

Table S1. SAXS data collection and analyses

(a) Sample details		Rad5
Organism	Saccharomyces cerevisiae	
Source	Escherichia coli expressed	
Construct Description	Full length Rad5 (His- and Twin-Strep-tagged)	
Extinction coefficient	124,720 M ⁻¹ cm ⁻¹	
M from chemical composition	137,694 Da	
Sample volume, concentration, flow rate	175 µl, 7.75 mg/ml, 0.7 ml/min	
FPLC and Column	AKTA Pure, Superdex 200 Increase 10/300 GL column	
Solvent details	40 mM Tris pH 8.0, 150 mM KCl, 5 mM DTT, 5% glycerol	
(b) SAXS data collection parameters		Rad5
X-ray beam Source	BioCAT facility at the Advanced Photon Source beamline 18ID	
Detector (Distance)	Pilatus3 1M (Dectris) detector (3.5 m)	
Wavelength	1.033 Å (12KeV)	
Beam size	150 (h) x 25 (v) µm ²	
q-measurement range	0.004-0.4 Å ⁻¹	
Absolute scaling method	N/A	
Basis for normalization to constant counts	To incident intensity, by ion chamber counter	
Method for monitoring radiation damage	Automated frame-by-frame comparison of relevant regions	
Exposure time, number of exposures	0.5 s exposure with a 2 s total exposure period (0.5 s on, 1.5 s off) of entire SEC elution	
Sample configuration	SEC-SAXS. Size separation by an AKTA Pure with a Superdex 200 Increase 10/300 GL column. SAXS data measured in a 1.5 mm ID quartz capillary.	
Sample temperature	20°C	
(c) Software employed for SAXS data reduction		Rad5
SAXS data reduction and solvent subtraction	Radial averaging; frame comparison, averaging, and subtraction done using BioXTAS RAW 1.6.0 (Hopkins <i>et al.</i> , 2017)	
Basic analyses: Guinier Rg and P(r)	Guinier fit using BioXTAS RAW 1.6.0, P(r) function using GNOM (Svergun, 1992)	

(d) Structural parameters	Rad5
Guinier Analysis	
I(0)	0.00006043 +/- 0.0000002302
R_g	47.0079 +/- 0.3058
qR_g range	0.2704 - 1.2842
Coefficient of correlation, R^2	0.9877
P(r) analysis	
I(0)	0.000061 +/- 0.000000232
R_g	49.18 +/- 0.3102
D_{max}	178
q range	0.0058 - 0.3627
χ^2 (total estimate from GNOM)	1.0914