;

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Varga-Weisz et al., 1997), human (LeRoy et al., 1998; LeRoy et al., 2000; Poot et al., 2000; Strothner et al., 2001), and *Saccharomyces cerevisiae* (Iida and Araki, 2004; Tsukiyama et al., 1999), as summarized in Table 1.

Upon binding ATP, the ISWI-family chromatin remodeling complexes are capable of changing the translational position of the histone octamer along the nucleosomal DNA (Eberharter et al., 2001; Eberharter et al., 2004; Kang et al., 2002; Langst et al., 1999). The catalytic SWI2/SNF2 ATPase subunit disrupts DNA-histone interactions (Schwanbeck et al., 2004; Zofall et al., 2006), and generates super-helical torsion, forming a diffusing twist (Havas et al., 2000) or a propagating loop (Langst and Becker, 2001). Meanwhile, the non-catalytic BAZ/WAL subunit provides anchor sites on the nucleosome through its C-terminal PHD finger (Eberharter et al., 2004), and additional binding sites to the nucleosomal DNA through its N-terminal WAC domain (Fyodorov and Kadonaga, 2002). Other small subunits might provide anchor sites on the histone octamer and/or extranucleosomal DNA (Dang et al., 2007).

The mechanism of the ISWI-family remodeling processes is not fully understood. Structurally, only a few peptide fragments or small regulatory subunits related to the ISWI family of remodeling complexes have been solved at atomic resolution using X-ray crystallography (Durr et al., 2005; Grune et al., 2003; Hartlepp et al., 2005; Li et al., 2006). The structure of *Drosophila* ISWI C-terminus region (PDB ID 1OFC), a fragment of 301 residues out of the complete 1027-residue ISWI, reveals three structural domains, HAND, SANT, and SLIDE (Grune et al., 2003). The structure of the ATPase domain, close to the N-terminus, of ISWI-family complexes has not been solved yet, but the ATPase domain of RAD54-family complexes from *Sulfolobus solfataricus* was obtained (PDB ID 1Z63), showing two lobes (Durr et al., 2005). One of them is referred to as the DEXD domain that may interact with and move along the DNA minor groove, generating DNA torsion or contraction. The structures of the BRD domain and PHD finger in the BAZ/WAL-family non-catalytic subunit have been solved for the SWI/SNF-family human BPTF (PDB ID 2F6J), showing interactions between the PHD finger and histone H3 tails (Li et al., 2006). The only solved structure of a complete subunit in the ISWI family of remodeling complexes is the small *Drosophila* CHRAC14-16 heterodimer (PDB ID 2BYK) (Hartlepp et al., 2005). It shows a similar geometry and electrostatic distribution to the histone H2B-H2A heterodimer, suggesting its binding to the nucleosomal DNA in the chromatin remodeling processes.

The three-dimensional (3D) architecture of any ISWI-family remodeling complex containing complete subunits has not yet been reported. The dimension and architecture of these complexes are unknown, and the lack of higher order structural detail about these complexes hinders understanding of the chromatin remodeling mechanism. Electron microscopy has emerged as a useful technique for the structural characterization of large macromolecular assemblies that are either refractory to crystallization or difficult to over-express and/or purify in the quantities required for X-ray crystallography. In this study, we determined the 3D structure of human chromatin accessibility complex, hCHRAC, using single particle reconstruction by electron microscopy. hCHRAC is a homolog of the *Drosophila* CHRAC, and composed of four components some of which are included in multiple copies: 135 kDa hSNF2H, 185 kDa hACF1, 15 kDa hCHRAC15, and 17 kDa hCHRAC17 (Poot et al., 2000). The dimension of our reconstructed hCHRAC structure suggests that it may consist of two hSNF2H, two hACF1, and one heterodimer of hCHRAC15-17. The structure has a roughly disk shape with a little larger size than a nucleosome. We found several lobes protruding out of the hCHRAC concave surface which could form a multiple-site contact motif to the nucleosome. The 3D structural determination of hCHRAC also provides insights into the mechanism of similar ISWI-family chromatin remodeling homologues, such as ACF and NURF, and SWI2/SNF2-type chromatin remodeling complexes.

2. Materials and methods

2.1. Protein purification and hCHRAC complex reconstitution

C-terminally 6-histidine tagged hACF1 and hSNF2H proteins were coexpressed in Sf9 insect cells using a recombinant baculovirus overexpression system (Aalfs et al, 2001; Phelan et al, 1999). Proteins were purified using Ni-NTA affinity chromatography. The other two components, hCHRAC15 and hCHRAC17 proteins were produced in E.coli BL21 (DE3) cells using a bacterial T7 overexpression system and purified using Ni-NTA affinity and size exclusion chromatography in a buffer solution (20 mM HEPES, 0.5 M NaCl, 10% v/v glycerol, 0.01% v/v NP40, pH = 7.5). Figure 1 shows the in vitro reconstitution and size-exclusion chromatography (BioSep-SEC-S 3000, Phenomenex) purification of the hCHRAC complex. The peak fractions of the hCHRAC complex were analyzed by 10% SDS-PAGE gel and the components visualized by Coomassie staining. Peak fractions collected from 15 to 16 min containing the complete complex and showing a stoichiometry of hACF1:hSNF2H $\approx$ 1:1 were used for electron microscopy.

2.2. Electron microscopy

hchrac was diluted to 0.02 mg/mL using a buffer solution (20 mM HEPES, 0.5 M NaCl, pH = 7.5). A carbon coated copper grid (Electron Microscopy Sciences, G400) was glow-discharged (Edwards, Auto 306) for 1 min in argon to make it hydrophilic. A 5- μ l drop of hCHRAC solution was applied onto the grid. After 1 min, excess buffer was removed by blotting, carefully touching the edge of the grid with a piece of filter paper (Whatman). The grid was washed three times with the buffer, then stained with a 2% uranyl acetate solution for 1 min, and blotted and air-dried at least for 30 min. Electron microscopy imaging was performed on a JEM-1200EX (JEOL) operating at 120 kV. Micrographs were recorded on Kodak SO163 film at a nominal magnification of 50,000 with an electron dose < 10 e/ $\text{\AA}^2$.

2.3. Image analysis and data processing

Micrographs were digitized on a Super Coolscan 8000 scanner (Nikon) at a depth of 8 bit/pixel and a step size of 2000 pixel/inch, corresponding to 2.54 $\text{\AA}$ /pixel at the specimen level. The pixel value histogram of each negative film was normalized by adjusting the densitometer parameters. Single particle reconstruction was performed with EMAN (Ludtke et al., 1999), SPIDER (Frank et al., 1996), and IMAGIC (van Heel et al., 1996). Seventy two micrographs were selected that displayed minimal drift and astigmatism. A total of 12,875 particles were manually selected and extracted as 128 $\times$ 128 pixel images using EMAN. The optical density histogram of each image was normalized to the mean density. The defocus values were estimated for each micrograph using SPIDER, showing a distribution from 0.95 to 3.08 μ m with an average of 2.04 μ m (Supplementary Fig. 1). The series of defocus values gave their first zero cross points ranging from 20 to 30 $\text{\AA}$ in the contrast transfer function (CTF). The CTF parameters were determined from the computed Fourier transform of each micrograph, and phase corrections were then applied to each particle image to compensate for information loss at the zero cross points in the CTF and to avoid resulting artifacts in structural reconstruction. The corrected particle images were centered and rotationally aligned using the reference-free method in SPIDER (Penczek et al., 1992). These particle images were classified into 100 classes based on multivariate statistical analysis in IMAGIC, where 20% of the particles and 5% of the classes with the worst fit were discarded. The starting model for reference-based refinement was an average of low-pass filtered four intermediate models (Supplementary Fig. 2). The first and second intermediate models were obtained from a coarse refinement of a Gaussian sphere and cylinder, respectively; the third and last ones were obtained from a coarse refinement of a common-line based initial model from two groups of 20 selected class averages. The averaged model showed similar features in total shape and positions of lobes, and cross-correlation coefficients of 0.73, 0.91, 0.93, and 0.94 with the four

intermediate models, respectively (Supplementary Fig. 2 and Table 1). A refinement was performed using the reference-based back projection algorithm. The initial model bias was minimized by three steps during the refinement. The first was to remove 20% of the particles having poor cross correlation with projections of the initial model before the refinement. The second was to use a large angle interval (15°) during several first loops and a small interval (8°) during several last loops in the refinement. The third was to use conservative parameters during first several loops (classiter = 15, classkeep = 1.0) and during several last loops (classiter = 4, classkeep = 0.6) in the refinement. The convergence of the refinement process was monitored by examining the Fourier shell correlation (FSC) between two successive iterations. The final 3D model was obtained after 20 computational iterations from a total of 10,237 images. An estimate of the resolution of the final 3D model was computed by separating the classified images into two random groups and using the FSC = 0.5 criterion (Bottcher et al., 1997; Conway et al., 1997). An isosurface threshold was set to correspond to the hCHRAC molecular weight of 670 kDa assuming a protein density of 1.35 g/cm³ (0.81 Da/Å³). The model was low-pass filtered to the estimated resolution and visualized by using CHIMERA (Pettersen et al., 2004). There were no significant or rapid structural changes at this resolution as the threshold was changed from 600 to 800 kDa (Supplementary Fig. 3).

3. Results

3.1. Composition analysis of hCHRAC complexes

Size-exclusion chromatography of the reconstituted hCHRAC complex showed an apparent molecular weight of ~670 kDa (Fig. 1a). The assignment of peaks was based on Coomassie blue staining SDS-PAGE analysis of each fraction. The reconstituted complex included all four subunits, hACF1 between 220 and 160 kDa, hSNF2H between 160 and 120 kDa, hCHRAC17 and hCHRAC15 between 20 and 10 kDa (Fig. 1b). They agree well with their reported molecular weights of 185, 135, 17, and 15 kDa, respectively (Poot et al., 2000). It is known that the hCHRAC complex has a stoichiometry ratio of hSNF2H to hACF1 of 1:1 (Poot et al., 2000). Recent studies on both human and *Drosophila* CHRAC complexes have shown that the two small CHRAC subunits do not associate with SNF2h, but with the N-terminus of ACF1 (Hartlepp et al, 2005;Kukimoto et al., 2004). Therefore, the fractions containing the complete complex and showing a stoichiometry of hACF1:hSNF2H ≈ 1:1 were selected for the complete hCHRAC complex, which minimizes the potential heterogeneity of protein composition.

3.2. Structural reconstruction by electron microscopy

Single particle reconstruction (Penczek et al, 1992) was performed to obtain a 3D structure of the hCHRAC complex from negative-stain electron micrographs. The complex has a size of 10–15 nm in diameter in electron microscopy images, depending on different views (Fig. 2a). The final 3D structure was reconstructed from an averaged initial model using a total of 10,237 particle images (Supplementary Fig. 2). We compared 336 class averages obtained from the reference-free alignment with 2246 projections from the final model (at 3 degree intervals). The cross correlation coefficient histogram showed an average value of 0.88 with a standard deviation of 0.05 (Supplementary Fig. 4), indicating consistency of the final model with the primary data. Fig. 2b shows some examples of the comparison of these class averages and model projections. An analysis of the three eulerian angles of each particle showed a uniform distribution of particle orientation in angular space suggesting a nearly random orientation of hCHRAC particles on the carbon film (Fig. 2c). This ruled out significant artifacts due to missing angles during the 3D structural reconstruction. The final refinement resulted in a 3D structure with a resolution of 27 Å (Fig. 2d). This was assessed by calculating the signal-to-noise ratio of the reconstructed 3D structure using the Fourier shell correlation (FSC). The FSC

showed a smooth curve without oscillation at FSC = 0.5, suggesting the absence of serious structural artifacts during image processing (Cheng et al., 2006).

The reconstructed 3D model of the hCHRAC complex at this resolution shows an asymmetric 15×10×12 nm disk-shaped structure with globular protrusions (Fig. 3a and Supplementary Movie). The isosurface was set for a volume containing a mass of 670 kDa. The size of this volume is similar to the protein particle projections in negative-stain images, indicating that the surface threshold determination was reasonable. Two large surfaces are present in the disk-shaped structure. One is relatively flat, and another shows a convex contour (Fig. 3b). There are several prominent lobes (number 1–4) protruding out of the flat surfaces and an additional one (number 5) out of the convex side. These lobes showed smooth density changes when the isosurface threshold was adjusted around 670 kDa (Supplementary Fig. 3). Two-axis rotational views showed that hCHRAC has a solid volume without any large cavity or holes (Fig. 3b). Lobes 1–4 are located on one side of hCHRAC, while lobe 5 is at the top of hCHRAC on the opposite side. At the center of the lobe 1–4 side, there are two small protrusions (numbers 6 and 7).

4. Discussion

4.1. Reliability of complex reconstitution and structural reconstruction

Size-exclusion chromatography showed the reconstituted hCHRAC complex has an apparent molecular weight of ~670 kDa, which agrees with a previous report (Poot et al., 2000). It is known that the hCHRAC complex has a stoichiometry ratio of hSNF2H to hACF1 of 1:1 (Poot et al., 2000), and the *Drosophila* ACF, a homologue of hCHRAC, consists of two ISWI and two ACF1 subunits (Strohner et al., 2005). Thus, it is reasonable to infer that hCHRAC also consists of two hSNF2H, two hACF1, and one heterodimer of hCHRAC15-17, giving a molecular weight of 670 kDa. The small ambiguity in molecular weight would probably not affect prominent structural features of the reconstructed 3D volume (Supplementary Fig. 3). Despite the ambiguity in molecular weight and minor contamination or degradation impurities in small quantities (Fig. 1b), there was no indication of obvious artifacts in image processing, such as poor correlation between volume projections and class averages, preferred orientation of particles, and oscillation of the FSC curve (Figs. 2b-d).

4.2. Hypothetical binding models between hCHRAC and nucleosome

We propose a multiple-site binding model between hCHRAC and the nucleosome based on their structural features. The reconstructed volume of hCHRAC showed a disk-shaped architecture with a flat and a convex side (Fig. 3b). Because the chromatin remodeling processes require multiple interactions of the subunits in hCHRAC with the nucleosome and DNA, association of hCHRAC and the nucleosome should have maximum contact area and minimum steric hindrance. Among three models that possibly satisfy the above assumption, the binding mode directly involving lobes 1–4 on the flat side of hCHRAC seems most reasonable (Fig. 4c). In this mode, lobes 1–4 form a binding surface with small protrusions 6 and 7 at the center (Fig. 4a), and this region has a diameter of ~10 nm comparable to the size of a disk-shaped nucleosome (Fig. 4b). Other binding modes from the convex side or other surfaces of hCHRAC either have larger steric hindrance (Fig. 4d) or involve fewer interacting surfaces (Fig. 4e) with the nucleosome. Conformational changes upon nucleosome and/or ATP binding might favor other binding configurations. However, considering the 3D structure of hCHRAC found, the multiple-site contact mode (Fig. 4c) is consistent with the current three-site binding model (Cairns, 2007). In that model, the ATPase domain binds to the position of two helical turns from the dyad axis, i.e., superhelical location 2 (SHL2) within the nucleosome, and the HAND domain in the C-terminus binds to the entry/exist site of nucleosomal DNA on the histone octamer (Dang and Bartholomew, 2007), together with a hypothetical hinge domain

on the remodeling complex being affixed to the nucleosome (Eberharter and Becker, 2004; Hartlepp et al., 2005). Lobes 1–4 could provide interacting translocation and stationary tracking sites to drive DNA sliding on the nucleosome in a repetitive release and rebinding process (Cairns, 2007). The small protrusions 6 and 7 and its surrounding surfaces could provide additional contact sites with the histone octamer. The conserved SANT/SLIDE domain in hSNF2H is considered to bind the linker DNA (Corona et al., 2007). Although we cannot localize the position of hSNF2H, some surfaces of lobes 1–4 are still exposed after hCHRAC binds to the nucleosome. Some of these exposed surfaces could enable their interaction with the linker or extranucleosomal DNA in addition to the core histone (Hartlepp et al., 2005).

4.3. Comparison with other chromatin remodeling complexes

Such a binding geometry and remodeling mechanism may be shared by other chromatin remodeling complexes. A reconstructed 3D structure of yeast SWI/SNF complex shows a rim structure on its surface, 15 nm in diameter and 5 nm in depth, possibly functioning as a nucleosome-binding pocket (Smith et al., 2003). However, two other reconstructed 3D structures of SWI/SNF complexes, yeast RSC (Asturias et al., 2002; Leschzner et al., 2007; Skiniotis et al., 2007) and human PBAF (Leschzner et al., 2005), show a cavity inside the complexes to encapsulate the nucleosome. All of these SWI/SNF-family complexes are composed of > 10 subunits with much larger molecular weights > 1 MDa. Although the ISWI-family complex, hCHRAC, has a smaller size and molecular weight, the multiple-site motif allows maximum contact area with minimum steric hindrance between hCHRAC and the nucleosome, and leaves the other side of hCHRAC open for interactions with ATP and other regulators.

4.4. Outlook

Further clarification of chromatin remodeling mechanism by hCHRAC requires identification of subunits in the complex. In this regard we have labeled the His-tagged ISWI with Ni-NTA 5-nm gold cluster and it can next be used to mark this protein in the complex (Reddy et al., 2005). Another approach is to dock X-ray crystallography structure of subunits into the EM 3D density map. Currently, the reported X-ray ISWI structure is only a C-terminus region (Grune et al., 2003), a fragment of 301 residues (36 kDa, PDB ID 1OFC) out of the complete 1027-residue ISWI (140 kDa). The CHRAC15-17 (32 kDa) structure is unknown, but its *Drosophila* CHRAC14-16 homologue (30 kDa, PDB ID 2BYK) is solved (Hartlepp et al., 2005). In addition, a 802-residue ATPase domain of RAD54-family complexes from *Sulfolobus solfataricus* (93 kDa, PDB ID 1Z63) is reported (Durr et al., 2005). However, all of these are too small (36 and 32 kDa) to give a precise fitting into the hCHRAC 3D density map. The difference map method, such as structural reconstruction of hCHRAC and nucleosome binding complex (Leschzner et al., 2005), is also useful to confirm the contact points and binding/releasing mode between hCHRAC and the nucleosome.

Additional structural study by higher resolution cryo-electron microscopy, gold cluster labeling, additional X-ray crystallography, study of hCHRAC subcomplexes, and hCHRAC-nucleosome assemblies may be expected to identify the location of hCHRAC subunits and their precise interaction sites with the nucleosome and DNA, which will provide further insight into the important mechanism of chromatin remodeling.

5. Conclusions

We determined the 3D structure of the hCHRAC complex using negative-stain single particle reconstruction by transmission electron microscopy to a resolution of 27 Å. The reconstructed hCHRAC volume has an asymmetric 15×10×12 nm disk structure with globular protrusions. The assignment of molecular weight of 670 kDa is consistent with its molecular composition

of two hSNF2H and two hACF1, and one heterodimer of hCHRAC15-17. Four large lobes (number 1–4) are present on the flat side of the disk-shaped hCHRAC structure. Because the nucleosome is slightly smaller than the hCHRAC complex, a tentative assignment of its binding to the surfaces where lobes 1–4 are located maximizes surface contacts and interactions. The additional non-histone binding surfaces might provide linker and extranucleosomal DNA interactions. While this initial structure provides a basic framework, additional higher resolution studies are required to fully identify and characterize the complex and its function in chromatin remodeling.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:

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Fig. 1. Reconstitution and composition analysis of hCHRAC complexes. (a) Size-exclusion chromatogram of the reconstituted hCHRAC complex at a flow rate of 0.2 ml/min. The complete complex shows an apparent molecular weight of ~670 kDa. (b) SDS-PAGE analysis of fractions collected from the chromatography at a retention time interval of 20 s. The complete complex showed four major bands corresponding to hACF1, hSNF2H, hCHRAC17, and hCHRAC15, respectively. Some contamination or degradation bands were visible in small quantities. Fractions collected from 15 to 16 min were combined and used for electron microscopy because they contained the complete complex and showed a stoichiometry of hACF1:hSNF2H $\approx$ 1:1.

Fig. 2.

Single particle reconstruction of hCHRAC complexes from electron microscopy. (a) Negative-stain electron microscopy image of hCHRAC particles visible as bright spots under defocus = 2.0 μm and magnification = 50,000. (b) Typical projections of the final 3D model (left column) compared to the corresponding class averages obtained from the reference free alignment and classification (right column), independent of the reconstruction, showing a cross correlation coefficient of 0.92, 0.94, 0.91, 0.93, 0.92, and 0.93, respectively. (c) Eulerian angle distribution of the particle images used in the final refinement. The two out-of-plane eulerian angles, θ and ϕ , are plotted (the third angle ψ , which is not shown, is an in-plane rotation). (d) FSC curve of the two 3D models derived from the even and odd numbered particles, respectively. FSC = 0.5 corresponds to a spatial frequency of 27 Å.

Fig. 3.

Three-dimensional structure of hCHRAC derived from electron microscopy single particle reconstruction. (a) A surface view of the 15×10×12 nm hCHRAC structure with five large lobes labeled from 1 to 5, and two small protrusions labeled by 6 and 7. (b) Rotational views around a vertical axis (upper row) and a horizontal axis (lower row) from the orientation shown in (a), where the rotation angles are noted under each view. The flat and convex surfaces of the hCHRAC are indicated by red lines and curves, respectively.

Fig. 4. Hypothetical binding of hCHRAC to a nucleosome. (a) Side view of the reconstructed hCHRAC structure. Lobes 1–4 in the hCHRAC structure form a multiple-site binding motif. The small protrusions 6 and 7 at the center may provide additional contacts with the histone octamer. A nucleosome outline is shown as a red annulus. (b) Face view of the nucleosome composed of a histone octamer and a double strand DNA (PDB ID 1AOI). The two dotted rings have a diameter of 6 and 10 nm, respectively. (c)–(e) Possible interaction modes between hCHRAC and nucleosome through lobes 1–4 on the flat side, lobes 2, 3, and 5 on the convex side, and lobes 1, 2, and 5 on other side of the disk-shaped hCHRAC. The structure with the

maximum contact between hCHRAC and the nucleosome with the least common density overlap is shown in (c) and is therefore the proposed binding configuration.

Table 1

Members of ISWI-family chromatin remodeling complexes.

	Remodeling Complex	SWI2/SNF2 ATPase subunit	BAZ/WAL family non-catalytic subunit	Other regulatory subunit
<i>Drosophila</i>	ACF	ISWI	ACF1	
	CHRAC	ISWI	ACF1	CHRAC14, CHRAC16
	NURF	ISWI	NURF301	p55, Pyrophosphatase
	hACF	hSNF2H	hACF1	
Human	hCHRAC	hSNF2H	hACF1	hCHRAC15, hCHRAC17
	hNURF	hSNF2L	BPTF	RbAP46, RbAP48
	RSF	hSNF2H	RSF1	
	NoRC	hSNF2H	hTIP5	
<i>S. cerevisiae</i>	ISW2	Isw2p	Itc1p	
	yCHRAC	Isw2p	Itc1p	Dpb4p, Dls1p