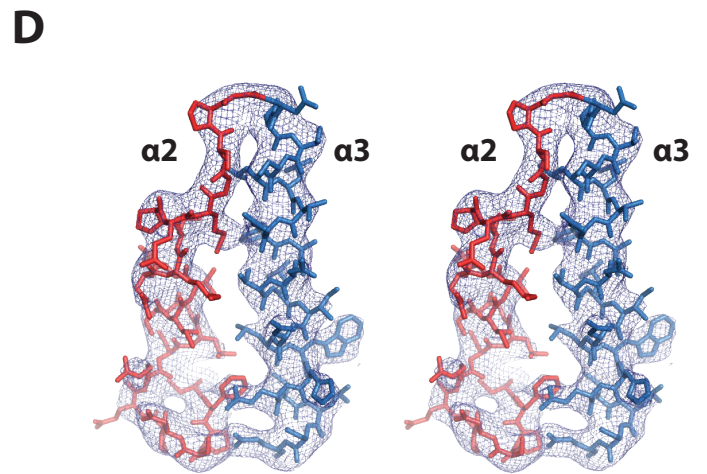
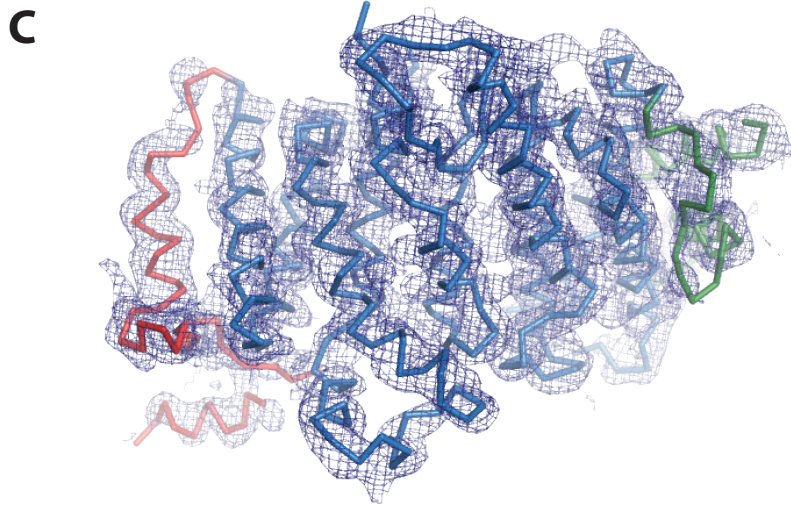
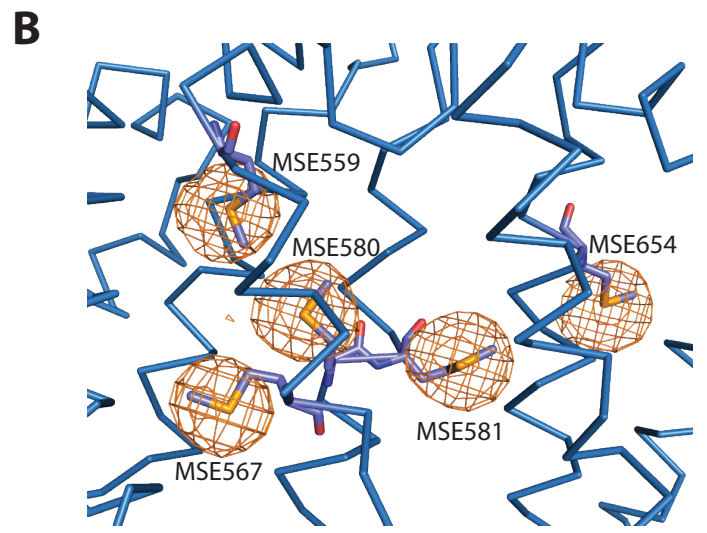
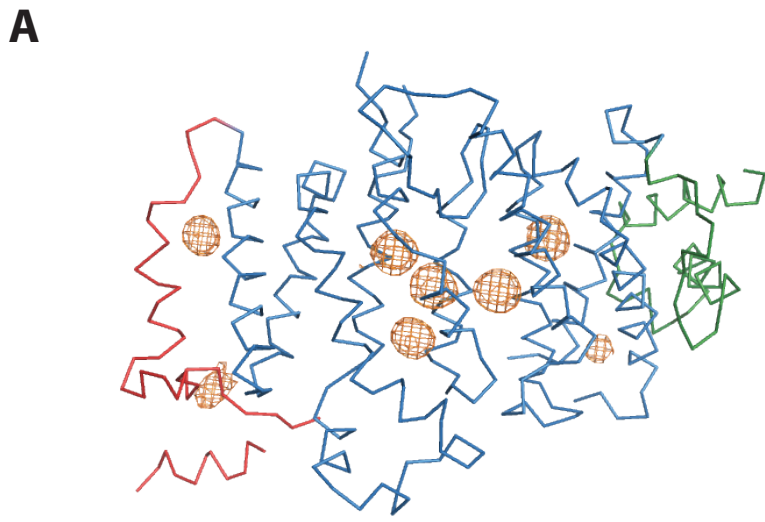
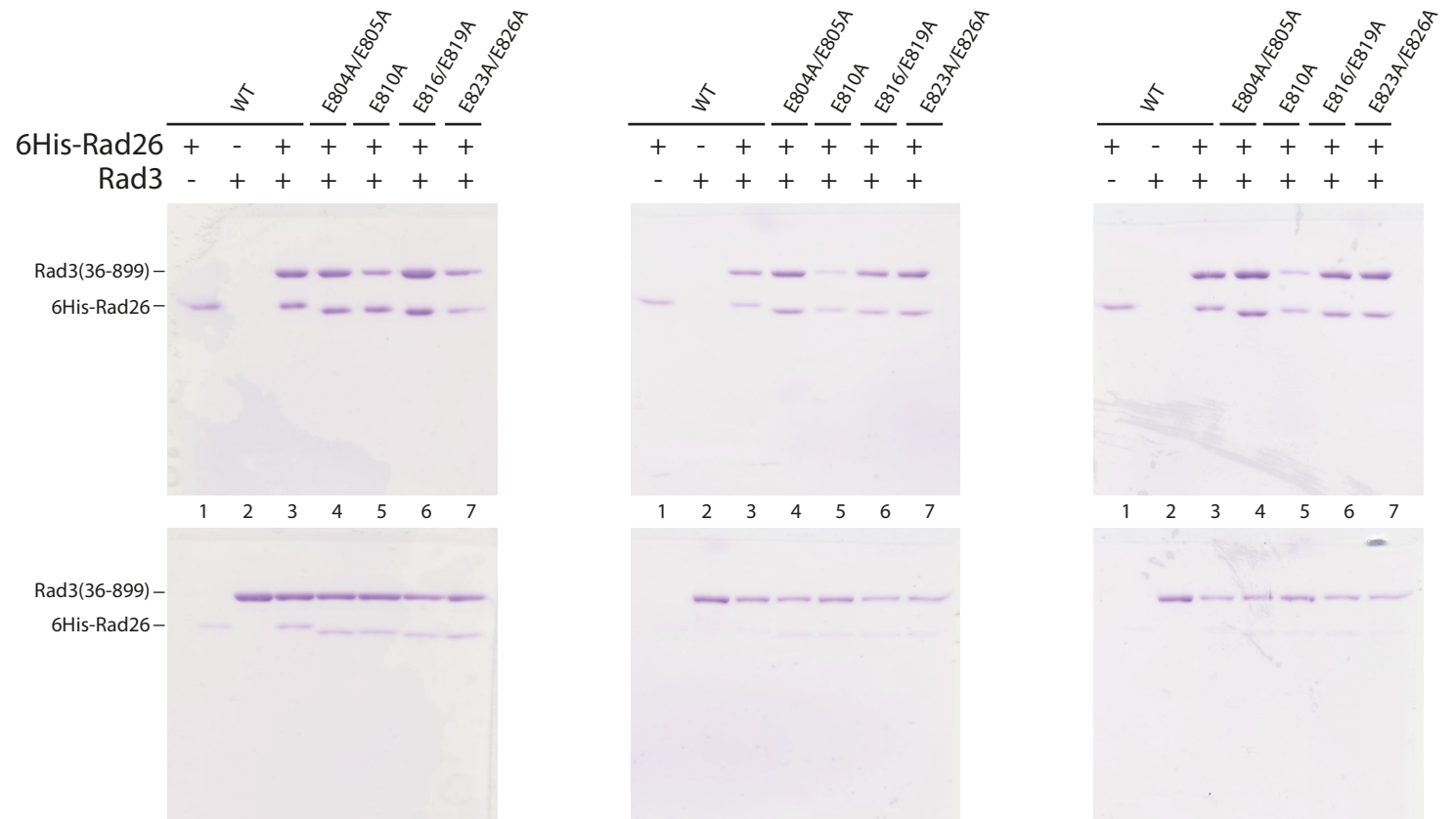


SUPPLEMENT Table 1. SAXS data

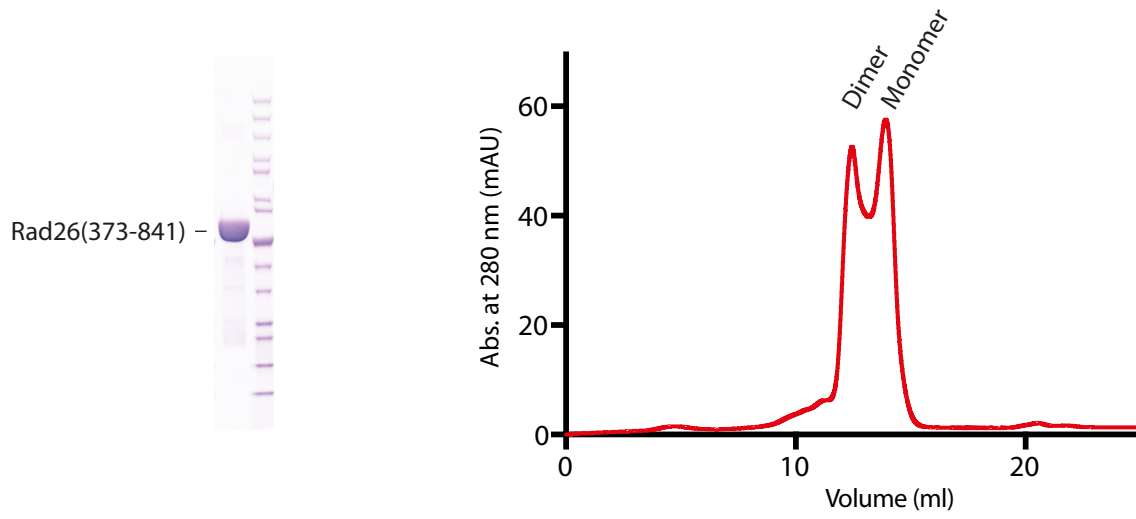
Data collection	
Instrument	EMBL P12 beamline, PETRA III
Wavelength (Å)	1.224
Exposure time (s)	1.0
Detector distance (m)	3.0
Concentration (mg/ml)	0.76
Temperature (°C)	20
Structural parameters	
R_g (Å)	41.5
D_{max} (Å)	133
Porod volume estimate (nm ³)	190
M_r (kDa)	160
Software	
Data reduction	Automated pipeline, EMBL P12 beamline, PETRA III
<i>Ab initio</i> analysis	DAMMIN/CRY SOL



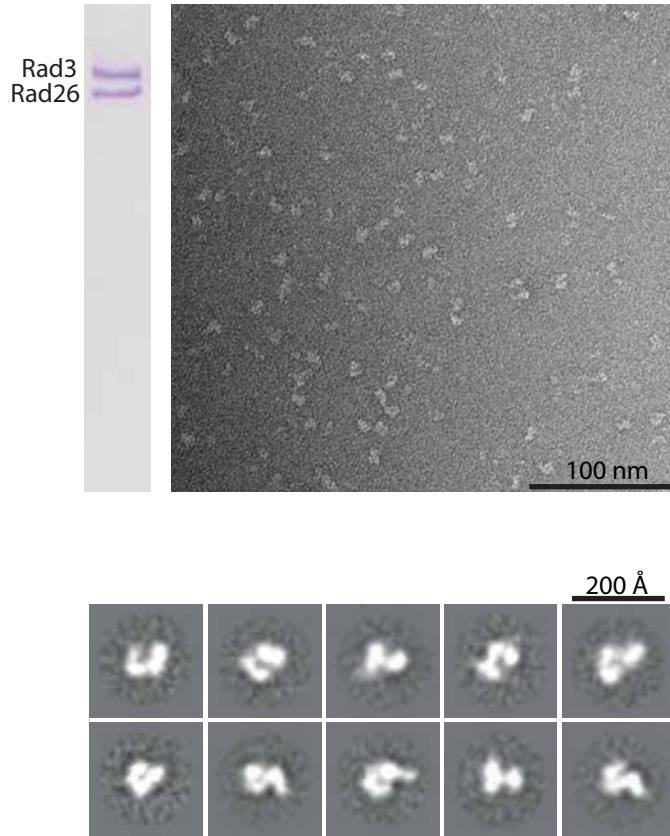
SUPPLEMENT FIGURE 1. *A-B*, Anomalous difference Fourier map contoured at 5σ showing location of selenium atoms. *C*, Experimental SAD electron density map contoured at 1σ together with the final Rad26 model. *D*, Stereo view of helix 2 and 3 in the final electron density (2mFo-DFc) contoured at 1σ.

A

SUPPLEMENT FIGURE 2. A, Three pull down experiments of Rad3 using tagged Rad26 mutated in the acidic patch as indicated. Top gel is the bound fraction and the bottom gel is the corresponding unbound fraction from each pull down experiment.

A

SUPPLEMENT FIGURE 3. A, Analytic gel filtration of the Rad26(residues 373-841) protein suggest that it exist as a mixture of monomers and dimers.

A

SUPPLEMENT FIGURE 4. A, SDS-PAGE of the purified Rad3-Rad26 complex and the associate micrograph of negative-stained particles with the reference-free 2D class averages shown below.