Table S1. Crystallographic Statistics, Related to Figure 2

	hcGAS–DNA	hcGAS–DNA ATP
Data Collection		
Resolution (Å)[a]	48.21–2.30 (2.38–2.30)	49.15–2.79 (2.95–2.79)
Wavelength (Å)	0.97918	0.97918
Space group	P 6_1 2 2	P 6_1 2 2
Unit cell: a, b, c (Å)	101.17, 101.17, 241.06	100.49, 100.49, 236.75
Unit cell: α, β, γ (°)	90.0, 90.0, 120.0	90.0, 90.0, 120.0
Molecules per ASU	1	1
No. reflections: total	438690	356853
No. reflections: unique	33460	18321
Completeness (%)[a]	99.6 (96.4)	99.8 (98.5)
Multiplicity[a]	13.1 (12.1)	19.5 (18.2)
$I/\sigma I$[a]	10.9 (1.1)	10.0 (1.6)
CC(1/2)[b] (%)[a]	99.8 (31.7)	99.8 (31.9)
Rpim[c] (%)[a]	4.5 (79.6)	8.6 (118.0)
Refinement		
Resolution (Å)	48.21–2.30	49.15–2.79
Free reflections (%)	10	10
R-factor / R-free	19.9 / 22.8	21.1 / 24.6
Bond distance (RMS Å)	0.006	0.002
Bond angles (RMS °)	0.720	0.543
Structure/Stereochemistry		
No. atoms: protein	2859	2826
No. atoms: DNA	592	592
No. atoms: ligand	1 (Zn)	34 (ATP, Mg, Zn)
No. atoms: water	103	21
Average B-factor: protein	57.0	66.1
Average B-factor: DNA	98.2	103.3
Average B-factor: ligand	43.4	56.3
Average B-factor: water	53.7	61.3
Ramachandran plot: favored	97.93%	96.71%
Ramachandran plot: allowed	1.77%	2.99%
Ramachandran plot: outliers	0.30%	0.30%
Rotamer outliers:	1.87%	1.57%
MolProbity[d] score	1.52	1.46
Protein Data Bank ID	6CT9	6CTA

[a] Highest resolution shell values in parenthesis
[b] (Karplus and Diederichs, 2012)
[c] (Weiss, 2001)
[d] (Chen et al., 2010)