Supplemental Figures

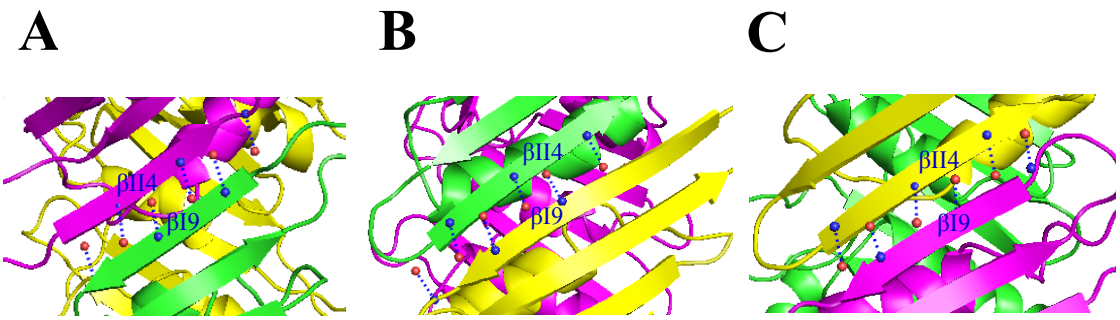

Figure S1. The zipper-like series of hydrogen bonds between each two components of the human 9-1-1 complex. hRad9 is shown in magenta, hHus1 in green, and hRad1 in yellow. The zipper-like series of hydrogen bonds is formed between βII4 of C-terminal domain of one molecule and βI9 of N-terminal domain of the next molecule.

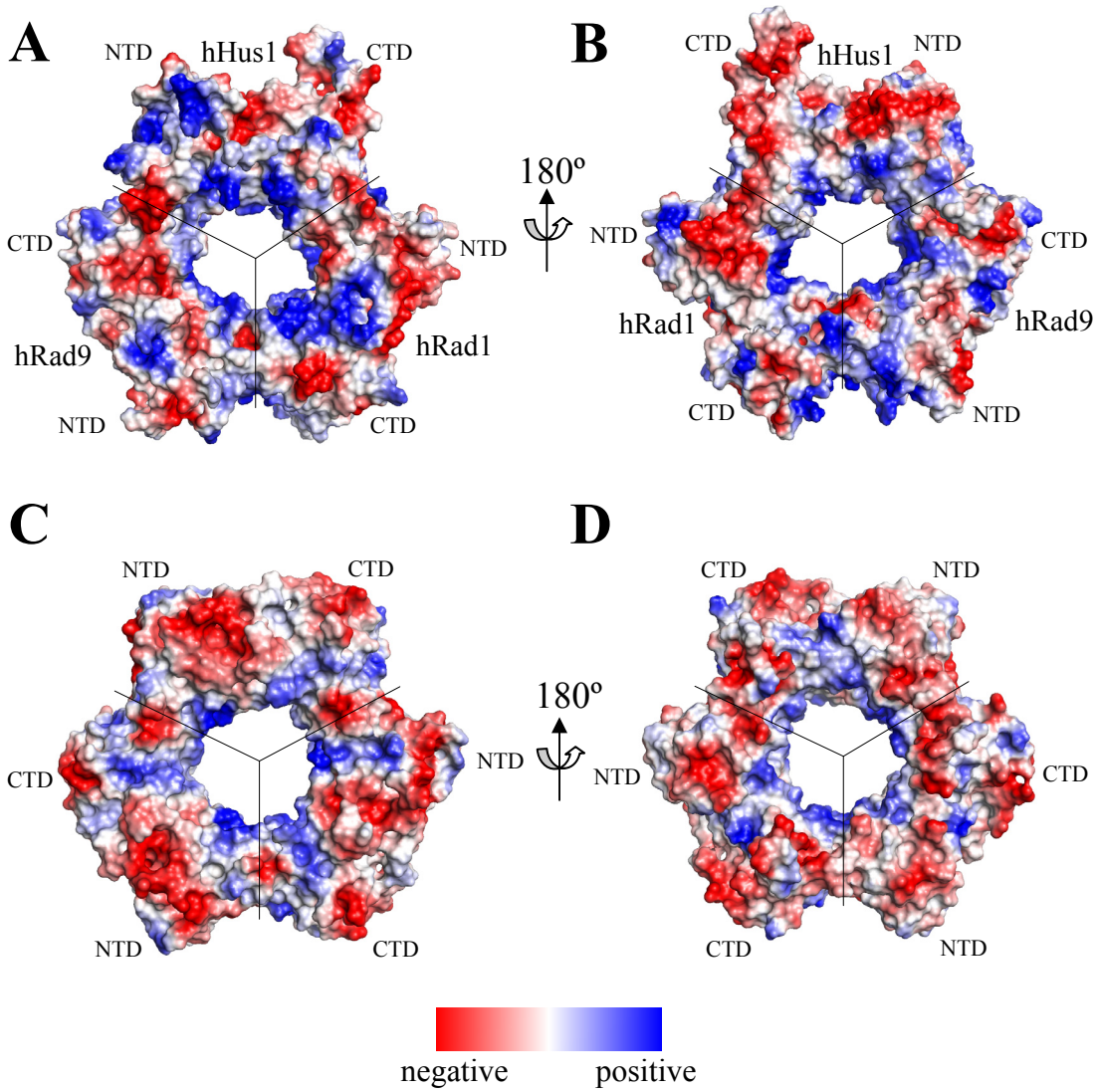

Figure S2. The net charge distribution on the surface of the human 9-1-1 complex and PCNA. A, B, The net charge distribution on the surface of the human 9-1-1 complex. **C, D,** The net charge distribution on the surface of the human PCNA (PDB code: 1vym).

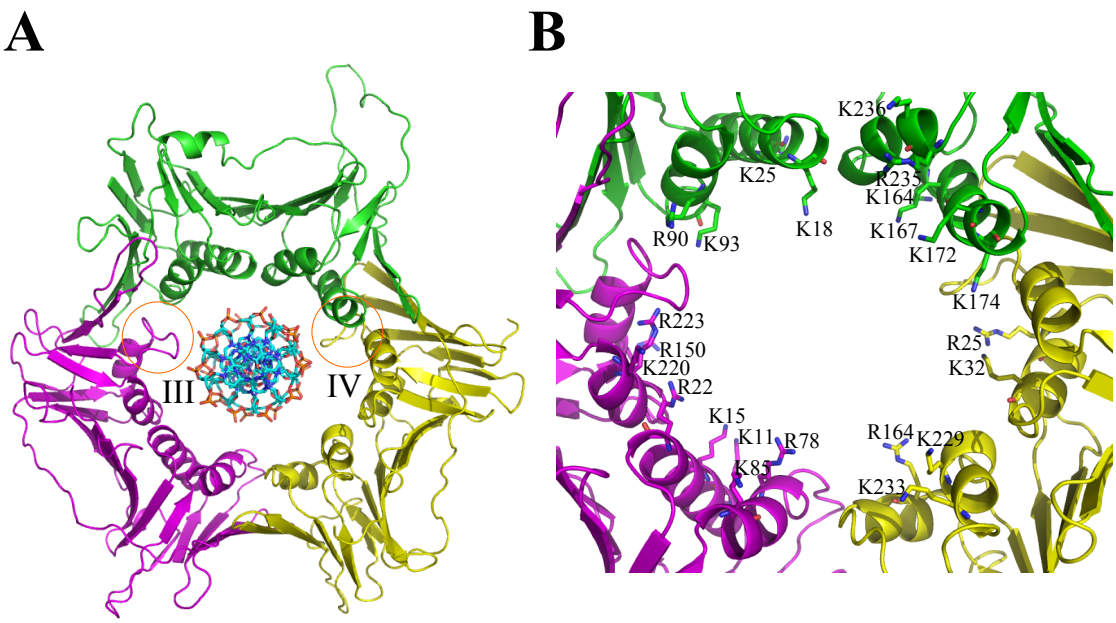

Figure S3. Potential interactions between the human 9-1-1 complex and dsDNA. hRad9 is shown in magenta, hHus1 in green, and hRad1 in yellow. **A,** An interaction model of the 9-1-1 complex and duplex B-form DNA. III indicates the αII1-βII2 loop of hRad9 near the channel in the 9-1-1 complex; IV indicates the αI2-βI7 loop of hRad1near the channel in the 9-1-1 complex. **B,** Lysine and arginine residues in the 12 α helices extend into the channel in the 9-1-1 ring.

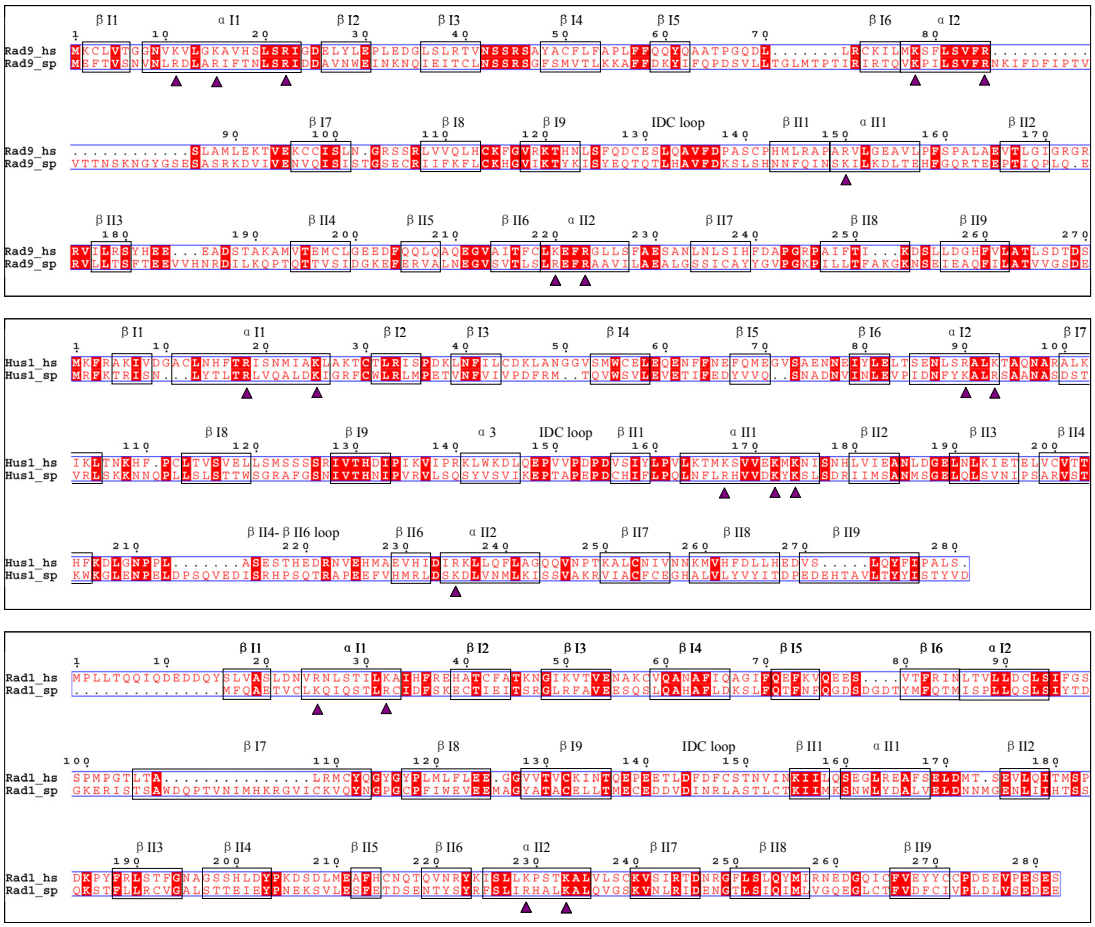

Figure S4. Sequence alignments between human and fission yeast Rad9, Hus1, and Rad1. Purple triangles indicate the conserved lysine and arginine residues in the α helices of these proteins which extend into the channel of the human 9-1-1 complex. Red shadow shows the conserved residues of each protein pair by sequence alignment from human and fission yeast sources. hs represents *human*, sp represents *Saccharomyces pombe*. The sequence alignments between *human* and *Saccharomyces pombe* sources were generated by ESPript (1).

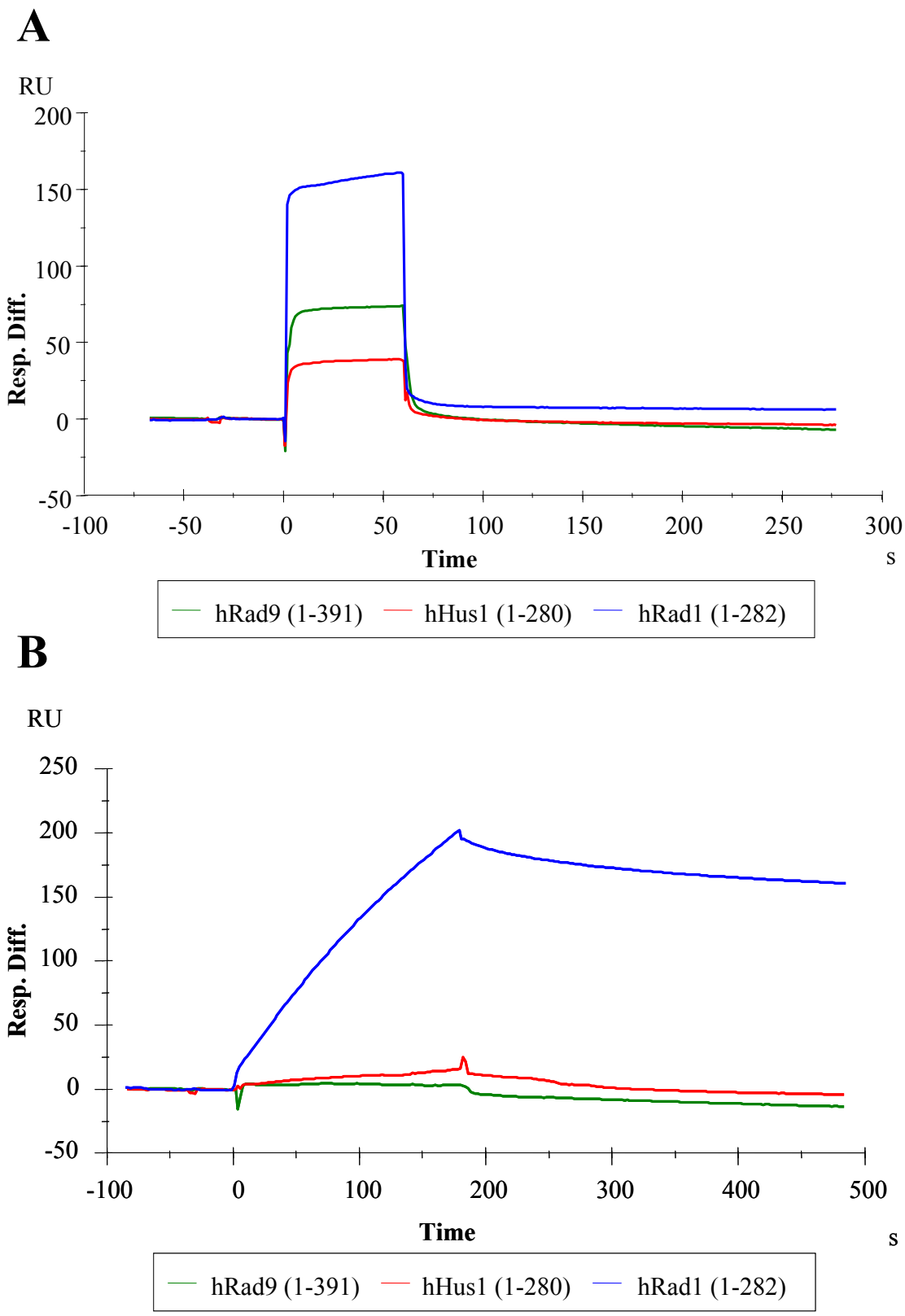

Figure S5. Biacore analysis. A, Biacore analysis of the hFen1 peptide (residues 335-364) binding to immobilized hRad9, hHus1, and hRad1. hRad1 has the highest binding affinity, hRad9 has the intermediate, and hHus1 has the lowest. **B,** Biacore

analysis of truncated hRad17 (residues 78-337) binding to immobilized hRad9, hHus1, and hRad1. Truncated hRad17 (residues 78-337) interacts with hRad1, but not with hHus1 or hRad9.

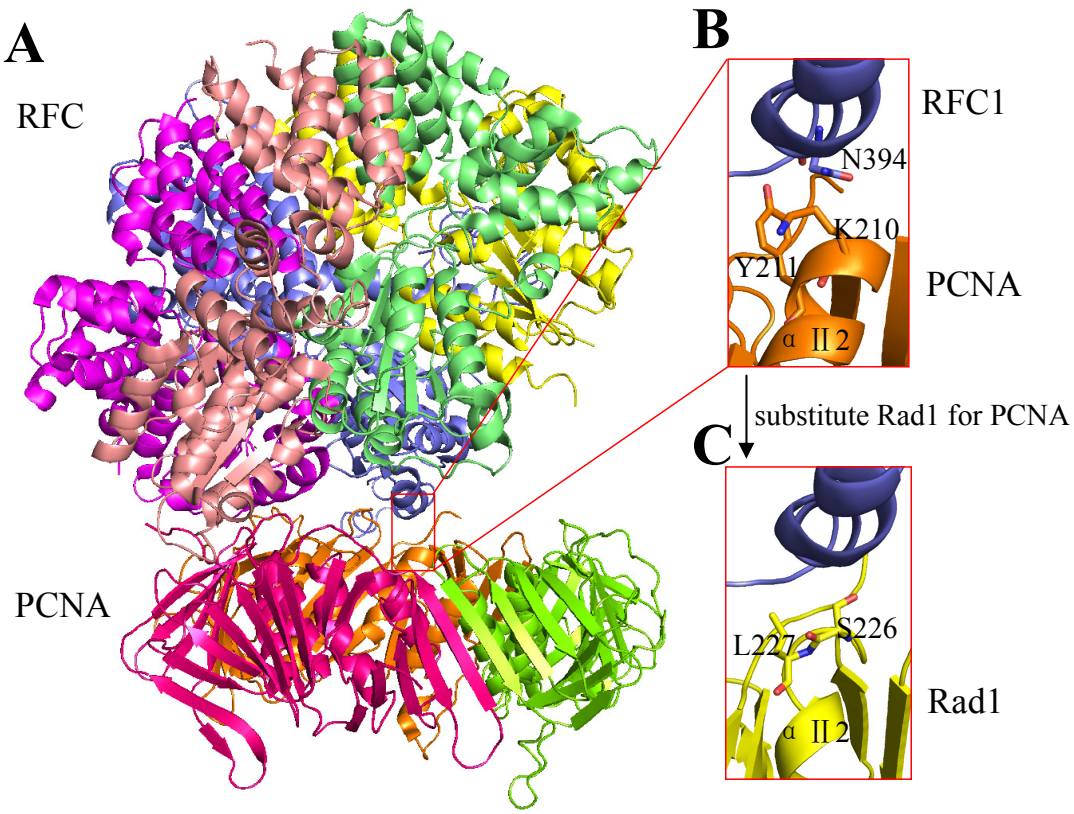

Figure S6. ***Saccharomyces cerevisiae*** **PCNA/RFC complex. A,** Stereoview of the *Saccharomyces cerevisiae* PCNA/RFC complex. PDB code: 1SXJ. **B,** The interface between RFC1 and the N-terminal residues of PCNA αII2 helix. The interacting residues in the interface are indicated. **C,** Substitution of hRad1 for PCNA. The residues 226-227 in αII2 helix of hRad1 corresponding to that of PCNA are indicated.

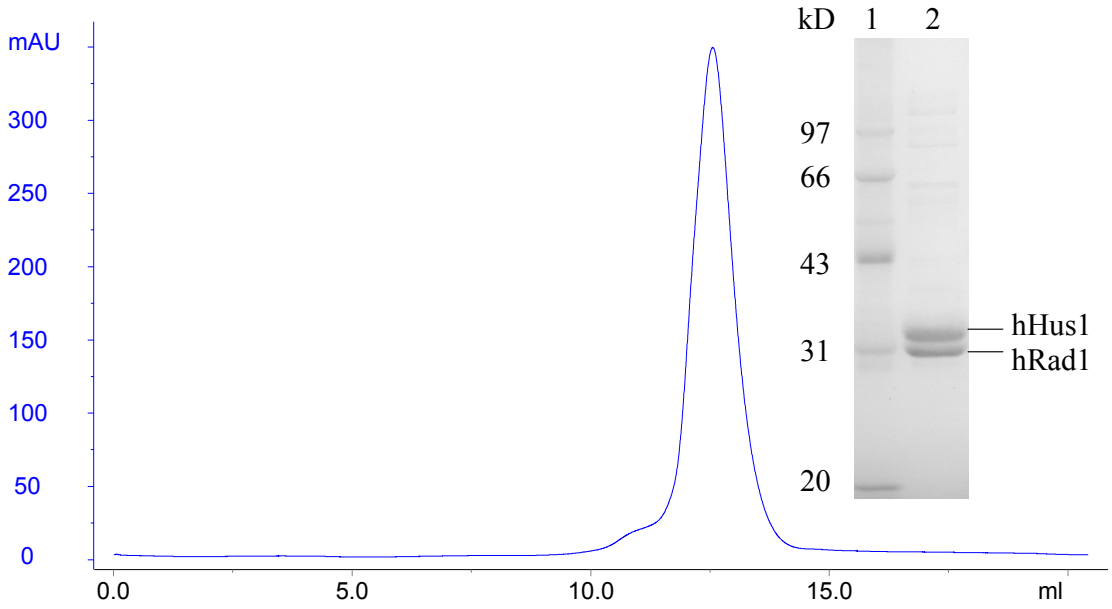

Figure S7. Size-exclusion column chromatography and SDS-PAGE of human Hus1-Rad1 complex. Line 1 shows the Protein markers. Line 2 shows the purified proteins obtained via size-exclusion column chromatography.

Supplemental tables

Table S1. Data Collection and Refinement Statistics

	Native	Hg Derivative
Data collection		
X-ray source	BL41XU at Spring-8 (Japan)	PX at SLS (Switzerland)
Wavelength (Å)	1.0716	1.0063
Resolution (Å)	15-3.2 (3.31-3.2)	15-3.2 (3.31-3.2)
Space group	$P2_1$	$P2_1$
Unit cell (Å)	a=71.03, b=67.17, c=83.41, β=97.58	a=70.54, b=67.38, c=82.97, β=97.85
Unique reflections	13,001(1272)	12,762 (1879)
Average redundancy	6.5	5.7
Anomalous redundancy		2.9
I/σ (I)	17.22(4.5)	24.6 (4.1)
Completeness (%)	99.8 (99.5)	99 (100)
Anomalous Completeness (%)		98.2 (99.7)
R_{merge} (%)[a]	8.0 (43.2)	8.7 (29.0)
Refinment		
Resolution (Å)	15-3.2	
$R_{working}$ (%)[b]	28.9	

R_{free}(%)[c]	30.6
Average B factor (Å)	67.8
rmsd bounds (Å)	0.011
rmsd angles (^{o})	1.728

Numbers in parentheses represent statistics for the highest resolution shell.

[a]$R_{merge} = \sum|I - \langle I \rangle| / \sum I$, where I is the measured intensity for reflections with indices *hkl*.

[b]$R_{working} = \sum||F_{obs}| - |F_{calc}|| / \sum|F_{obs}|$.

[c]R_{free} = R factor for a selected subset (10%) of the reflections that were not included in prior refinement calculations.

Table S2. Interface parameters of the human 9-1-1 complex.

Calculated using the CCP4 PISA server (2) and the CCP4 SC program (3).

Interface	Complexation Significance Score (CSS)*	Shape Complementarity (SC)**
hRad9-hHus1	1.0	0.609
hHus1-hRad1	1.0	0.649
hRad1-hRad9	0.24	0.540

* Complexation Significance Score (CSS) ranges from 0 to 1 as the interface relevant to complexation increases.

** Shape Complementarity (SC) is in the range 0–1 (1 = best fit).

Supplemental References

1. Gouet, P., Courcelle, E., Stuart, D. I., and Metoz, F. (1999) *Bioinformatics* **15**, 305-308

2. Krissinel, E., and Henrick, K. (2007) *J. Mol. Biol.* **372**, 774-797

3. Lawrence, M. C., and Colman, P. M. (1993) *J. Mol. Biol.* **234**, 946-950