Supplementary legends

Movie S1. Model for the molecular architecture of SAGA complex. Same 3D model as shown in Fig. 7. The movie was prepared using UCSF Chimera (Pettersen *et al*, 2004).

Table S1. Sequence coverage of WT SAGA complex. Sequence coverage was calculated using MaxQuant. Subscript a-d denotes uncrosslinked SAGA preparations that were the same data set as in the iBAQ analysis. 2mM and 5mM indicate the crosslinked complexes in 2mM and 5mM BS3 crosslinking experiments, respectively.

Table S2. Summary of the BS3 crosslinks within SAGA complex. The BS3 modified lysine in each peptide is indicated by an asterisk (*). "type" is either 1 (intra-links) or 2 (inter-links). "experiment" indicates the crosslinks identified in either 2mM BS3 experiment or 5mM BS3 experiment or both experiments. Number of spectra is the total number of spectra used to identify each crosslink.

Table S3. Distance measurements of crosslinked residues in known 3D structures.

Table S4. (A) List of iBAQ values for SAGA subunits. (B) List of adjNSAF values for SAGA subunits. Subscript a-d indicates MS analysis of independent SAGA preparations.

Table S5. (A) Yeast strains used in this study. (B) Plasmids used in this study.

Figure S1. BS3 crosslinking of SAGA complex. (**A**) Chemical structure of BS3 (upper panel) and crosslinking mechanism (lower panel). (**B**) Silver stained protein gel showing the crosslinking of SAGA complex with increasing amounts of BS3. (**C**) Venn diagram showing the number of crosslinks identified in experiments with 2 mM or 5 mM

BS3. 199 total intermolecular and 240 intramolecular crosslinks were identified. Data is from Table S1.

Figure S2. SAGA intramolecular crosslinking map. Similar to Figure 2, but only the identified intramolecular crosslinks are shown.

Figure S3. Crosslinks of Sgf73, Ada2 and Ada3. (**A**) Intermolecular crosslinking map between Sgf73, Ada2 and Ada3. (**B**) Intermolecular crosslinking map between Sgf73 and Taf or core subunits of SAGA. (**C**) Intermolecular crosslinking map between Ada2/3 and Taf or core subunits of SAGA. Also shown in all three maps are the deletions designed in Sgf73, Ada2 and Ada3 (see also Fig. 5 and Fig. S4).

Figure S4. Growth phenotypes of DUB and HAT mutants. Serial dilutions of yeast strains bearing mutations within (**A**) *SGF73*, (**B**) *ADA2*, and (**C**) *ADA3* were spotted onto minimal media and incubated at 30°C and 37°C for two days. WT, wild type.

Figure S5. Consequences of eliminating the SAGA HAT and DUB modules. **(A)** iBAQ analysis of WT, Sgf73 Δ2A, Ada3 Δ2A, and Sgf73 Δ4 SAGA complexes. iBAQ values were normalized to that of Spt7. Also see Fig. 6B and Table S3A. Error bars represent standard deviation from 4 replicates for WT complex, 2 replicates for all three mutant complexes. Color scheme is the same as in Fig. 6B. **(B)** The DUB module does not affect the lysine specificity of Gcn5 HAT module. An *in vitro* HAT assay using mono-nucleosome as substrate was performed at 30°C for 30 min with both wild type (WT) and Sgf73 Δ2A SAGA complexes. Reactions were analyzed by SDS-PAGE gel and Western blot or silver staining. Equivalent amounts of Gcn5 and all 4 histones were present in each sample, as shown in the top and bottom panels. Histone acetylation was monitored using antibodies against acetylated H3K14 (H3K14Ac) or H3K23 (H3K23Ac). Quantification of the relative intensity ratio is shown as bar graph on the right. Error bars represent standard deviation from the two independent experiments for both complexes shown on the left. **(C)** *in vitro* HAT assays. Same as in Fig. 6C and 6D, but

with free histone H3 as substrate. Color scheme is the same as in Fig. 6C and 6D. Error bars represent standard deviations from two biological replicates.

Figure S6. Representative MS2 spectra. MS2 spectra for identified crosslinks between (**A**) Taf12 K284 and Ada1 K234, (**B**) Sgf73 K40 and Ubp8 K22, (**C**) Ada3 K381 and Sgf73 K448, (**D**) Spt20 K161 and Tra1 K2713, (**E**) Gcn5 K111 and Spt7 K797, (**F**) Taf5 K209 and Taf6 K466, (**G**) Spt3 K190 and TBP K167, (**H**) Spt8 K548 and TBP K138. b and y ions are colored blue and red, respectively. Immonium ions are shown in green, and precursor ion is shown in yellow. Peptide sequences are listed below the spectra with modification mass shown in brackets following the modified residue.