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Supporting Information

Accommodation of a 1*S* (–)-Benzo[*c*]phenanthrenyl-N^6-dA Adduct in a Y Family Dpo4 DNA Polymerase Active Site: Structural Insights through Molecular Dynamics Simulations

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Running Title: Benzo[*c*]phenanthrenyl-N^6-dA adduct in Dpo4

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Tables

Table S1. Torsion angles in modeled Dpo4 ternary complexes from Type I and Type II crystal structures. [a]

Model	Residue	α (°)	β (°)	γ (°)	δ (°)	ε (°)	ζ (°)	χ (°)
Control and Major Groove Type I	tG_1	N/A	N/A	36.4	156.4	155.0	–94.6	116.0
	tG_2	139.8	–132.8	*116.1*	*146.1*	*–103.2*	*127.8*	*–139.1*
Intercalation	tG_1	N/A	N/A	36.3	156.4	155.0	–95.2	–97.8
	tG_2	–46.8	–146.0	36.4	156.4	–62.3	–129.9	–97.8
	tA_3	–112.9	–150.7	–47.0	138.5	–177.0	–110.3	–114.0
	tC_4	–87.2	–94.3	36.3	156.4	107.0	–80.0	148.9
	tA^*_5	–114.3	125.7	132.6	135.4	–151.3	–89.1	–35.5
	tA_6	–79.2	–175.4	52.6	146.1	–161.0	–112.1	–99.3
	tG_7	–65.0	171.2	*47.6*	*119.8*	*–179.1*	*–120.7*	*–111.1*
–1 Deletion	tG_1	N/A	N/A	36.4	156.4	154.9	–95.2	–97.8
	tG_2	–46.8	–146.1	36.4	156.4	–62.3	–108.8	–97.7
	tA_3	–135.2	–172.2	–5.2	*–138.5*	*–143.3*	*–150.4*	*–114.1*

[a] N/A denotes values not applicable to the terminal residue. Italicized numbers denote crystal values.

Table S2. Hydrogen bonding interactions of > 10% occupancy or bifurcated hydrogen bonds between polymerase residues and the sugar–triphosphate backbone of the incoming dNTP.

Model	**Hydrogen Bond** [a]	**Occupancy** [b]
Control	(Arg51)Nη1–Hη12…O2γ(dTTP)	100%
	(Arg51)Nη2–Hη22…O3β(dTTP)	99.70%
	(Arg51)Nη2–Hη22…O2γ(dTTP)	90.90%
	(Thr45)Oγ1–Hγ1…O1β(dTTP)	99.5%
	(Tyr10)N–H…O2γ(dTTP)	95.60%
	(Tyr10)N–H…O1γ(dTTP)	61.40%
	(Tyr10)N–H…O3β(dTTP)	33.20%
	(Phe11)N–H…O2β(dTTP)	95.30%
	(Tyr12)N–H…O3′(dTTP)	81.75%
	(Lys159)Nζ–Hζ1…O3γ(dTTP)	44.65%
	(Lys159)Nζ–Hζ3…O3γ(dTTP)	32.50%
	(Lys159)Nζ–Hζ2…O3γ(dTTP)	21.70%
	(Lys159)Nζ–Hζ1…O2γ(dTTP)	6.60%
	(Lys159)Nζ–Hζ3…O2γ(dTTP)	4.65%
	(Lys159)Nζ–Hζ2…O2γ(dTTP)	4.10%
Intercalation	(Arg51)Nη1–Hη12…O1γ(dTTP)	98.75%
	(Arg51)Nη2–Hη22…O3γ(dTTP)	95.94%
	(Arg51)Nη2–Hη22…O1γ(dTTP)	40.62%
	(Arg51)Nη1–Hη12…O3γ(dTTP)	36.27%
	(Arg51)Nη1–Hη12…O1β(dTTP)	12.06%
	(Thr45)Oγ1–Hγ1…O3γ(dTTP)	36.51%
	(Tyr10)N–H…O1γ(dTTP)	16.41%
	(Tyr12)Oη–Hη…O3′(dTTP)	14.71%
	(Tyr12)Oη–Hη…375O4′(dTTP)	7.15%
	(Lys159)Nζ–Hζ1…O1β(dTTP)	42.47%
	(Lys159)Nζ–Hζ1…O1γ(dTTP)	18.51%
	(Lys159)Nζ–Hζ2…O1β(dTTP)	12.06%
	(Lys159)Nζ–Hζ3…O1β(dTTP)	12.01%
	(Lys159)Nζ–Hζ2…O1γ(dTTP)	10.86%
	(Lys159)Nζ–Hζ3…O1γ(dTTP)	9.65%
	(Arg51)Nη2–Hη22…O1γ(dCTP)	40.10%
	(Thr45)Oγ1–Hγ1…O3γ(dCTP)	99.9%
	(Tyr10)N–H…O1γ(dCTP)	30.10%
	(Tyr10)N–H…O2γ(dCTP)	19.75%
	(Tyr10)N–H…O3β(dCTP)	33.20%
	(Tyr12)Oη–Hη…375O2(dCTP)	99.95%
	(Lys159)Nζ–Hζ2…O1β(dCTP)	19.35%
	(Lys159)Nζ–Hζ3…O1β(dCTP)	12.80%
	(Lys159)Nζ–Hζ1…O1β(dCTP)	1.25%
	(Tyr12)Oη–Hη…O3′(dATP)	98.60%
	(Arg51)Nη1–Hη12…O1γ(*syn*-dATP)	99.50%
	(Arg51)Nη2–Hη22…O3γ(*syn*-dATP)	92.35%
	(Arg51)Nη2–Hη22…O1γ(*syn*-dATP)	78.35%
	(Thr45)Oγ1–Hγ1…O3γ(*syn*-dATP)	39.65%
	(Tyr10)N–H…O1γ(*syn*-dATP)	27.00%
	(Tyr10)N–H…O2γ(*syn*-dATP)	7.55%
	(Tyr10)N–H…O3β(*syn*-dATP)	33.20%
	(Tyr12)Oη–Hη…O3′(*syn*-dATP)	88.70%
	(Lys159)Nζ–Hζ3…O1β(*syn*-dATP)	65.90%
	(Lys159)Nζ–Hζ2…O1β(*syn*-dATP)	18.20%

	(Lys159)Nζ–Hζ1…O1β(*syn*-dATP)	15.25%
Intercalation (Cont'd)	(Arg51)Nη2–Hη22…O3γ(dGTP)	89.40%
	(Arg51)Nη1–Hη12…O1γ(dGTP)	72.90%
	(Arg51)Nη2–Hη22…O1γ(dGTP)	22.60%
	(Arg51)Nη1–Hη12…O3γ(dGTP)	16.15%
	(Thr45)Oγ1–Hγ1…O3γ(dGTP)	16.05%
	(Tyr12)Oη–Hη…375O4′(dGTP)	10.65%
	(Lys159)Nζ–Hζ2…O1β(dGTP)	32.55%
	(Lys159)Nζ–Hζ1…O1β(dGTP)	32.00%
	(Lys159)Nζ–Hζ3…O1β(dGTP)	28.30%
	(Lys159)Nζ–Hζ2…O1γ(dGTP)	9.350%
	(Lys159)Nζ–Hζ1…O1γ(dGTP)	6.30%
	(Lys159)Nζ–Hζ3…O1γ(dGTP)	4.70%
	(dGTP)O3′– HO3′…Oδ2(Asp105)	64.15%
	(Arg51)Nη1–Hη12…O1γ(*syn*-dGTP)	99.40%
	(Arg51)Nη2–Hη22…O3γ(*syn*-dGTP)	99.00%
	(Arg51)Nη2–Hη22…O1γ(*syn*-dGTP)	70.00%
	(Thr45)Oγ1–Hγ1…O3γ(*syn*-dGTP)	26.20%
	(Tyr10)N–H…O1γ(*syn*-dGTP)	57.80%
	(Tyr10)N–H…O2γ(*syn*-dGTP)	9.30%
	(Phe11)N–H…O2γ(*syn*-dGTP)	67.55%
	(Phe11)N–H…O3γ(*syn*-dGTP)	5.25%
	(Tyr12)N–H…O3′(*syn*-dGTP)	11.30%
	(Lys159)Nζ–Hζ1…O1β(*syn*-dGTP)	48.20%
	(Lys159)Nζ–Hζ2…O1β(*syn*-dGTP)	26.75%
	(Lys159)Nζ–Hζ3…O1β(*syn*-dGTP)	21.05%
Major Groove Type I	(Arg51)Nη1–Hη12…O3γ(dTTP)	99.80%
	(Arg51)Nη2–Hη22…O3β(dTTP)	83.80%
	(Arg51)Nη2–Hη22…O3γ(dTTP)	19.30%
	(Arg51)Nη1–Hη12…O3β(dTTP)	17.95%
	(Arg51)Nη2–Hη22…O1β(dTTP)	12.40%
	(Tyr10)N–H…O2γ(dTTP)	100%
	(Phe11)N–H…O1β(dTTP)	27.45%
	(Tyr12)N–H…O3′(dTTP)	91.75%
	(Tyr12)Oη–Hη…375O2(dTTP)	7.90%
	(Tyr48)Oη–Hη…O3γ(dTTP)	93.35%
	(Lys159)Nζ–Hζ3…O1γ(dTTP)	51.20%
	(Lys159)Nζ–Hζ1…O1γ(dTTP)	44.40%
	(Arg51)Nη2–Hη22…O3β(dCTP)	87.25%
	(Arg51)Nη1–Hη12…O2γ(dCTP)	85.40%
	(Arg51)Nη2–Hη22…O2γ(dCTP)	34.80%
	(Arg51)Nη2–Hη22…O1β(dCTP)	22.10%
	(Arg51)Nη1–Hη12…O3β(dCTP)	15.35%
	(Thr45)Oγ1–Hγ1…O1β(dCTP)	100%
	(Tyr10)N–H…O2γ(dCTP)	88.20%
	(Tyr10)N–H…O3β(dCTP)	57.20%
	(Tyr10)N–H…O1γ(dCTP)	37.65%
	(Phe11)N–H…O2β(dCTP)	22.25%
	(Tyr12)Oη–Hη…375O2(dCTP)	88.85%
	(Tyr12)N–H…O3′(dCTP)	83.45%
	(Tyr48)Oη–Hη…O2γ(dCTP)	37.75%
	(Lys159)Nζ–Hζ1…O3γ(dCTP)	45.95%
	(Lys159)Nζ–Hζ3…O3γ(dCTP)	36.95%
	(Lys159)Nζ–Hζ2…O3γ(dCTP)	14.55%

Major Groove Type I (Cont’d)	(Lys159)Nζ–Hζ1…O2γ(dCTP)	13.75%
	(Lys159)Nζ–Hζ3…O2γ(dCTP)	9.10%
	(Lys159)Nζ–Hζ2…O2γ(dCTP)	4.50%
	(Arg51)Nη2–Hη22…O3β(dATP)	72.95%
	(Arg51)Nη1–Hη12…O2γ(dATP)	70.05%
	(Arg51)Nη1–Hη12…O3β(dATP)	56.35%
	(Arg51)Nη2–Hη22…O1β(dATP)	53.30%
	(Arg51)Nη2–Hη22…O2γ(dATP)	15.50%
	(Arg51)Nη1–Hη12…O3γ(dATP)	13.45%
	(Thr45)Oγ1–Hγ1…O3′(dATP)	86.30%
	(Thr45)Oγ1–Hγ1…O1β(dATP)	7.25%
	(Tyr10)N–H…O2γ(dATP)	98.65%
	(Tyr10)N–H…O3β(dATP)	38.65%
	(Tyr10)N–H…O1γ(dATP)	27.50%
	(Tyr48)Oη–Hη…O2γ(dATP)	97.50%
	(Tyr48)Oη–Hη…O3γ(dATP)	8.10%
	(Lys159)Nζ–Hζ2…O3γ(dATP)	46.60%
	(Lys159)Nζ–Hζ1…O3γ(dATP)	27.55%
	(Lys159)Nζ–Hζ3…O3γ(dATP)	19.90%
	(Lys159)Nζ–Hζ1…O1γ(dATP)	7.30%
	(Lys159)Nζ–Hζ2…O1γ(dATP)	6.90%
	(Lys159)Nζ–Hζ3…O1γ(dATP)	1.40%
	(Arg51)Nη2–Hη22…O3β(*syn*-dATP)	99.90%
	(Arg51)Nη1–Hη12…O2γ(*syn*-dATP)	99.50%
	(Arg51)Nη2–Hη22…O2γ(*syn*-dATP)	48.05%
	(Arg51)Nη1–Hη12…O3γ(*syn*-dATP)	21.00%
	(Arg51)Nη2–Hη22…O1β(*syn*-dATP)	11.65%
	(Arg51)Nη1–Hη12…O3β(*syn*-dATP)	8.30%
	(Arg51)Nη2–Hη22…O3γ(*syn*-dATP)	6.80%
	(Thr45)Oγ1–Hγ1…O1β(*syn*-dATP)	98.25%
	(Thr45)Oγ1–Hγ1…O3′(*syn*-dATP)	13.35%
	(Tyr10)N–H…O2γ(*syn*-dATP)	100%
	(Tyr10)N–H…O3β(*syn*-dATP)	34.70%
	(Tyr12)N–H…O3′(*syn*-dATP)	19.45%
	(Lys159)Nζ–Hζ1…O1γ(*syn*-dATP)	34.95%
	(Lys159)Nζ–Hζ1…O3γ(*syn*-dATP)	26.95%
	(Lys159)Nζ–Hζ3…O1γ(*syn*-dATP)	20.55%
	(Lys159)Nζ–Hζ3…O3γ(*syn*-dATP)	16.50%
	(Lys159)Nζ–Hζ2…O1γ(*syn*-dATP)	15.00%
	(Lys159)Nζ–Hζ2…O3γ(*syn*-dATP)	14.00%
	(Arg51)Nη2–Hη22…O3β(dGTP)	100%
	(Arg51)Nη1–Hη12…O2γ(dGTP)	97.60%
	(Arg51)Nη2–Hη22…O2γ(dGTP)	32.70%
	(Arg51)Nη1–Hη12…O3β(dGTP)	27.95%
	(Arg51)Nη2–Hη22…O1β(dGTP)	25.90%
	(Arg51)Nη1–Hη12…O3γ(dGTP)	18.40%
	(Thr45)Oγ1–Hγ1…O1β(dGTP)	99.95%
	(Tyr10)N–H…O2γ(dGTP)	79.10%
	(Tyr10)N–H…O3β(dGTP)	42.25%
	(Phe11)N–H…O2β(dGTP)	98.95%
	(Tyr12)N–H…O3′(dGTP)	81.25%
	(Tyr48)Oη–Hη…O2γ(dGTP)	33.00%
	(Lys159)Nζ–Hζ3…O3γ(dGTP)	43.20%
	(Lys159)Nζ–Hζ2…O3γ(dGTP)	40.15%

Major Groove Type I (Cont'd)	(Lys159)Nζ–Hζ1…O3γ(dGTP)	15.05%
	(Lys159)Nζ–Hζ2…O2γ(dGTP)	14.45%
	(Lys159)Nζ–Hζ3…O2γ(dGTP)	11.60%
	(Lys159)Nζ–Hζ1…O2γ(dGTP)	4.60%
	(Arg51)Nη2–Hη22…O3β(*syn*-dGTP)	99.95%
	(Arg51)Nη1–Hη12…O3γ(*syn*-dGTP)	99.10%
	(Arg51)Nη1–Hη12…O2γ(*syn*-dGTP)	33.65%
	(Arg51)Nη2–Hη22…O3γ(*syn*-dGTP)	19.65%
	(Arg51)Nη1–Hη12…O3β(*syn*-dGTP)	12.15%
	(Arg51)Nη2–Hη22…O1β(*syn*-dGTP)	11.55%
	(Thr45)Oγ1–Hγ1…O1β(*syn*-dGTP)	100%
	(Tyr10)N–H…O2γ(*syn*-dGTP)	99.95%
	(Tyr10)N–H…O3β(*syn*-dGTP)	43.90%
	(Phe11)N–H…O2β(*syn*-dGTP)	85.00%
	(Phe11)N–H…O1β(*syn*-dGTP)	6.40%
	(Tyr12)N–H…O3′(*syn*-dGTP)	51.10%
	(Tyr48)Oη–Hη…O2γ(*syn*-dGTP)	100%
	(Lys159)Nζ–Hζ1…O3γ(*syn*-dGTP)	41.90%
	(Lys159)Nζ–Hζ3…O3γ(*syn*-dGTP)	40.70%
	(Lys159)Nζ–Hζ2…O3γ(*syn*-dGTP)	16.80%
	(Lys159)Nζ–Hζ3…O2γ(*syn*-dGTP)	3.90%
	(Lys159)Nζ–Hζ1…O2γ(*syn*-dGTP)	3.80%
	(Lys159)Nζ–Hζ2…O2γ(*syn*-dGTP)	1.15%
–1 Deletion	(Tyr10)N–H…O1γ(dGTP)	47.45%
	(Tyr10)N–H…O2γ(dGTP)	19.40%
	(Phe11)N–H…O3γ(dGTP)	12.50%
	(Phe11)N–H…O2γ(dGTP)	9.80%

[a] Hydrogen bonds are specified in the format (A)B–C…D(E), where A is the residue name of the donor atom, B is the name of the donor atom, C is the name of the hydrogen atom, D is the name of the acceptor atom, and E is the residue name of the acceptor atom. ***** denotes 1*S* (–)-B[c]Ph-dA modification.
[b] Criterion for hydrogen bond occupancy is: heavy-to-heavy distance ≤ 3.4 Å and bond angle ≤ 135°.

Table S3. Hydrogen bonding interactions of >10% occupancy between the adducted adenine and neighboring bases or protein residues other than the incoming dNTP.

Model	**dNTP**	**Hydrogen Bond** [a]	**Distance (Å)** [b]	**Angle (°)** [b]	**Occupancy** [c]
Intercalation	dTTP	(tA$_3$)N6–H61…O4Z(tA*$_5$)	3.08 ± 0.16	160.5 ± 10.3	71.59%
		(tA*$_5$)O2Z–HO2Z…O4(pT$_{13}$)	2.86 ± 0.18	158.0 ± 8.4	63.48%
		(tC$_4$)N4–H42…O3Z(tA*$_5$)	3.06 ± 0.17	150.2 ± 10.1	35.22%
		(tA$_3$)N6–H61…O3Z(tA*$_5$)	3.07 ± 0.18	150.0 ± 10.6	16.66%
	dCTP	(tA*$_5$)O4Z–HO4Z…O(Gly58)	2.81 ± 0.17	166.6 ± 9.1	56.10%
		(tA*$_5$)O2Z–HO2Z…O4(pT$_{13}$)	2.91 ± 0.19	154.9 ± 8.5	52.20%
		(tA*$_5$)O3Z–HO3Z…N3(tC$_4$)	2.94 ± 0.18	165.1 ± 8.3	49.35%
		(tA$_3$)N6–H61…O3Z(tA*$_5$)	3.06 ± 0.17	155.8 ± 12.7	42.50%
		(tA$_6$)N6–H61…O2Z(tA*$_5$)	3.00 ± 0.16	151.1 ± 9.9	33.75%
		(tA*$_5$)N6–H6…O(Gly58)	3.18 ± 0.15	164.7 ± 7.8	29.65%
		(tA$_3$)N6–H61…O4Z(tA*$_5$)	3.12 ± 0.16	158.2 ± 10.0	27.45%
		(tA*$_5$)O4Z–HO4Z…N1(tA$_3$)	2.95 ± 0.17	161.5 ± 11.3	25.70%
		(tA*$_5$)O3Z–HO3Z…N1(tA$_3$)	2.90 ± 0.16	162.8 ± 10.8	20.75%
		(tC$_4$)N4–H41…O3Z(tA*$_5$)	3.16 ± 0.18	155.3 ± 10.9	12.85%
	dATP	(tA*$_5$)O2Z–HO2Z…O4(pT$_{13}$)	2.82 ± 0.16	153.6 ± 8.2	78.35%
		(tA$_3$)N6–H61…O4Z(tA*$_5$)	3.03 ± 0.16	162.9 ± 10.2	73.75%
		(tA$_6$)N6–H61…O2Z(tA*$_5$)	2.96 ± 0.14	150.5 ± 9.7	61.65%
		(tA*$_5$)O4Z–HO4Z…N1(tA$_3$)	2.86 ± 0.14	165.8 ± 8.6	24.25%
		(tA$_3$)N6–H61…O3Z(tA*$_5$)	3.11 ± 0.16	152.4 ± 11.4	14.60%
		(tA*$_5$)O2Z–HO2Z…N1(tA$_6$)	2.91 ± 0.21	165.9 ± 9.7	12.75%
		(tC$_4$)N4–H42…O3Z(tA*$_5$)	3.03 ± 0.17	144.8 ± 7.6	7.60%
		(tC$_4$)N4–H41…O3Z(tA*$_5$)	2.99 ± 0.16	154.2 ± 11.8	5.85%
	syn-dATP	(tA*$_5$)O2Z–HO2Z…O4(pT$_{13}$)	2.81 ± 0.15	158.4 ± 8.1	95.75%
		(tA$_3$)N6–H61…O4Z(tA*$_5$)	3.02 ± 0.16	158.1 ± 10. 7	74.95%
		(tA$_6$)N6–H61…O2Z(tA*$_5$)	2.92 ± 0.14	159.3 ± 9.9	66.75%
		(tC$_4$)N4–H42…O3Z(tA*$_5$)	3.02 ± 0.16	149.2 ± 9.4	29.25%
	dGTP	(tA*$_5$)O2Z–HO2Z…O4(pT$_{13}$)	2.81 ± 0.17	158.5 ± 8.1	76.00%
		(tA$_6$)N6–H61…O2Z(tA*$_5$)	2.95 ± 0.15	155.1 ± 10.3	57.20%
		(tC$_4$)N4–H41…O3Z(tA*$_5$)	2.99 ± 0.16	156.7 ± 10.9	18.45%
	syn-dGTP	(tA*$_5$)O2Z–HO2Z…O4(pT$_{13}$)	2.93 ± 0.20	157.8 ± 9.6	55.25%
		(tC$_4$)N4–H42…O3Z(tA*$_5$)	3.01 ± 0.17	154.4 ± 10.6	34.60%
		(tC$_4$)N4–H41…O3Z(tA*$_5$)	3.00 ± 0.16	159.1 ± 11.8	20.60%
		(tA$_6$)N6–H62…N7(tA*$_5$)	3.18 ± 0.13	155.1 ± 10.3	17.40%
		(tA$_3$)N6–H61…O4Z(tA*$_5$)	3.11 ± 0.17	162.8 ± 10.3	14.00%
Major Groove Type I	dTTP	(tA*$_5$)O3Z–HO3Z…O(Val43)	2.66 ± 0.10	169.4 ± 6.2	99.85%
		(Gly58)N–H…O3Z(tA*$_5$)	2.90 ± 0.12	164.8 ± 8.8	96.00%
	dCTP	(tA*$_5$)O3Z–HO3Z…O(Val43)	2.66 ± 0.10	169.4 ± 6.0	92.55%
		(Gly58)N–H…O3Z(tA*$_5$)	2.95 ± 0.15	157.9 ± 10.4	85.70%
	dATP	(tA*$_5$)O3Z–HO3Z…O(Ala57)	2.77 ± 0.16	167.7 ± 7.9	67.30%
		(tA*$_5$)O3Z–HO3Z…O(Val43)	2.84 ± 0.19	165.5 ± 10.2	31.45%
	syn-dATP	(tA*$_5$)O3Z–HO3Z…O(Val43)	2.67 ± 0.10	169.6 ± 5.9	100%
		(Gly58)N–H…O3Z(tA*$_5$)	2.92 ± 0.12	164.6 ± 8.1	98.95%
	dGTP	(tA*$_5$)O3Z–HO3Z…O(Val43)	2.69 ± 0.11	168.8 ± 6.9	99.40%
		(Gly58)N–H…O3Z(tA*$_5$)	2.90 ± 0.12	163.3 ± 8.3	97.70%
		(tA*$_5$)O2Z–HO2Z…O(Gly58)	3.02 ± 0.20	152.0 ± 9.5	12.15%
	syn-dGTP	(tA*$_5$)O3Z–HO3Z…O(Val43)	2.68 ± 0.11	169.5 ± 6.3	99.85%
		(Gly58)N–H…O3Z(tA*$_5$)	2.93 ± 0.13	161.3 ± 10.4	84.00%
–1 Deletion	dGTP	(tC$_4$)N4–H42…O3Z(tA*$_5$)	3.00 ± 0.15	163.8 ± 7.9	79.35%
		(tA*$_5$)O2Z–HO2Z…N7(tA$_3$)	3.12 ± 0.16	151.6 ± 8.3	31.70%

[a–c] See footnotes of Table 1.

Figure Legends

Figure S1. RMSDs for the Dpo4 ternary complexes over the 1 ns MD simulations. **(A)** RMSDs for the unmodified control with incoming dTTP and 1*S* (–)-B[*c*]Ph-dA intercalation models with varying incoming dNTPs. Color code: control, black; dTTP, green; dCTP, orange; dATP, red; *syn*-dATP, cyan; dGTP, blue; *syn*-dGTP, magenta. **(B)** RMSDs for the major groove Type I models with varying dNTPs and –1 deletion model with incoming dGTP. Color code: same as in **(A)** except that *black* represents the –1 deletion case.

Figure S2. Time dependence of the linkage site torsional angles α′, β′ and χ over 1 ns time frame for unmodified control and 1*S* (–)-B[*c*]Ph-dA intercalation structures in the Dpo4 DNA polymerase. See Figure 1 for definition of the torsion angles. Color code: same as in Figure S1A.

Figure S3. Time dependence of the linkage site torsional angles α′, β′ and χ over 1 ns time frame for 1*S* (–)-B[*c*]Ph-dA major groove Type I structures and –1 deletion model in the Dpo4 DNA polymerase. See Figure 1 for definition of the torsion angles. Color code: same as in Figure S1B.

Figure S4. Time dependence of distances and angles of significantly occupied hydrogen bonds (> 50% occupancy) between the templating residue and incoming dNTP in unmodified control and 1*S* (–)-B[c]Ph-dA intercalation structures in the Dpo4 DNA polymerase. Refer to Table 1 for complete specifications of these hydrogen bonds. Color code: the same as in Figure S1A.

Figure S5. Stacking interactions in the unmodified control and in the 1*S* (–)-B[*c*]Ph-dA intercalation structures of the Dpo4 ternary complexes after 1 ns of MD. **(A)–(G)** are the same as in Figure 2. Color code: unmodified or modified adenine, green; incoming dNTP, purple; B[*c*]Ph, red; tA_6, magenta; pT_{13}, cyan. The view is along the DNA helix axis from 5′ to 3′ end of the template strand. All stereo images are constructed for viewing with a stereoviewer.

Figure S6. Time dependence of the distances between C1′s of the nascent base pair and distances between Pα of dNTP and O3′ of the primer terminus, in the unmodified control and 1*S* (–)-B[c]Ph-dA intercalation structures in the Dpo4 DNA polymerase. Color code: the same as in Figure S1A.

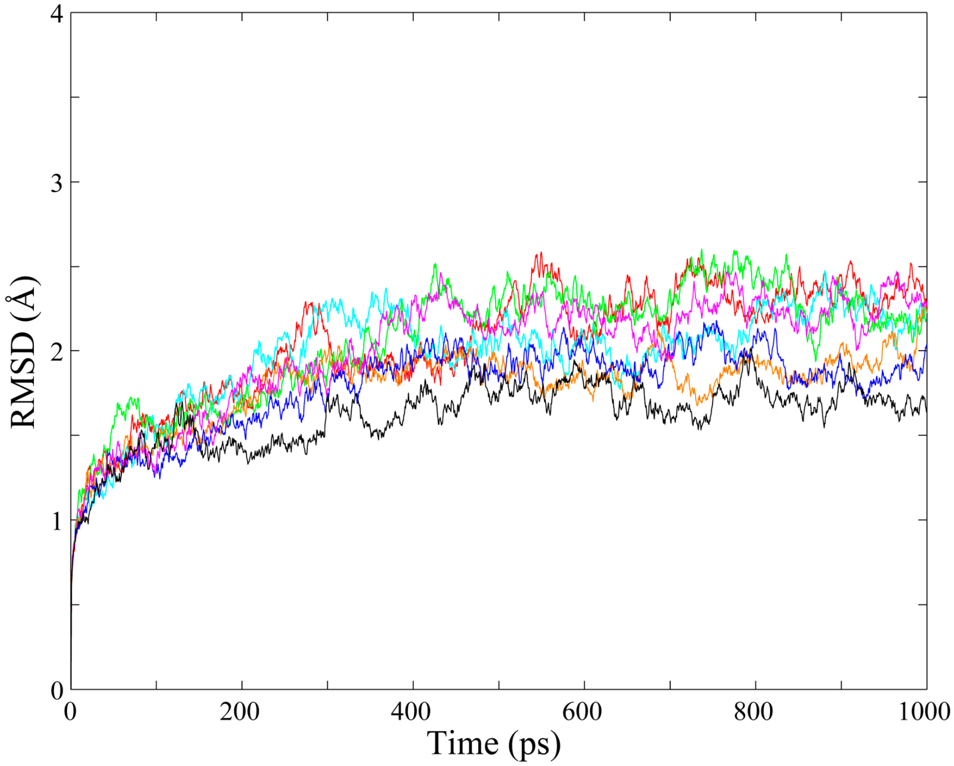
Figure S7. Time dependence of the distances between C1′s of the nascent base pair and distances between Pα of dNTP and O3′ of the primer terminus, in the 1*S* (–)-B[*c*]Ph-dA major groove and –1 deletion models of the Dpo4 ternary complexes. Color code: the same as in Figure S1B.

Figure S8. Time dependence of distances and angles of significantly occupied hydrogen bonds (> 50% occupancy) between the templating residue and incoming dNTP in the 1*S* (–)-B[*c*]Ph-dA major groove and –1 deletion models of the Dpo4 ternary complexes. Refer to Table 1 for complete specifications of these hydrogen bonds. Color code: the same as in Figure S1B.

Figure S9. Stacking interactions in the unmodified control and in the 1*S* (–)-B[*c*]Ph-dA major groove and –1 deletion models of the Dpo4 ternary complexes after 1 ns of MD. **(A)–(G)** are the same as in Figure 5. Color code: the same as in Figure S5 except that tC_4 is shown in orange in **(G)**. All stereo images are constructed for viewing with a stereoviewer.

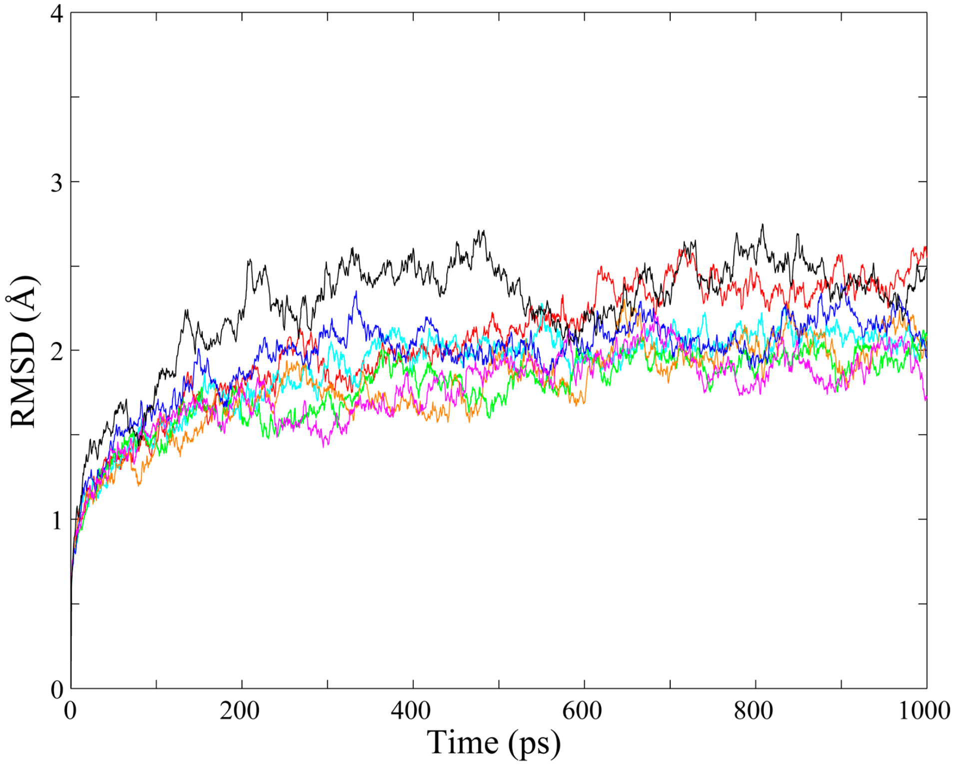
Figure S1

(A)



RMSD (Å)
Time (ps)
0
1
2
3
4
0
200
400
600
800
1000

(B)



RMSD (Å)
Time (ps)
0
1
2
3
4
0
200
400
600
800
1000

Figure S2

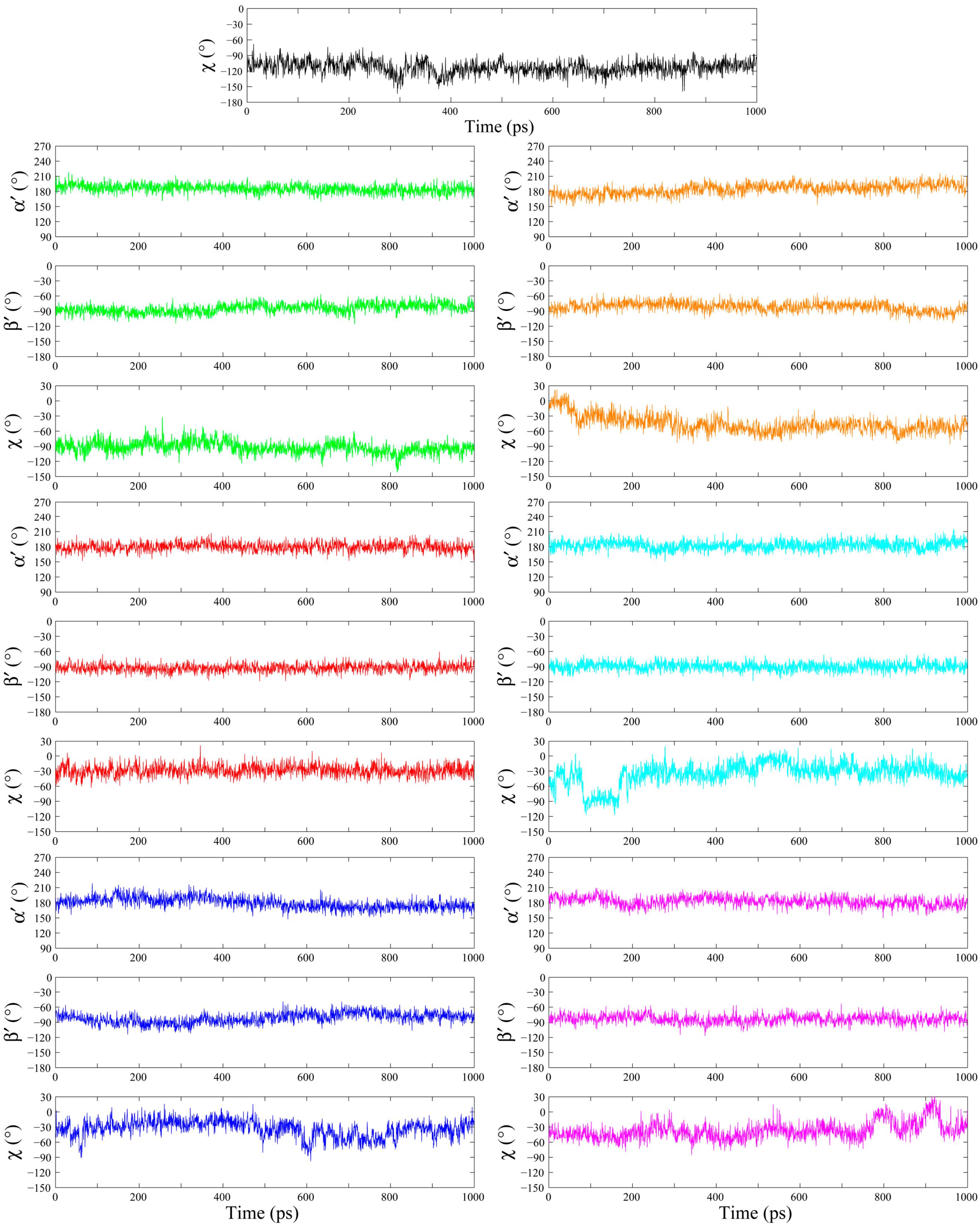


Figure S3

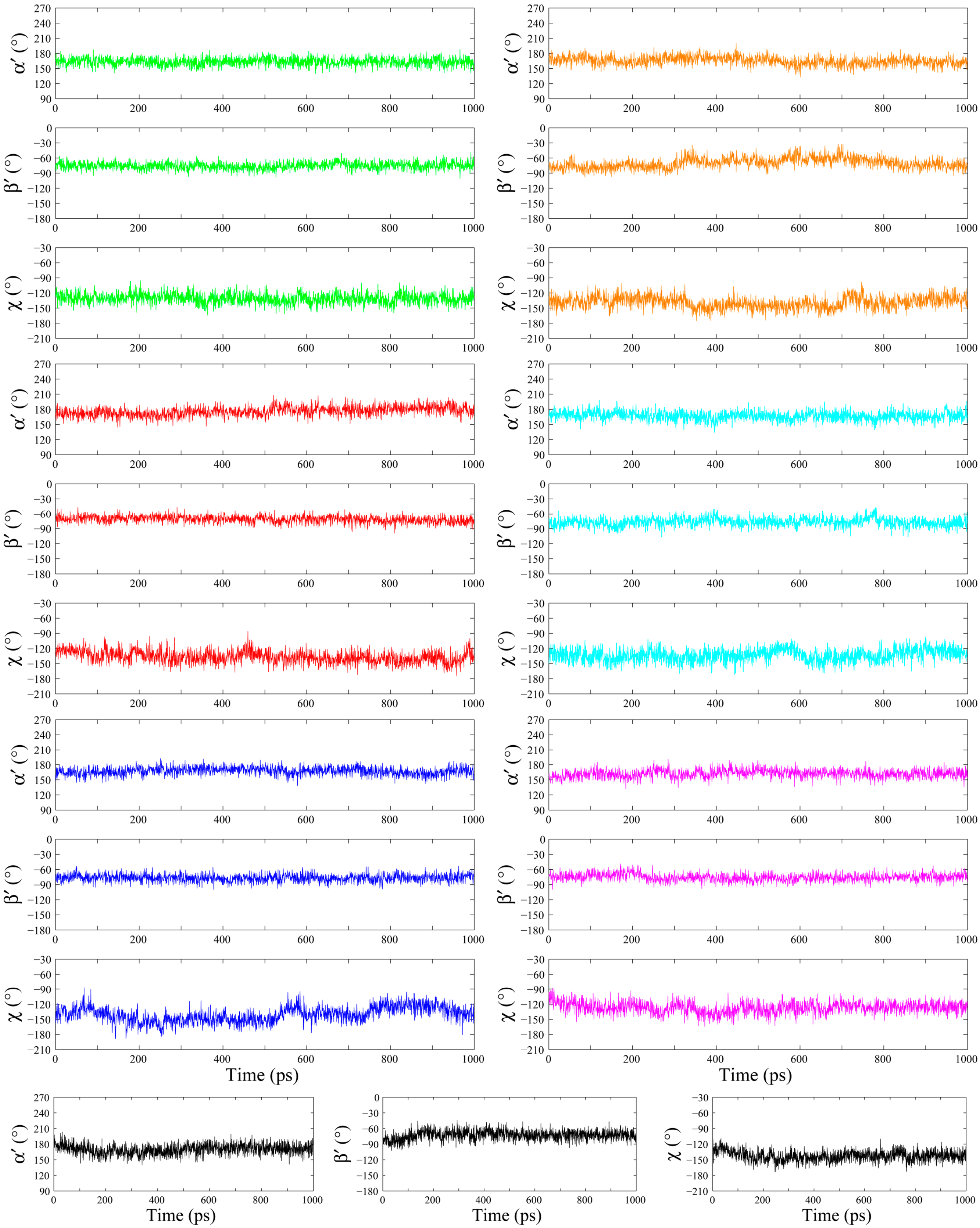


Figure S4

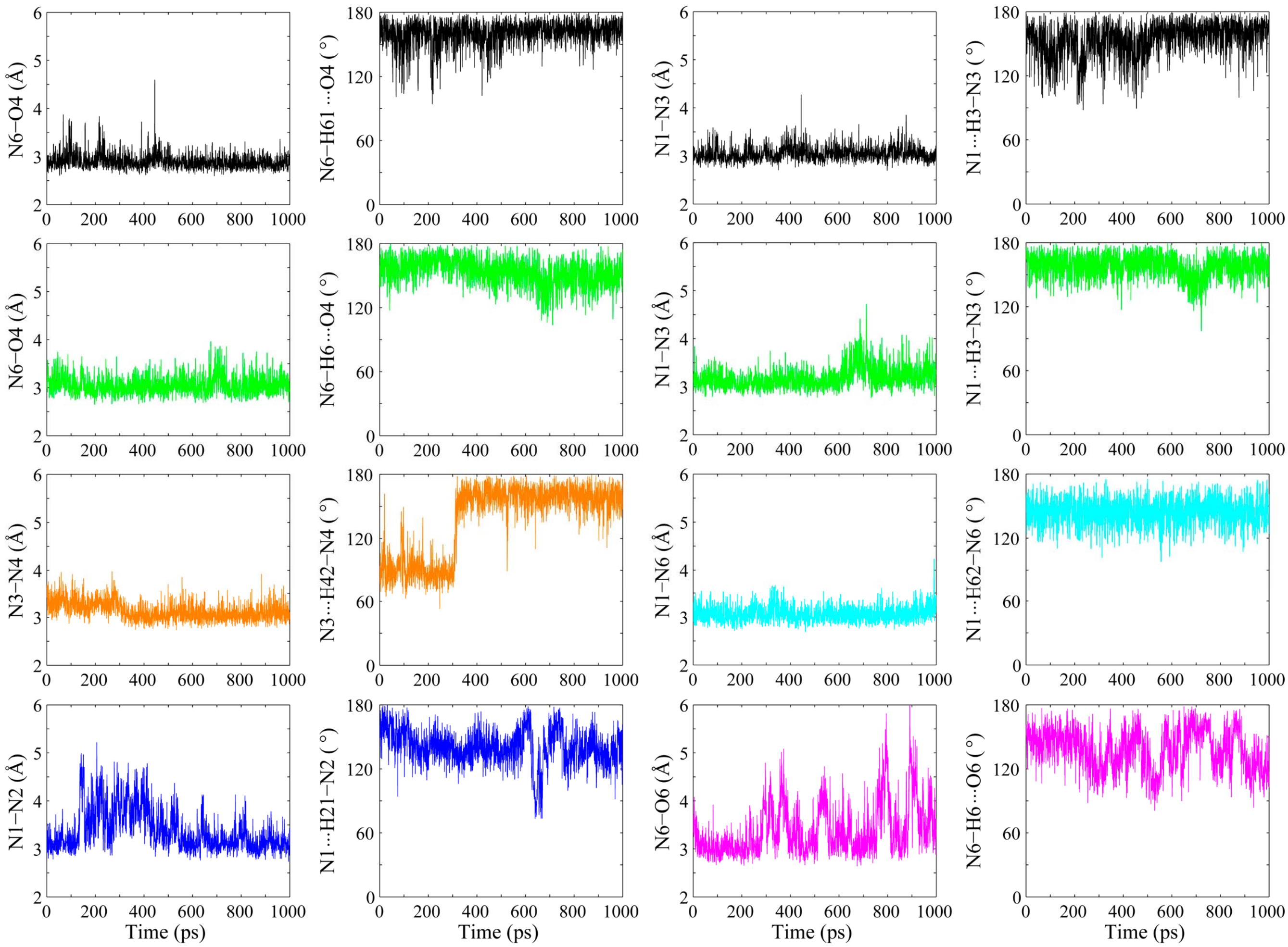
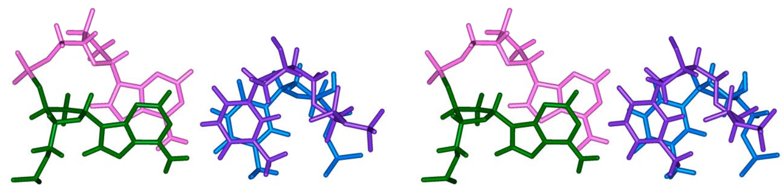
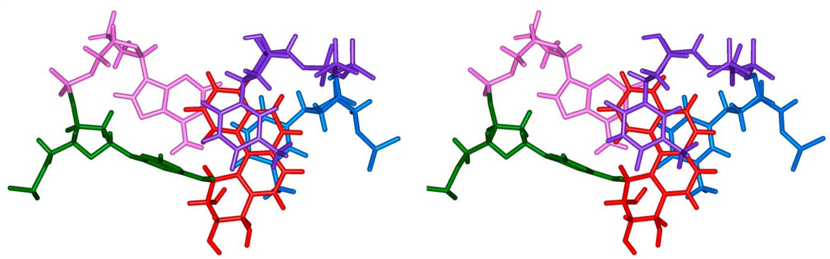

N6−O4 (Å)
N6−H61···O4 (°)
N1−N3 (Å)
N1···H3−N3 (°)
N6−O4 (Å)
N6−H6···O4 (°)
N1−N3 (Å)
N1···H3−N3 (°)
N3−N4 (Å)
N3···H42−N4 (°)
N1−N6 (Å)
N1···H62−N6 (°)
N1−N2 (Å)
N1···H21−N2 (°)
N6−O6 (Å)
N6−H6···O6 (°)
Time (ps)
Time (ps)
Time (ps)
Time (ps)

Figure S5

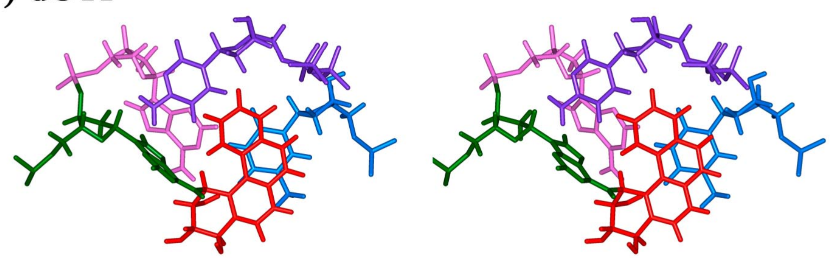
(A) Control



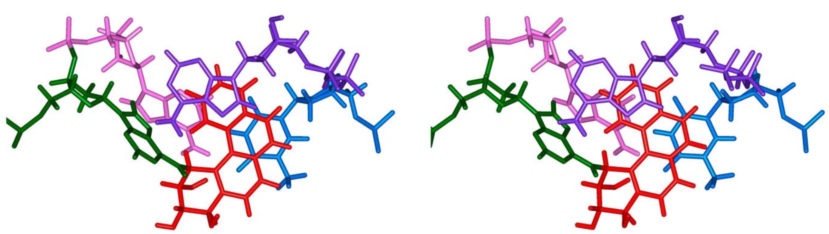
(B) dTTP



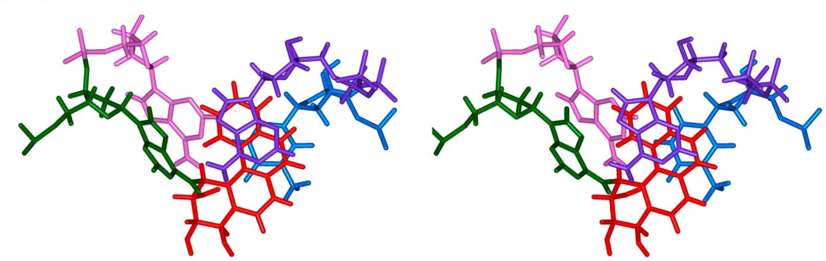
(D) dCTP



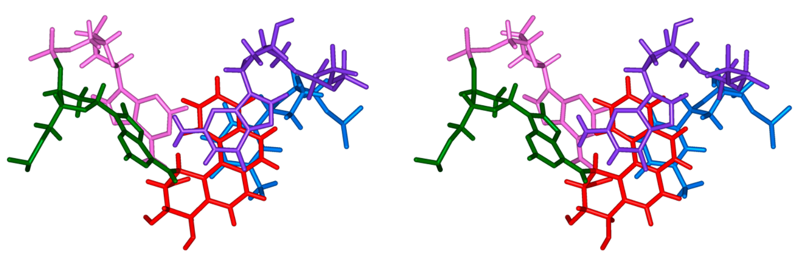
(D) dATP



(E) *syn*-dATP



(F) dGTP



(G) *syn*-dGTP

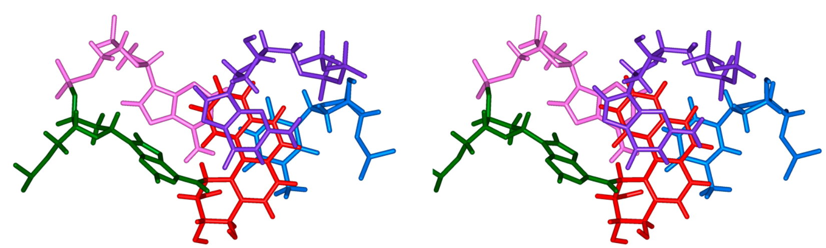


Figure S6

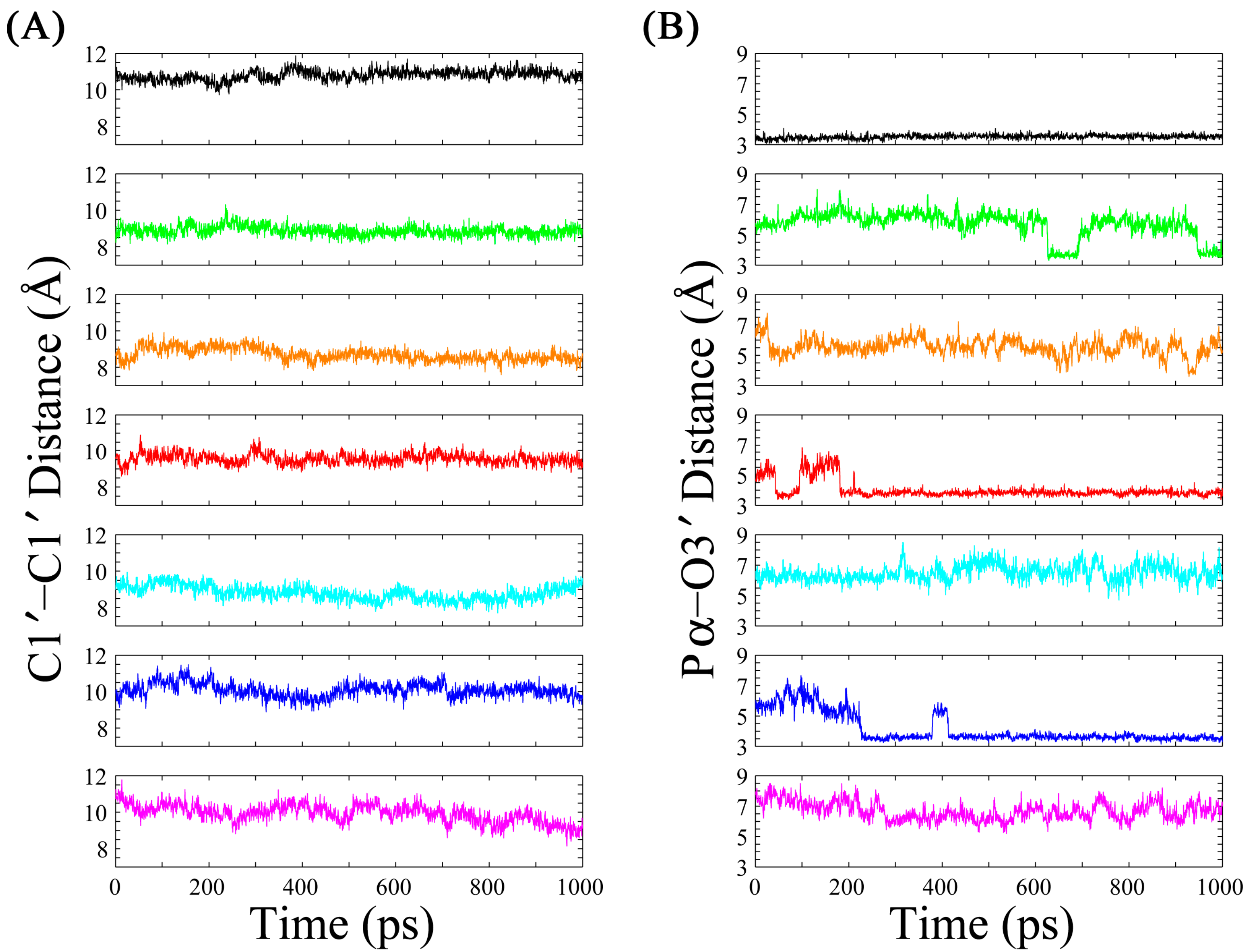

(A)
(B)
C1′–C1′ Distance (Å)
Pα–O3′ Distance (Å)
Time (ps)
Time (ps)
12
10
8
9
7
5
3
0
200
400
600
800
1000

Figure S7

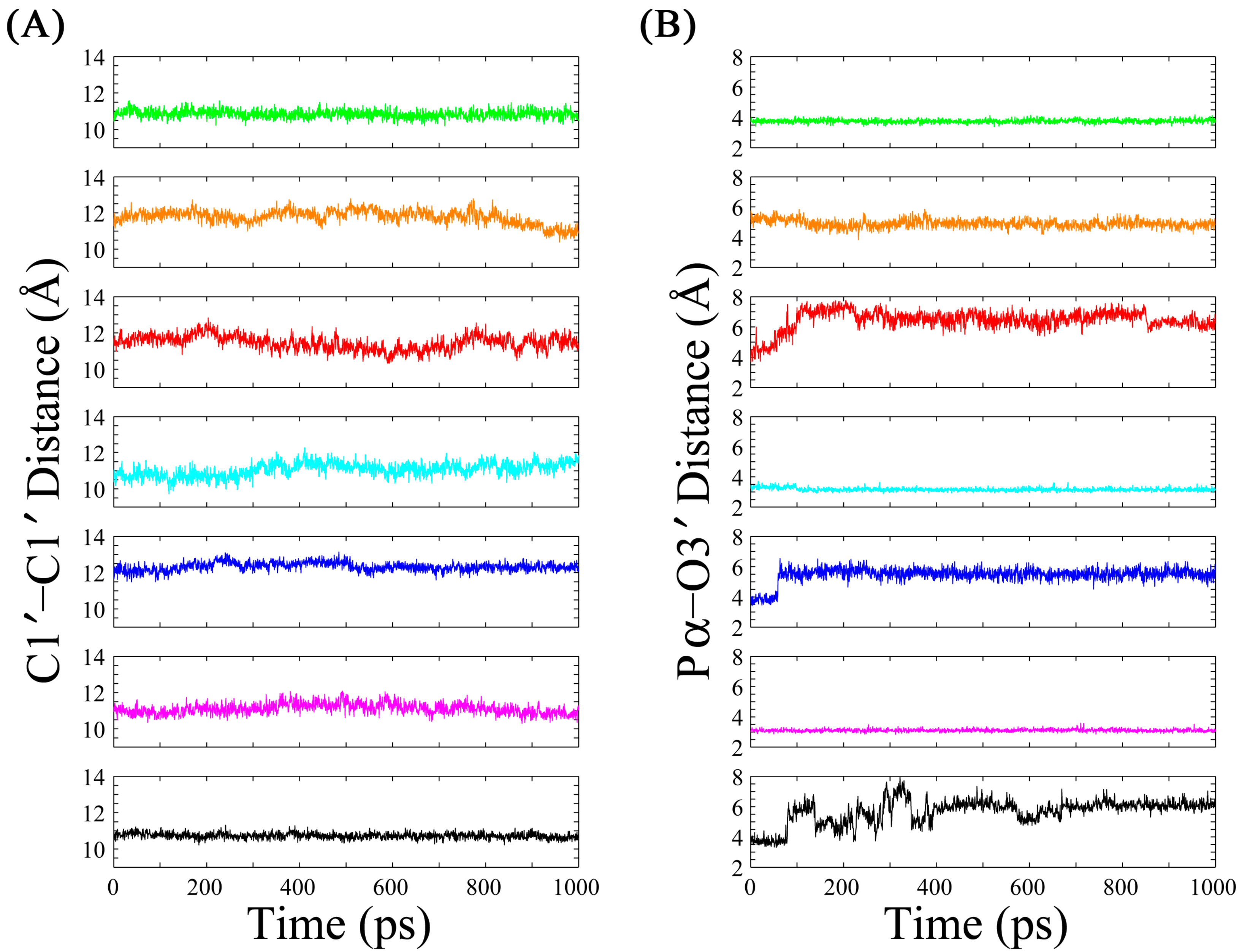

(A)
C1′–C1′ Distance (Å)
14
12
10
0
200
400
600
800
1000
Time (ps)
(B)
Pα–O3′ Distance (Å)
8
6
4
2
0
200
400
600
800
1000
Time (ps)

Figure S8

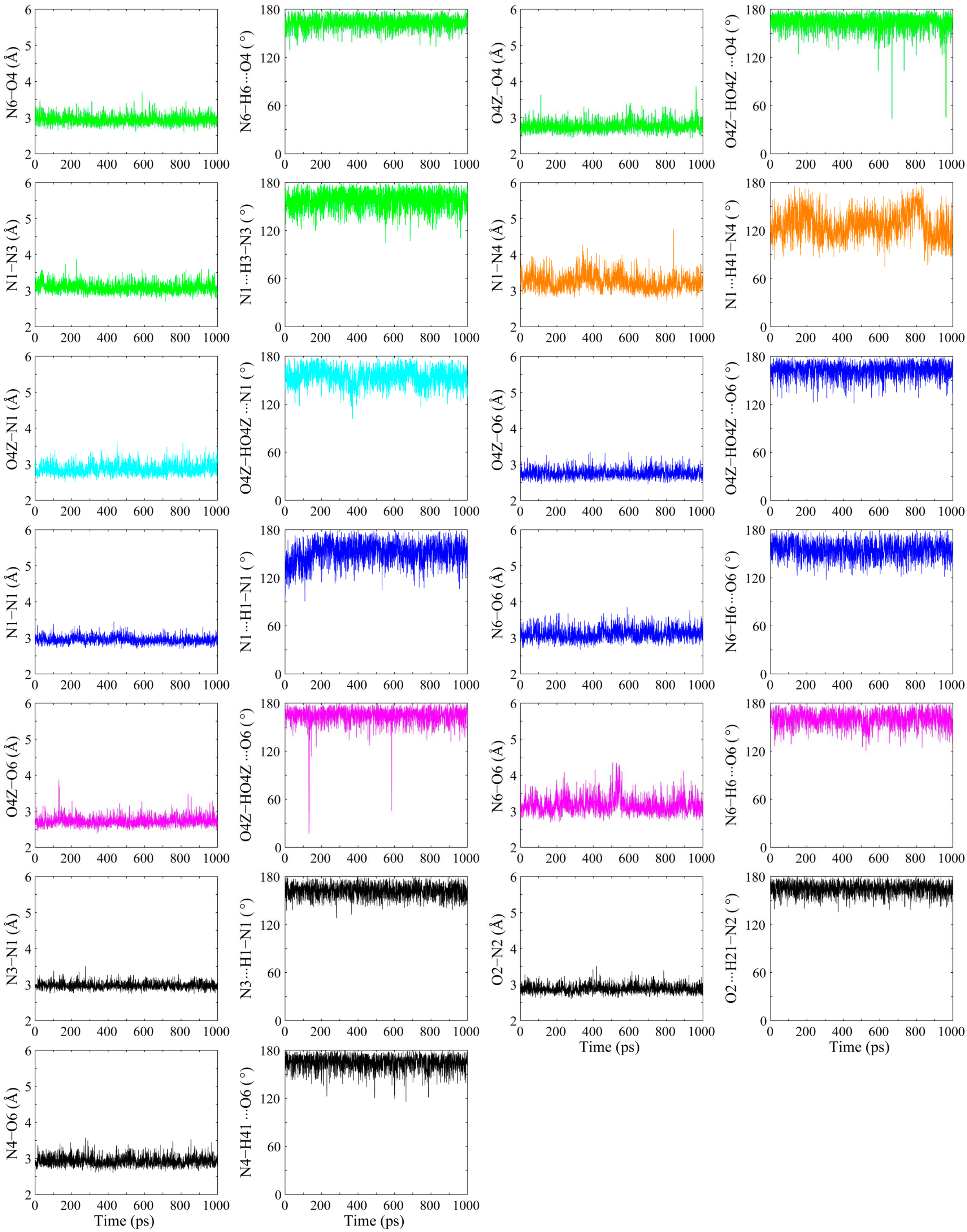
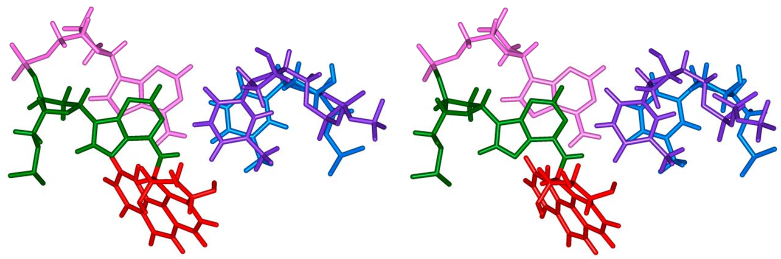
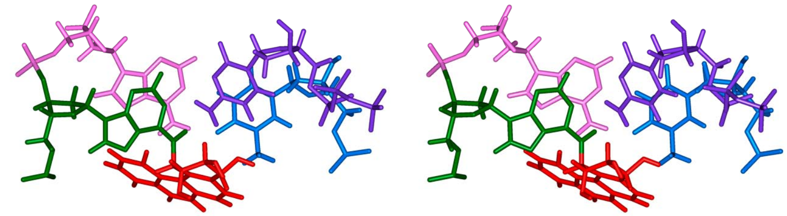

N6−O4 (Å)
N6−H6···O4 (°)
O4Z−O4 (Å)
O4Z−HO4Z ···O4 (°)
N1−N3 (Å)
N1···H3−N3 (°)
N1−N4 (Å)
N1···H41−N4 (°)
O4Z−N1 (Å)
O4Z−HO4Z ···N1 (°)
O4Z−O6 (Å)
O4Z−HO4Z ···O6 (°)
N1−N1 (Å)
N1···H1−N1 (°)
N6−O6 (Å)
N6−H6···O6 (°)
O4Z−O6 (Å)
O4Z−HO4Z ···O6 (°)
N6−O6 (Å)
N6−H6···O6 (°)
N3−N1 (Å)
N3···H1−N1 (°)
O2−N2 (Å)
O2···H21−N2 (°)
N4−O6 (Å)
N4−H41 ···O6 (°)
Time (ps)

Figure S9

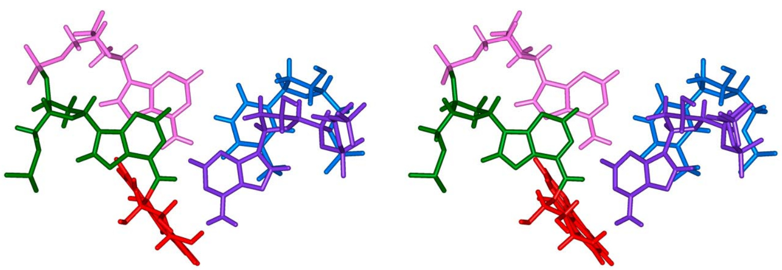
(A) dTTP



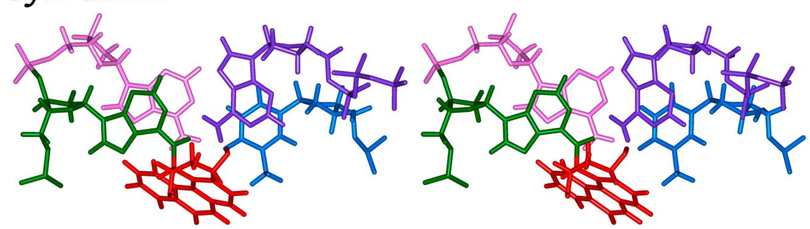
(B) dCTP



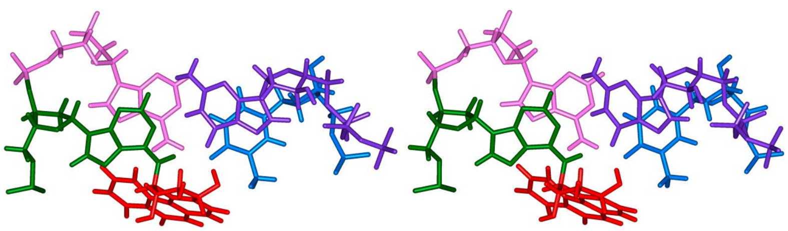
(C) dATP



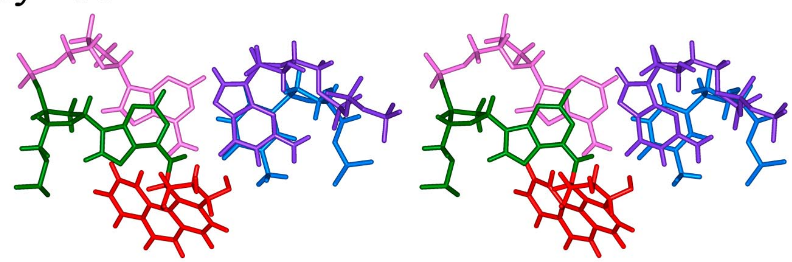
(D) *syn*-dATP



(E) dGTP



(F) *syn*-dGTP



(G) –1 Deletion