Supplementary Methods

GST-pull down assay

Glutathione sepharose beads (GE Healthcare) equilibrated in binding buffer (50 mM Tris-HCl, pH 8.0, 150 mM NaCl, 0.1% NP40, 10 µM $ZnCl_2$, 1 mM DTT and protease inhibitors), were incubated with bacterial lysates containing GST or GST-SCA7 domains of hATXN7, hATXN7L3 or ySgf73. Mononucleosomes, recombinant H2A-H2B dimers and H3-H4 tetramers or recombinant tail-less histone octamers were prepared as described (Hamiche et al., 2001) and added to the GST-coated sepharose beads and incubated overnight at 4°C in binding buffer. Beads were washed with binding buffer containing 250 mM NaCl. 30% of the bound proteins were analysed by SDS-PAGE followed by Coomassie blue R250 coloration and 30% were analysed by immunoblot analysis. A monoclonal anti-H2B antibody (5HH2-2A8) was obtained by immunization of mice with a peptide corresponding to residues 111-125 (VSEGTKAVTKYTSSK) of H2B. An antibody against H3 (ab1791) was obtained from Abcam.

Cell Extraction and Tandem Affinity Purifications

Cell extracts were prepared from *S. cerevisiae* strains TAP-tagged on Spt20 (WT, Δsgf73 and Sgf73ΔSCA7, Supplementary Table 1). Cells were harvested from a 2 L suspension culture in CSM minus Leucine at an OD-600 of 2, disrupted by glass bead homogenization in extraction buffer (20 mM HEPES-NaOH, pH 8.0, 150 mM sodium chloride, 10% glycerol, 0.1% Tween 20, and Protease Inhibitor Cocktail (Sigma-Aldrich)) and cleared by ultracentrifugation.

40 µL of biotinylated rabbit anti goat IgG (Bethyl Laboratoties) were incubated with 400 µL of Dynabeads® M-280 Streptavidin (Invitrogen). After extensive washes in extraction buffer, the resin was incubated for 2 h with 10 mL of cell extract and subsequently washed with 30 mL of extraction buffer and 10 mL of cleavage buffer (10 mM Tris-HCl, pH 8.0, 150 mM sodium chloride, 0.5 mM EDTA, pH 8.0, 0.1% Tween 20 and 1 mM DTT). The protein A

moiety of the tag was cleaved off with 10 µL of TEV protease (Invitrogen) in 1 mL of cleavage buffer for 2 h. Binding to calmodulin agarose (Stratagene) for 1 h in binding buffer (10 mM Tris-HCl, pH 8.0, 150 mM NaCl, 1 mM magnesium acetate, 1 mM imidazole, 2 mM calcium chloride, 10% glycerol, 0.1% Tween 20 and 10 mM mercaptoethanol) was followed by washing with 30 mL of binding buffer and elution in 400 µL of elution buffer (10 mM Tris-HCl, pH 8.0, 150 mM NaCl, 1 mM magnesium acetate, 1 mM imidazole, 2 mM EGTA, pH 8.0, 10% glycerol, 0.1% Tween 20 and 10 mM mercaptoethanol). The eluate was precipitated according to (Wessel and Flugge, 1984) and analysed on a NuPAGE® Novex 4-12% Bis-Tris Gel (Invitrogen), revealed by Coomassie blue staining or by western blotting using PAP (Sigma) or HA antibody (3F10, Roche).

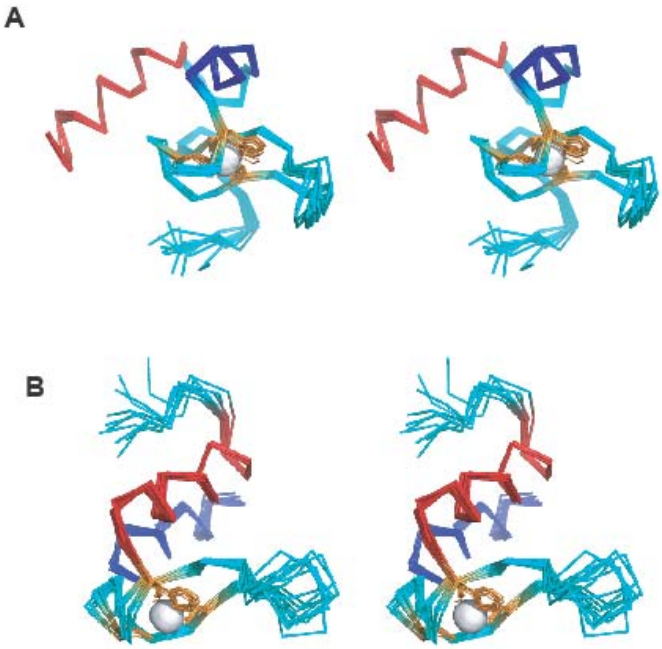
Supplementary References

Hamiche, A., Kang, J.G., Dennis, C., Xiao, H. and Wu, C. (2001) Histone tails modulate nucleosome mobility and regulate ATP-dependent nucleosome sliding by NURF. *Proc Natl Acad Sci U S A*, **98**, 14316-14321.

Wessel, D. and Flugge, U.I. (1984) A method for the quantitative recovery of protein in dilute solution in the presence of detergents and lipids. *Anal Biochem*, **138**, 141-143.

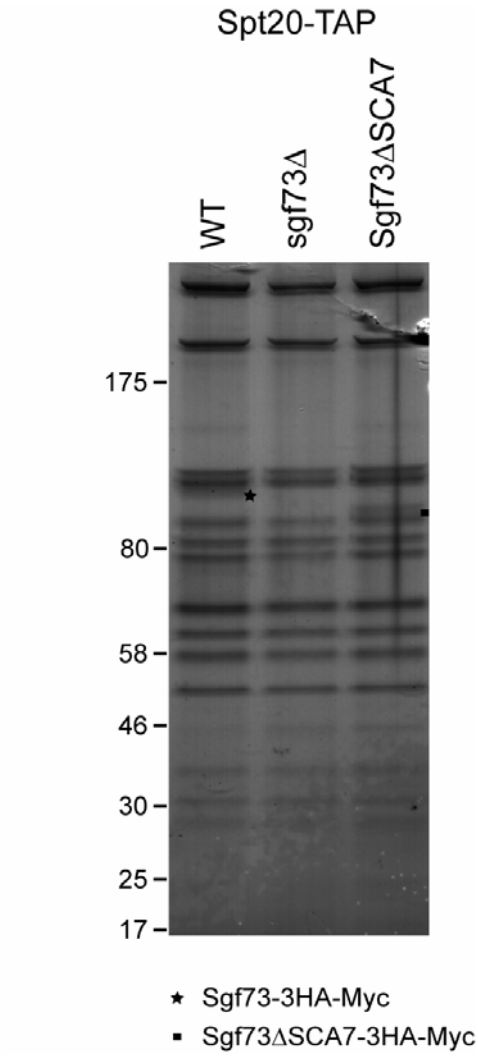
Supplementary Figure 1 : Solution structures of the SCA7 domains of human ATXN7 and ATXN7L3

(**A,B**) Stereoview of the C_α traces from the ten lowest energy structures of (**A**) ATXN7-SCA7 and (**B**) ATXNL3-SCA7 ZnFs. Only the folded parts of the proteins are represented. The heavy atoms of the zinc-coordinating residues are shown in orange and the position of the zinc ion is indicated by a gray sphere. Helices α_1 and α_2 are coloured in blue and red respectively.



Supplementary Figure 2 : Sgf73-SCA7 is not required for Sgf73 incorporation into SAGA

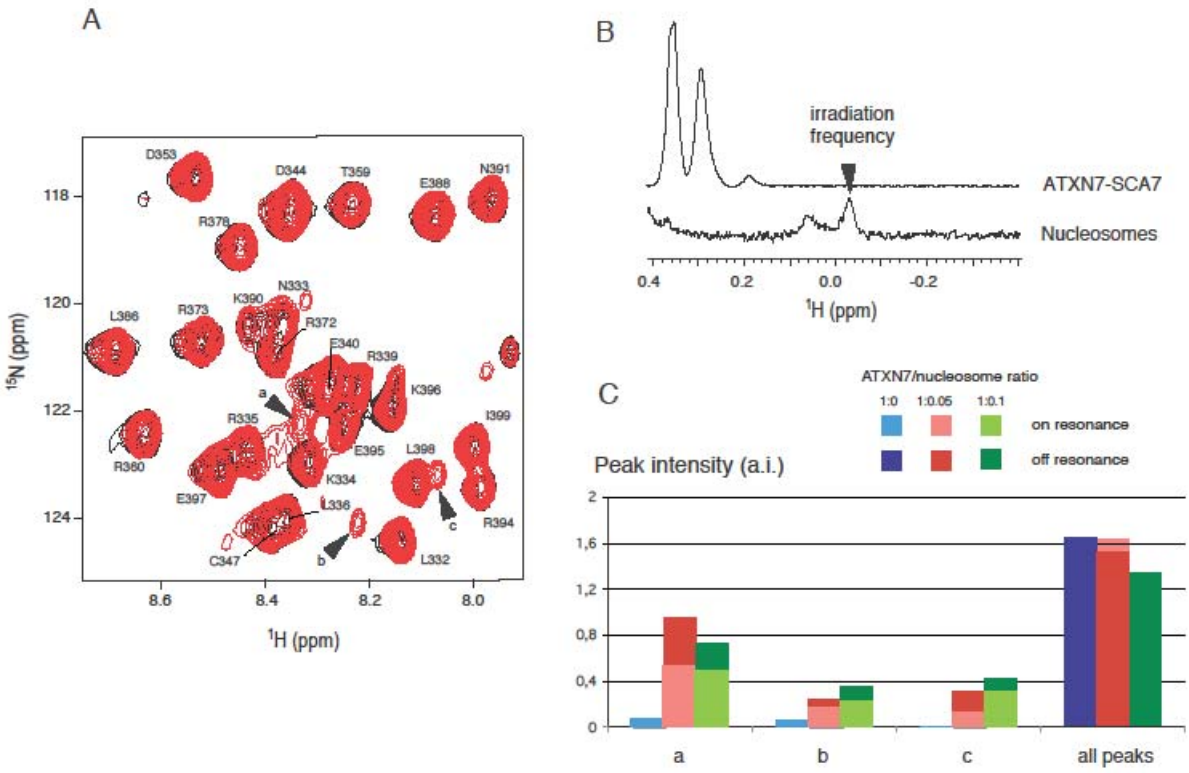
Tandem affinity purification of SAGA complexes using Tap-tagged Spt20 from the indicated strains were analyzed by Coomassie staining.



Supplementary Figure 3 : Interaction of ATXN7-SCA7 domain with nucleosomes

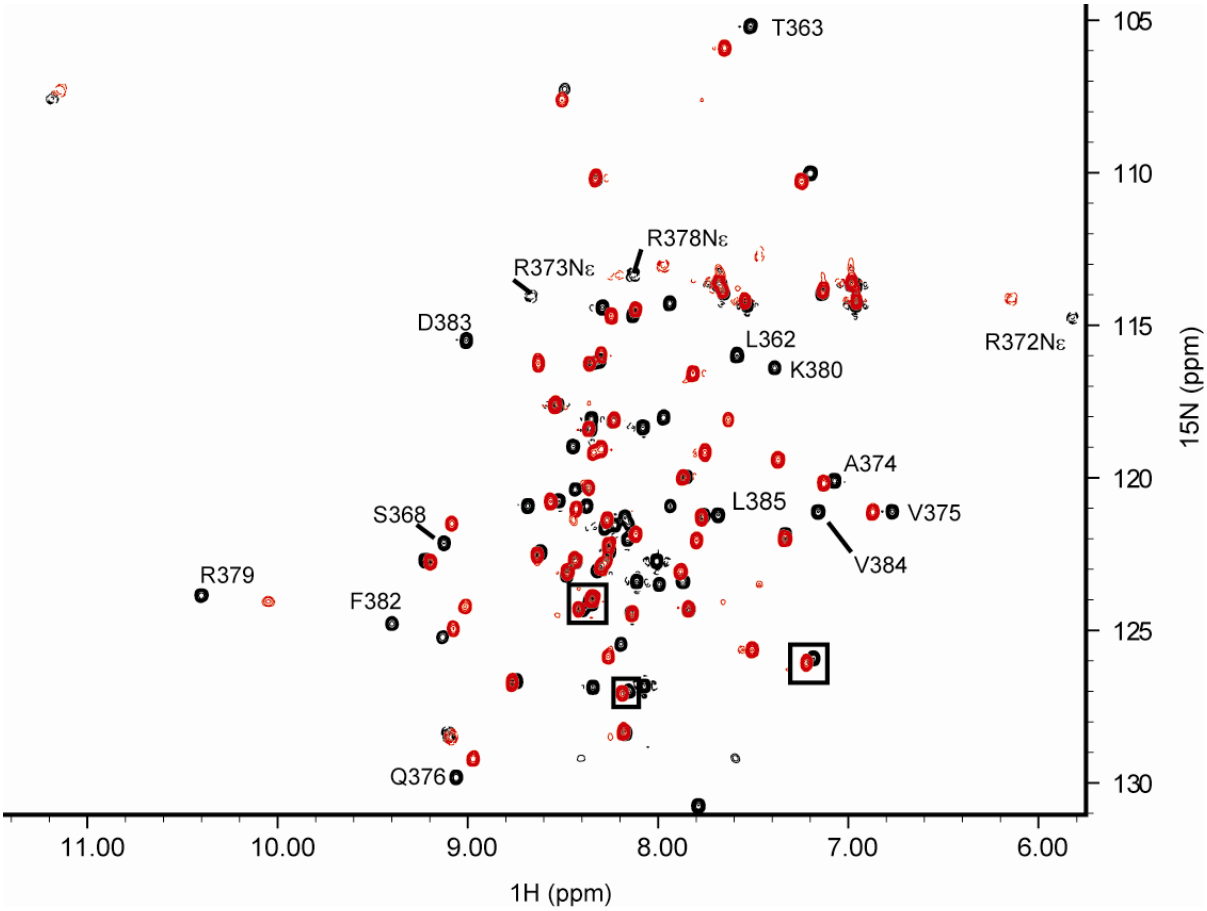
(**A**) The interaction between the SCA7 domain of ATXN7 and nucleosome particles was probed using NMR by mixing ^{13}C, ^{15}N uniformly labelled ATXN7-SCA7 domain with different amounts of a preparation of purified nucleosomes. (**B**) The presence of an isolated methyl resonance at -0.015 ppm observed in the NMR spectrum of the nucleosome preparation was used to assess the relative concentration of nucleosome as compared to that of ATXN7 (B). The ratio of 1:30 (stock solution of nucleosome versus ATXN7) was found to be compatible to the 1:20 ratio found by Bradford assay. The absence of peak overlap between free ATXN7 and the nucleosome signal allowed specific saturation of the nucleosome particles using selective irradiation at -0.015 ppm during the relaxation time of the ^{1}H-^{15}N HSQC experiments. (C) Peak intensities were measured in ^{1}H-^{15}N HSQC spectra of ATXN7-SCA7 domains recorded in absence and with two different substœchiometric amounts of nucleosome particles. In addition, peak intensities were recorded under a selective irradiation of the histone methyl resonance (light blue, red and green colours) or under off-resonance (-13.3 ppm) irradiation (dark blue, red and green colours). While the addition of increasing amounts of nucleosomes leads to an overall decrease of ATXN7 signals, a set of additional peaks, with increasing intensities could be observed in the region of the HSQC spectrum that corresponds to unfolded parts of the ATXN7 protein (see peaks labelled a,b and c in (A)). The intensity of these peaks is affected by nucleosome on-resonance irradiation, suggesting that they originate from a nucleosome bound form of ATXN7. Furthermore, analysis of frequencies of these secondary peaks suggests that they probably correspond to residues located at the edges of the SCA7 domain, where sufficient protein backbone flexibility is present in the complex to allow their observation, while frequencies are slightly affected by the nucleosome environment. The observation of a slow exchange regime between

free and nucleosome bound forms of ATXN7 suggests a tight binding involving all residues of the SCA7 domain, with an upper limit of the K_d of about 10 µM.



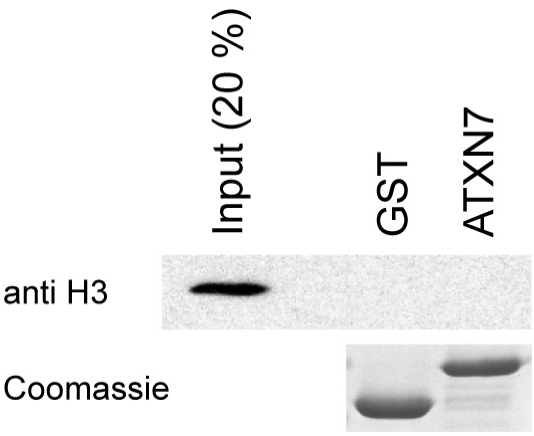
Supplementary Figure 4 :

Superposition of HSQC spectra from ATXN7-SCA7 (black) and the mutant ATXN7-ΔCter (red). Correlations with significant shifts upon mutation are labelled. Zinc-coordinating residues are boxed.



Supplementary Figure 5 : ATXN7-SCA7 does not interact with H3H4 tetramers *in vitro*

GST-pull down experiments using H3-H4 tetramers were analyzed by Coomassie blue staining or western blotting using anti-H3 antibodies.



Supplementary Table 1

Ramachandran statistics of ATXN7 and ATXN7L3 structures

	ATXN7	ATXN7L3
Backbone dihedral angles statistics		
Residues in most favorable regions (%)	72.4	76.0
Residues in additional favorable regions(%)	27.1	21.0
Residues in generously favorable regions (%)	0.6	2.0
Residues in disallowed regions (%)	0.0	1.1

Supplementary Table 2

Name	Strain	Genotype	Source
	YGL066W	*Mat a; his3D1; leu2D0; lys2D0; ura3D0; sgf73Δ::Kan*	Euroscarf
	YMR223W	*Mat a; his3D1; leu2D0; lys2D0; ura3D0; ubp8Δ::Kan*	Euroscarf
Spt20-TAP sgf73Δ	YJB100	Isogenic to YGL066W except *SPT20-TAP::URA3; pRS315*	This study
Spt20-TAP WT	YJB101	Isogenic to YGL066W except *SPT20-TAP::URA3; pRS315-Sgf73-3HA-Myc*	This study
Spt20-TAP Sgf73ΔSCA7	YJB103	Isogenic to YGL066W except *SPT20-TAP::URA3; pRS315-Sgf73Δ 227-281-3HA-Myc*	This study
Flag-H2B sgf73Δ	YJB104	Isogenic to YGL066W except *pRS315; pRS413-FLAG-HTB1-HTA1*	This study
Flag-H2B WT	YJB105	Isogenic to YGL066W except *pRS315-Sgf73-3HA-Myc; pRS413-FLAG-HTB1-HTA1*	This study
Flag-H2B Sgf73ΔSCA7	YJB106	Isogenic to YGL066W except *pRS315-Sgf73Δ227-281-3HA-Myc; pRS413-FLAG-HTB1-HTA1*	This study
Flag-H2B-K123R WT	YJB107	Isogenic to YGL066W except *pRS315-Sgf73-3HA-Myc; pRS413-FLAG-htb1-K123R-HTA1*	This study
Flag-H2B ubp8Δ	YJB108	Isogenic to YMR223W except *pRS315; pRS413-FLAG-HTB1-HTA1*	This study