Supplementary Tables

Supplementary Table 1

Structure without DNA		
Model number	**Model obtained after:**	**Correlation coefficient after fitting**
Model 0	Initial model: composite structure without the N-terminus (residues 1-46) obtained after the superposition of the catalytic core of the following structures CC+Nter, CC+Cter, CC+IBD of LEDGF	
Model 1	1 mode fitting, use of 30% of the amplitudes, regularization with Refmac	0.531
Model 2	1 mode fitting, use of 50% of the amplitudes, regularization with Refmac	0.564
Model 3	1 mode fitting, use of 100% of the amplitudes, manually fitting of the N-terminus, regularization with Refmac	0.738
Model 4	Rigid body N-terminus fitting, use 100% of the amplitudes, regularization with Refmac	0.821
Model 5	12 modes fitting in model masked EM map, use 100% of the amplitudes, regularization with Refmac, generate the two fold symmetric related molecule.	0.830

Detailed fitting procedure in the structure without DNA. When one normal mode is used, it is the lowest frequency mode (mode 7). Frequency modes 7 to 18 are used in the 12 modes fitting. The correlation coefficient are calculated as defined in (Navaza *et al.*, 2002)

Supplementary Table 2

Structure with DNA		
Model number	**Model obtained after:**	**Correlation coefficient after fitting**
Model 4	Initial model obtained from the structure without DNA at the step 4	-
Model 6	1 modes fitting in model masked EM map, use 30% of the amplitudes, regularization with Refmac	0.471
Model 7	1 modes fitting in model masked EM map, use 50% of the amplitudes, regularization with Refmac	0.481
Model 8	12 modes fitting in model masked EM map, use 100% of the amplitudes, regularization with Refmac	0.550
Model 9	Rigid body N-terminus fitting, use 100% of the amplitudes, regularization with Refmac	0.772
Model 10	Manually fitting of the DNA molecules in the empty density remaining in the top region using difference map	-

Detailed fitting procedure in the structure with DNA. When one normal mode is used, it is the lowest frequency mode (mode 7). Frequency modes 7 to 18 are used in the 12 modes fitting. The correlation coefficient are calculated as defined in (Navaza *et al.*, 2002)

Supplementary Table 3

Structure	**Superposition of the catalytic core domain of :**	**Domain**	**Translation (Å)**	**Rotation (°)**
Without DNA	model 0 – model 5	Nter A	23.61	133.58
		Nter B	-44.75	-163.59
		Cter A	3.12	12.62
		Cter B	-2.14	-5.88
With DNA	model 4 – model 9	Nter A	16.44	30.21
		Nter B	-12.16	-51.02
		Cter A	15.78	-36.84
		Cter B	4.25	37.23

Movement of the Cter and Nter domains after superposition of the catalytic core domains.