

Supplementary Table 2 | Cryo-EM data collection, refinement and validation statistics.

	Map 1 (EMD-10465) (PDB 6TDA)	Map 2 (EMD-10465)	Map 3 (EMD-10465)	Map 4 (EMD-10465)
Data collection and processing				
Magnification	130,000	130,000	130,000	130,000
Voltage (kV)	300	300	300	300
Electron exposure (e ⁻ /Å ²)	47.8 / 45.4*	47.8 / 45.4*	47.8 / 45.4*	39.0 [†] / 45.2 [†] / 54.9 [‡]
Defocus range (μm)	0.4 – 2.9	0.4 – 2.9	0.4 – 2.9	0.8 – 4.8
Pixel size (Å)	1.05	1.05	1.05	1.05
Symmetry imposed	C1	C1	C1	C1
Initial particle images (no.)	1,232,532	1,232,532	1,232,532	1,009,020
Final particle images (no.)	372,442	106,474	35,972	176,594
Map resolution (Å)	~15 [#]	3.6	4.3	3.8
FSC threshold		0.143	0.143	0.143
Map resolution range (Å)		3.4 – 5.3	3.7 – 7.8	3.7 – 4.5
Refinement				
Initial model used (PDB code)	5Z3U, 3LJW, 1UHR, 2FQ3, 2YUS, 1TOT, 4V3Q, 6AX5			
Model resolution (Å)				
FSC threshold				
Map sharpening <i>B</i> factor (Å ²)				
Model composition				
Non-hydrogen atoms	42,578			
Protein / Nucleotide residues	4817 / 320			
Ligands	1x Zn			
<i>B</i> factors (Å ²)				
Protein				
Ligand				
Nucleotide				
R.m.s. deviations				
Bond lengths (Å)	0.005			
Bond angles (°)	0.947			
Validation				
MolProbity score	1.82			
Clashscore	7.27			
Poor rotamers (%)	1.37			
Ramachandran plot				
Favored (%)	95.50			
Allowed (%)	4.27			
Disallowed (%)	0.23			

	Map 5 (EMD-10465)	Map 6 (EMD-10465)	Map 7 (EMD-10465) (PDB 6TDA) [§]	Map 8 (EMD-10465) (PDB 6TDA) [§]
Data collection and processing				
Magnification	130,000	130,000	130,000	130,000
Voltage (kV)	300	300	300	300
Electron exposure (e ⁻ /Å ²)	39.0 [†] / 45.2 [†] / 54.9 [‡]	39.0 [†] / 45.2 [†] / 54.9 [‡]	47.8 / 45.4*	39.0 [†] / 45.2 [†] / 54.9 [‡]
Defocus range (μm)	0.8 – 4.8	0.8 – 4.8	0.4 – 2.9	0.8 – 4.8
Pixel size (Å)	1.05	1.05	1.05	1.05
Symmetry imposed	C1	C1	C1	C1
Initial particle images (no.)	1,009,020	1,009,020	1,232,532	1,009,020
Final particle images (no.)	176,594	176,594	106,474 / 35,972	176,594
Map resolution (Å)	3.6	3.6	3.9	3.6
FSC threshold	0.143	0.143	0.143	0.143
Map resolution range (Å)	3.5 – 5.4	3.5 – 5.7	3.5 – 7.5	3.5 – 5.5
Refinement				
Initial model used (PDB code)			5Z3U	3LJW, 1UHR, 2FQ3, 2YUS, 1TOT, 4V3Q, 6AX5
Model resolution (Å)			3.6	3.7
FSC threshold			0.5	0.5
Map sharpening <i>B</i> factor (Å ²)			-152.1	-105.7
Model composition				
Non-hydrogen atoms			13,648	20,260
Protein / Nucleotide residues			1,274 / 246	2646 / -
Ligands			0	1x Zn
<i>B</i> factors (Å ²)				
Protein			106.52	68.91
Ligand				61.21
Nucleotide			119.35	
R.m.s. deviations				
Bond lengths (Å)			0.004	0.005
Bond angles (°)			0.749	0.995
Validation				
MolProbity score			1.17	1.77
Clashscore			3.79	7.26
Poor rotamers (%)			0.00	0.05
Ramachandran plot				
Favored (%)			98.07	94.57
Allowed (%)			1.93	5.39
Disallowed (%)			0.00	0.05

Supplementary Table 1 | RSC subunit modelling.

Subunit / Chain ID	Domain	Residue range	PDB entry of homology model / Modelling algorithm	Changes to homology model
H2A / C + G	Histone	15-116	5Z3U, without chain O	UCSF Chimera, Namdinator, PHENIX real space refinement H4 (B) 15-22 stubbed Removed residues (see residue range)
H2B / D + H	Histone	15-116		
H3 / A + E	Histone	30-121		
H4 / B + F	Histone	30-121		
DNA / I	Nucl. DNA	39-134		
DNA / J	Nucl. DNA	40-134		
DNA / I	Upstream DNA	15-101		
DNA / J	Upstream DNA	21-102	B-DNA / 3D-DART	UCSF Chimera, PHENIX geometry minimization
		2-124		
		24-146		
Sfh1 / K	N-term.	1-150	not modelled	
Sfh1 / K		151-186	COOT, density guided <i>de novo</i> modelling	
Sfh1 / K		187-198	not modelled	
Sfh1 / K		198-201	COOT, density guided <i>de novo</i> modelling	
Sfh1 / K	RPT1	202-267	6ax5 / SWISS	UCSF Chimera, COOT, density + model guided building
Sfh1 / K		268-274	COOT, density guided <i>de novo</i> modelling	
Sfh1 / K	RPT2	275-341	6ax5 / SWISS	UCSF Chimera, COOT, density + model guided building
Sfh1 / K		342-346	COOT, density guided <i>de novo</i> modelling	
Sfh1 / K	Poly-alanine	347-360	COOT, density guided <i>de novo</i> modelling	
Sfh1 / K		361-372	not modelled	
Sfh1 / K	Docking helix	373-408	COOT, density guided <i>de novo</i> modelling	
Sfh1 / K	C-term.	408-426	not modelled	
Rsc8 / L	N-term.	1-58	not modelled	
Rsc8 / L		59-86	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	SWIRM	87-169	2FQ3 / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc8 / L		170-197	COOT, density guided <i>de novo</i> modelling	

Rsc8 / L		198-256	not modelled	
Rsc8 / L	Zn finger	257-307	1TOT / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc8 / L		308-314	not modelled	
Rsc8 / L	SANT	315-359	2YUS / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc8 / L		360-368	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L		369-385	not modelled	
Rsc8 / L	Long helix	386-401	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	Long helix	402-404	not modelled	
Rsc8 / L	Long helix	405-492	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	C-term.	493-557	not modelled	
Rsc8 / L	N-term.	1001-1081	not modelled	
Rsc8 / L		1082-1086	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	SWIRM	1087-1169	2FQ3 / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc8 / L		1170-1202	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	Zn finger	1203-1310	not modelled	
Rsc8 / L		1311-1314	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	SANT	1315-1359	2YUS / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc8 / L		1360-1370	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L		1371-1421	not modelled	
Rsc8 / L	Long helix	1422-1488	COOT, density guided <i>de novo</i> modelling	
Rsc8 / L	C-term.	1489-1557	not modelled	
Npl6 / M	N-term.	1-322	not modelled	
Npl6 / M		323-376	COOT, density guided <i>de novo</i> modelling	
Npl6 / M		377-380	not modelled	
Npl6 / M		381-434	COOT, density guided <i>de novo</i> modelling	
Npl6 / M	C-term.	435	not modelled	
Rsc9 / N	N-term.	1-55	not modelled	

Rsc9 / N		56-80	COOT, density guided <i>de novo</i> modelling	
Rsc9 / N	Armadillo	81-161	COOT, density guided <i>de novo</i> modelling	
Rsc9 / N	Armadillo	160-319	4V3Q / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc9 / N	Armadillo	320-346	COOT, density guided <i>de novo</i> modelling	
Rsc9 / N		347-359	COOT, density guided <i>de novo</i> modelling	
Rsc9 / N	Zn finger	360-516	not modelled	
Rsc9 / N		517-524	COOT, density guided <i>de novo</i> modelling	
Rsc9 / N	Armadillo	525-578	COOT, density guided <i>de novo</i> modelling	
Rsc9 / N	C-term.	579-581	not modelled	
Rsc6 / O	N-term.	1-5	not modelled	
Rsc6 / O		6-61	COOT, density guided <i>de novo</i> modelling	
Rsc6 / O		62-227	not modelled	
Rsc6 / O	SWIB	228-269	1UHR / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc6 / O		270-312	not modelled	
Rsc6 / O	SWIB	313-343	1UHR / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc6 / O		344-391	not modelled	
Rsc6 / O		392-462	COOT, density guided <i>de novo</i> modelling	
Rsc6 / O		463-468	not modelled	
Rsc6 / O		469-480	COOT, density guided <i>de novo</i> modelling	
Rsc6 / O	C-term.	481-483	not modelled	
Rsc58 / P	N-term.	1-9	not modelled	
Rsc58 / P	Bromo	10-36	COOT, density guided <i>de novo</i> modelling	
Rsc58 / P	Bromo	37-71	not modelled	
Rsc58 / P	Bromo	72-121	3LJW / SWISS	UCSF Chimera, COOT, density + model guided building
Rsc58 / P	Bromo	122-139	COOT, density guided <i>de novo</i> modelling	
Rsc58 / P		140-168	not modelled	
Rsc58 / P		169-316	COOT, density guided <i>de novo</i> modelling	

Rsc58 / P		317-387	not modelled	
Rsc58 / P		388-491	COOT, density guided <i>de novo</i> modelling	
Rsc58 / P	C-term.	492-502	not modelled	
Htl1 / Q	N-term.	1-16	not modelled	
Htl1 / Q		17-74	COOT, density guided <i>de novo</i> modelling	
Htl1 / Q	C-term.	75-78	not modelled	
Rsc4 / R	N-term. / Tandem bromo	1-443	not modelled	
Rsc4 / R	Sheet bundle 1	444-536	COOT, density guided <i>de novo</i> modelling	
Rsc4 / R		537-587	not modelled	
Rsc4 / R	Sheet bundle 2	588-625	COOT, density guided <i>de novo</i> modelling	
Sth1 / S	N-term.	1-47	not modelled	
Sth1 / S		48-134	COOT, density guided <i>de novo</i> modelling	
Sth1 / S		135-156	not modelled	
Sth1 / S		157-297	COOT, density guided <i>de novo</i> modelling	
Sth1 / S		298-321	not modelled	
				UCSF Chimera, rigid-body docking together with ARP module
Sth1 / S	HSA	322-369	4I6M:C / Used as deposited	Removed residues (see residue range)
				Amino acid residues mutated to Sth1-HSA (see Methods)
				Side chains stubbed
Sth1 / S		370-392	not modelled	
		modelled: 393-407 447-662, 677-734, 754-940,		UCSF Chimera, PHENIX real space refinement
Sth1 / S	ATPase	976-1006	5Z3U:O / Rosetta	Side chains stubbed
		not modelled: 408-446, 663-676, 735-753, 941-975		Removed residues (see residue range)

Sth1 / S	Bromo, C-term.	1007-1359	not modelled	
Arp7 / T				
Arp9 / U	ARP module	Same as in PDB entry	4I6M	UCSF Chimera, rigid-body docking
Rtt102 / V				
Chain X	poly-alanine		COOT, density guided <i>de novo</i> modelling	

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For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

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- ☒ ☐ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☒ ☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ A description of all covariates tested
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- ☒ ☐ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☒ ☐ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
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- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection FEI EPU 1.10, pLink 2 (version 2.3.1)

Data analysis RELION 3.0, Warp 1.0.6/1.0.7, UCSF Chimera (version 1.11.2), UCSF ChimeraX (version 0.91), COOT (version 0.8.9.2), PHENIX (version 1.16), PyMol (Schrödinger LLC version 1.8.4.1), Aline 1.0.025, XlinkAnalyzer 1.1.1, Namdinator (online version April 2019 - August 2019), 3D-DART (online version April 2019 - August 2019), MSAProbs (online version 0.9.7), ESPript (webserver July 2019 - August 2019), ROSETTA (online version February 2019 - August 2019), xVis (online version February 2019 - August 2019), Quick2D (online version August 2018 - August 2019), PSIPRED (online version February 2019 - July 2019), Molprobit plugin (PHENIX), XiNet (online version June 2019 - August 2019), SWISS-MODEL (online version October 2018 - August 2019), Molprobit (online version June 2019 - August 2019)

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Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

The coordinate file for the RSC-nucleosome complex structure was deposited with the Protein Data Bank with accession code 6TDA. The cryo-EM density maps used for model building were all deposited with the Electron Microscopy Data Base (EMDB) with accession code EMD-10465.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

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Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	Structural data was collected on two independently prepared samples. No statistical methods were used to predetermine the sample size. For cryo-EM, the sample sizes were determined by available electron microscopy measuring time and density of the particles on the sample grids. Statistics regarding cryo-EM analysis have all been detailed in the methods section.
Data exclusions	No data were pre-excluded from the analyses. Low quality data from cryo-EM was sorted out in RELION to reach high resolution with criteria pre-established in RELION.
Replication	Cross-linking mass spectrometry experiments were performed in duplicates with reproducible results.
Randomization	Samples were not allocated to groups.
Blinding	Investigators were not blinded during data acquisition and analysis because it is not a common procedure for the methods employed.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s)	Saccharomyces cerevisiae, RSC2-TAP-HIS3 yeast strain (YSC1177-YLR357W), Dharmacon TAP-tagged open reading frame (ORF) library
Authentication	N.A.
Mycoplasma contamination	Cells were not tested for mycoplasma.
Commonly misidentified lines (See ICLAC register)	none

Supplementary information

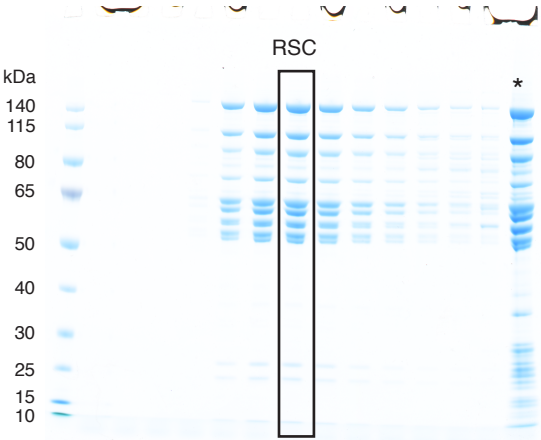
**Structure of SWI/SNF chromatin remodeller
RSC bound to a nucleosome**

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Felix R. Wagner, Christian Dienemann, Haibo Wang, Alexandra Stützer, Dmitry Tegunov,
Henning Urlaub & Patrick Cramer[✉]

Supplementary Figure 1

Extended Data Figure 1a



Extended Data Figure 1b

