

SUPPORTING INFORMATION

Exploring non-covalent interactions in guanine- and xanthine-based model DNA quadruplex structures: A comprehensive quantum chemical approach

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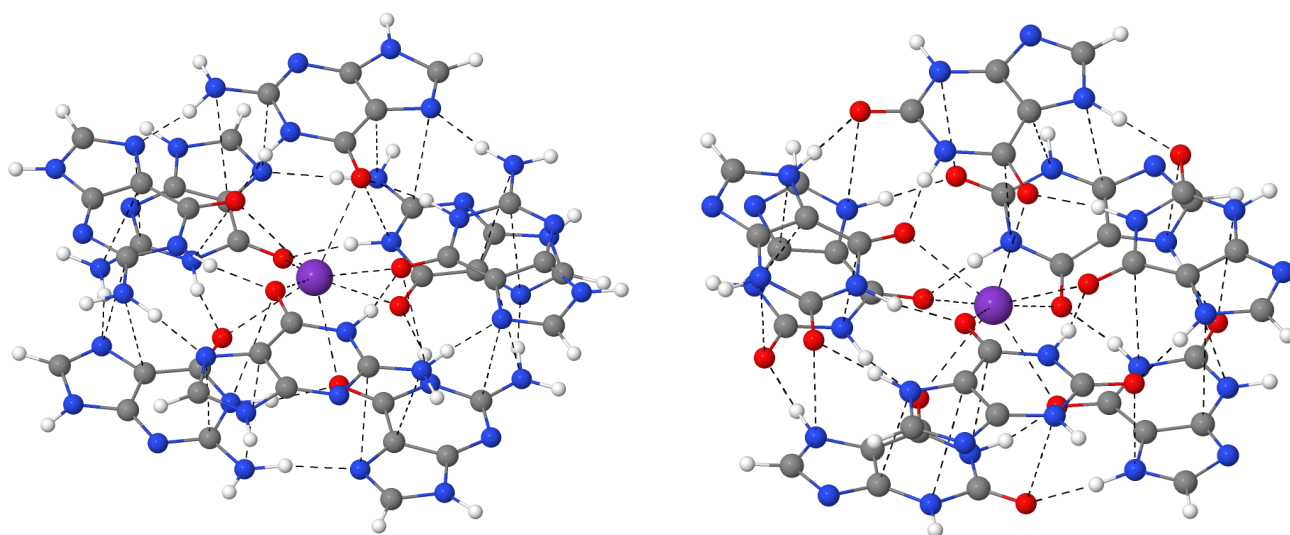


Figure S1. Optimized structures of guanine (left) and xanthine (right) (B4)₂ complexes with a K⁺ ion inside the central channel. Dotted lines designate non-covalent interactions (H-bonds, ion-base coordination, and van der Waals contacts) identified by the QTAIM approach. Wavefunctions for QTAIM analysis were calculated at the BLYP/def2-TZVPP level of theory in Gaussian 09 for TURBOMOLE geometries.

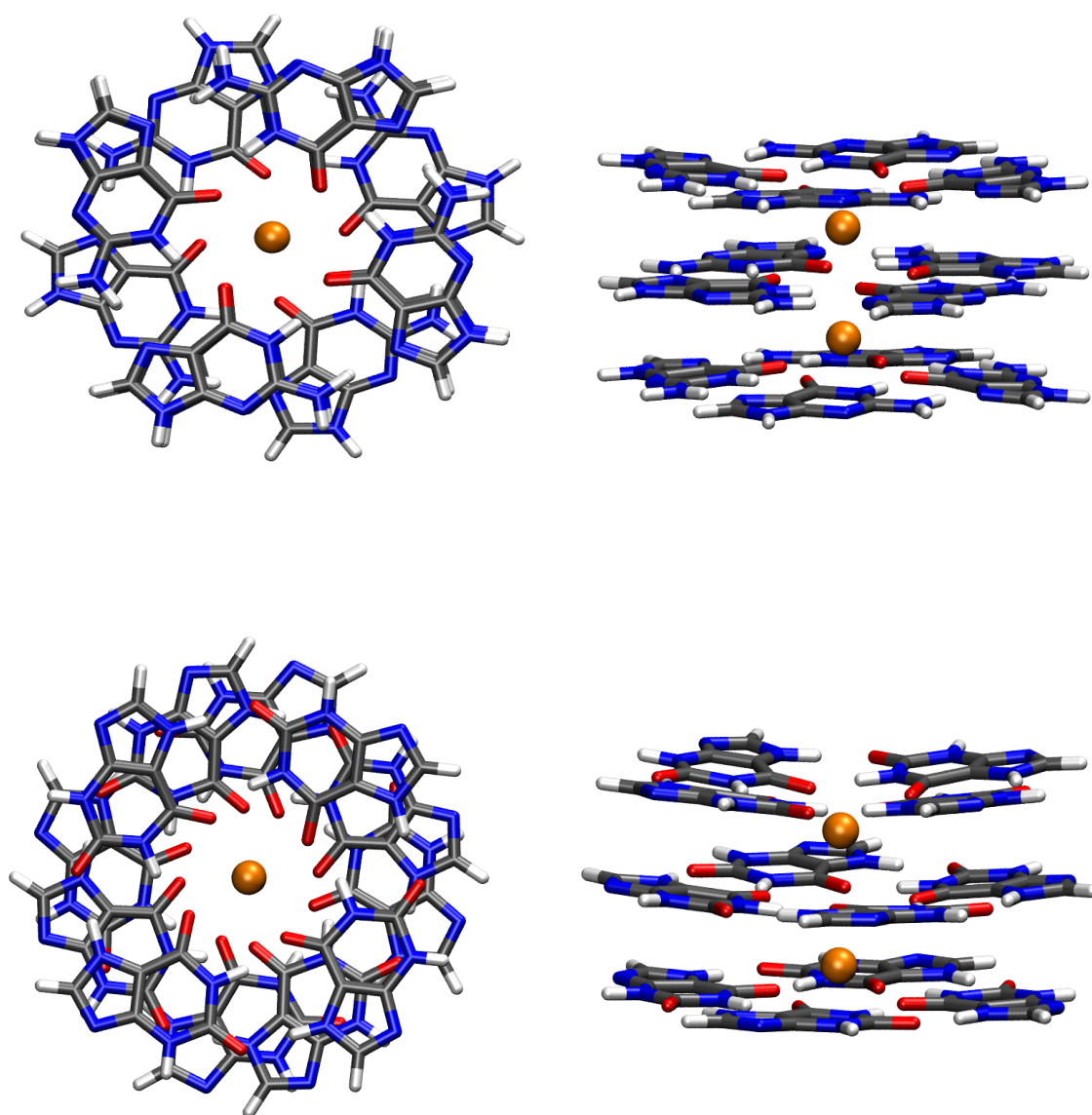


Figure S2. Optimized structures of Gua (upper) and Xan (lower) (B4)₃ complexes with two Na⁺ ions. The structures on the left display the view from the top, whereas complexes on the right show the lateral view.

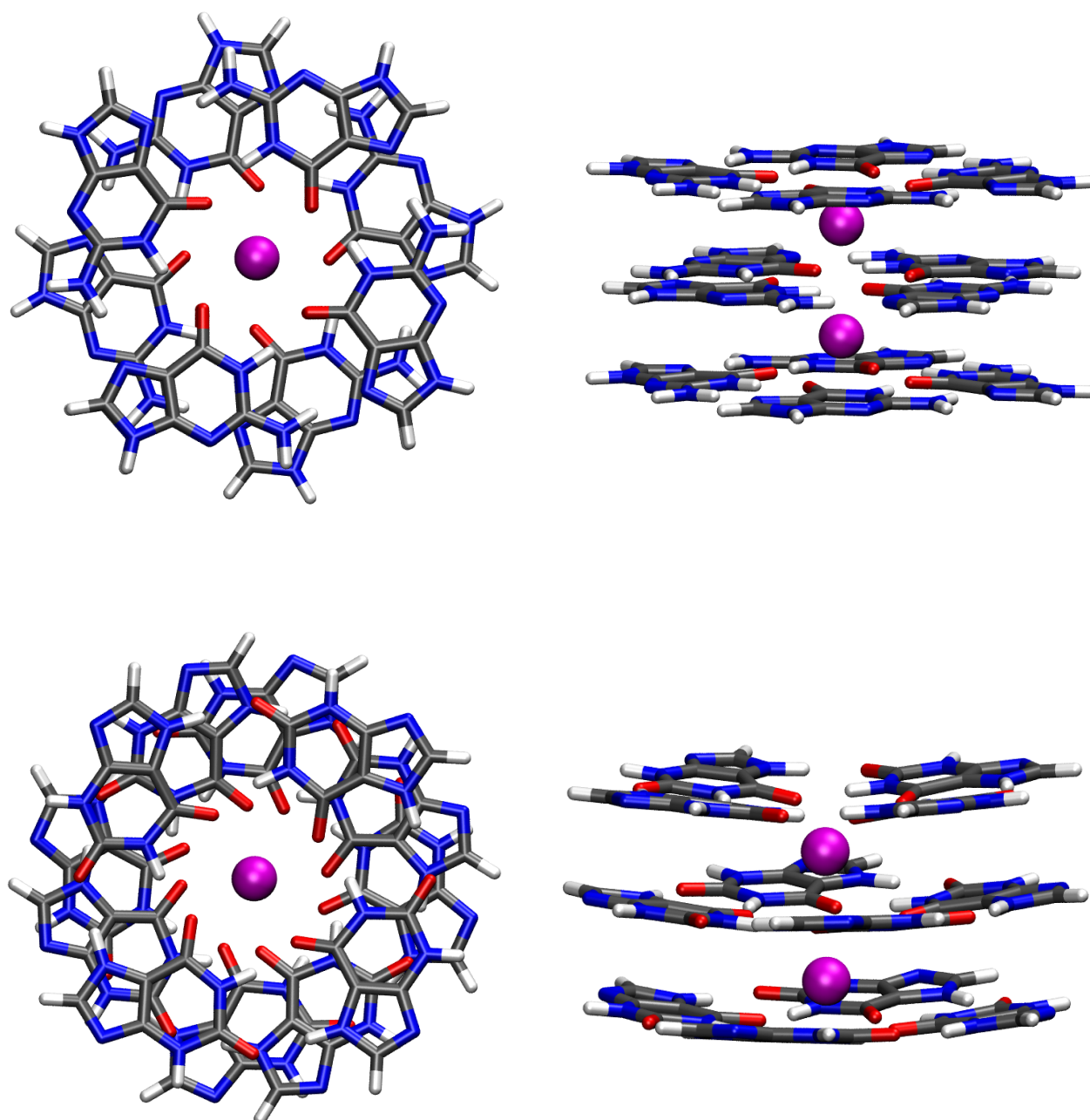


Figure S3. Optimized structures of Gua (upper) and Xan (lower) (B4)₃ complexes with two K⁺ ions. The structures on the left display the view from the top, whereas complexes on the right show the lateral view.

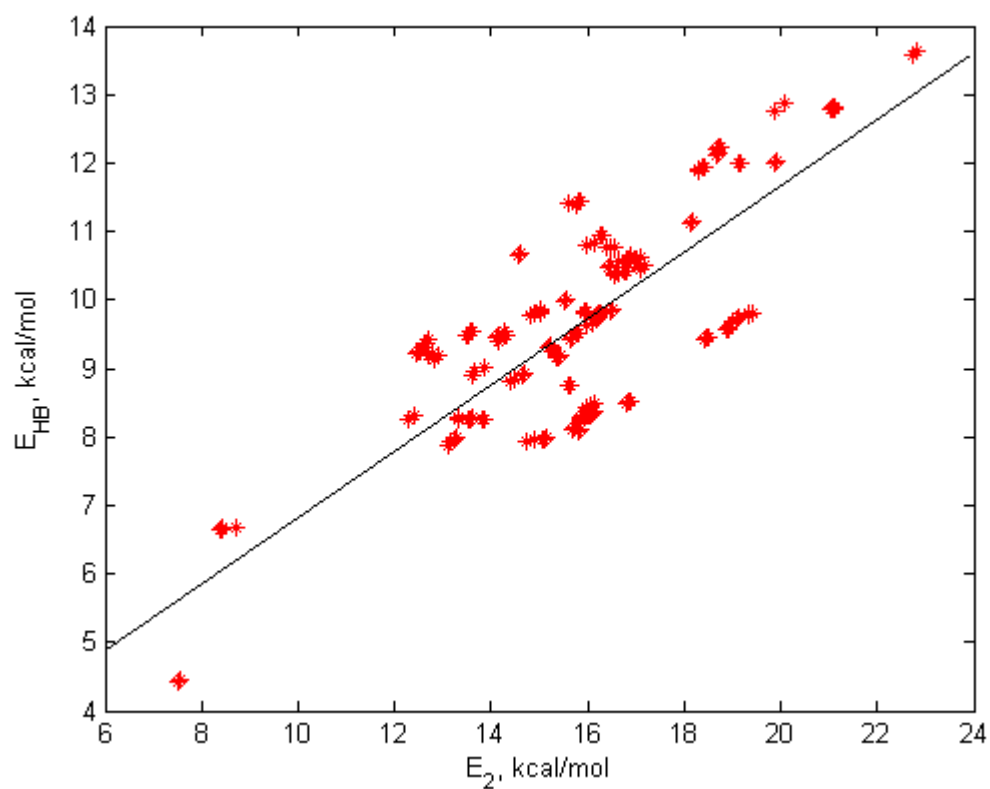


Figure S4. Correlation between the H-bond energy calculated by the EML formula and the donor-acceptor LP-BD* stabilization energy from NBO analysis (LP – lone pair(s) of the H-bond acceptor atom, BD* is the anti-bonding orbital of the H-bond donor group).

Table S1. Van der Waals volumes of Gua and Xan B4 and (B4)₂ DNA quadruplex models with/without Na⁺/K⁺. The geometries were optimized at the BLYP-D3/def2-TZVPP level of theory. Volumes were calculated by using the Vega ZZ program. Volume units are Å³.

Structure	Xan	Gua
B	115	117
B4	444	467
B4·Na ⁺	476	496
B4·K ⁺	514	530
(B4) ₂	886	930
(B4) ₂ ·Na ⁺	919	934
(B4) ₂ ·K ⁺	928	956

Table S2. Formation energies ΔE_{form} (in kcal/mol) of model quadruplex structures obtained at the BLYP-D3/def2-TZVPP level of theory using the COSMO model of water in TURBOMOLE. ΔE_{form} was calculated as the difference between the electronic energy of the whole optimized complex and its components (formula (1) in the manuscript).

Components/Optimized structure	ΔE _{form} (B = Gua)	ΔE _{form} (B = Xan)
4*B → B4	-33	-30
4*B + Na ⁺ → B4·Na ⁺	-63	-55
4*B + K ⁺ → B4·K ⁺	-57	50
8*B → (B4) ₂	-89	-87
(B4) ₂ + Na ⁺ → (B4) ₂ ·Na ⁺	-58	-44
(B4) ₂ + K ⁺ → (B4) ₂ ·K ⁺	-55	-42
12*B → (B4) ₃	-139	-145
(B4) ₃ + Na ⁺ → (B4) ₃ ·Na ⁺	-66	-49
(B4) ₃ + K ⁺ → (B4) ₃ ·K ⁺	-63	-45
(B4) ₃ ·Na ⁺ + Na ⁺ → (B4) ₃ ·2Na ⁺	-52	-35
(B4) ₃ ·K ⁺ + K ⁺ → (B4) ₃ ·2K ⁺	-48	-29

Table S3. Energetic contributions of H-bonding, stacking, and ion coordination to the total interaction energy ΔE_{int} in model guanine and xanthine quadruplex structures. The optimization of the geometry and subsequent EDA were performed at the BLYP-D3/TZP level of theory. The molecular regions were chosen in a way that allows separating the contributions from all three major types of non-covalent interactions (H-bonding, stacking, and ion coordination). All units are kcal/mol.

Base	Model	H-bonding ^a	Stacking ^b	Coordination ^c	ΔE_{int} ^d
Gua	B4	-88	-	-	-88
	B4·Na ⁺	-90	-	-111	-201
	B4·K ⁺	-90	-	-84	-174
	(B4) ₂	-179	-34	-	-213
	(B4) ₂ ·Na ⁺	-177	-34	-149	-360
	(B4) ₂ ·K ⁺	-179	-34	-126	-339
	(B4) ₃	-267	-70	-	-337
	(B4) ₃ ·2Na ⁺	-264	-66	-207	-537
	(B4) ₃ ·2K ⁺	-269	-67	-159	-495
Xan	B4	-76	-	-	-76
	B4·Na ⁺	-75	-	-90	-165
	B4·K ⁺	-76	-	-66	-142
	(B4) ₂	-152	-42	-	-194
	(B4) ₂ ·Na ⁺	-151	-38	-121	-310
	(B4) ₂ ·K ⁺	-150	-40	-98	-288
	(B4) ₃	-228	-85	-	-313
	(B4) ₃ ·2Na ⁺	-220	-88	-146	-454
	(B4) ₃ ·2K ⁺	-222	-85	-96	-403

Note: Energetic contributions of H-bonding, stacking, and ion coordination to the total interaction energies were evaluated in the following way. The H-bond energy was calculated as the sum of the interaction energies between four bases (regions 1, 2, 3 and 4) in each individual tetrad in the structure. Stacking was calculated as the interaction energy between two (in the case of two-stack models) or three (in three-stack structures) tetrads representing individual regions. The ion coordination energy was estimated as the interaction energy between the Na⁺/K⁺ ion (region 1) and the rest of the system (region 2). In the case of (B4)₃·2M⁺ models the ion coordination energy was the sum of the individual ion coordination interactions for both ions. ΔE_{int} was calculated as the interaction energy between all the monomeric units (bases and ions) in a structure, each representing a separate region. The ΔE_{int} energy is equal to the sum of the H-bonding, stacking, and ion coordination contributions.

Table S4. QTAIM and geometric characteristics of individual H-bonds and van der Waals contacts in B4 and (B4)₂ models for Gua and Xan. The geometries were optimized in TURBOMOLE at the BLYP-D3/def2-TZVPP level of theory. The wavefunctions for QTAIM analysis were obtained at the BLYP/def2-TZVPP level of theory in Gaussian 09.

Structure	Interaction	N ^a	ρ ^b	Δρ ^b	E _{bond} ^c	Σ E _{HB} ^d	d _{A...B} ^e	d _{H...B} ^f	AHB ^g
G4 (fully optimized)	N1H...O6	4	0.037	0.096÷0.097	10.76 [6.30]	78.01	2.82÷2.83	1.79÷1.80	170.8÷171.0
	N2H...N7	4	0.035	0.074	8.74		2.92	1.90	169.9÷170.0
G4 (planar)	N1H...O6	4	0.036	0.095	9.80÷9.82 [6.07]	71.69	2.83	1.80	169.6
	N2H...N7	4	0.035	0.074	8.09÷8.12		2.92	1.90	170.5÷170.6
G4·Na ⁺ (fully optimized)	O6...Na ⁺	4	0.020	0.133÷0.134	-	67.18	2.31	-	-
	N1H...O6	4	0.032	0.088	8.24÷8.32 [5.17]		2.87÷2.88	1.86÷1.87	164.4÷164.5
	N2H...N7	4	0.036	0.075	8.50-8.53		2.91	1.88	173.6÷173.7
G4·K ⁺ (fully optimized)	O6...K ⁺	4	0.014÷0.015	0.068÷0.076	-	68.00	2.74÷2.79	-	-
	N1H...O6	4	0.033÷0.034	0.090÷0.091	8.90÷9.02 [5.40-5.62]		2.86	1.84	166.8÷167.5
	N2H...N7	4	0.034÷0.035	0.073÷0.074	7.92÷8.13		2.93	1.90	171.7÷173.4
(G4) ₂ (fully optimized)	C2...C5	4	0.007	0.020	-	151.49	3.26÷3.27	-	-
	N3...N7	4	0.007	0.026	-		3.25÷3.27	-	-
	N2...N7	4	0.007	0.024	-		3.25÷3.27	-	-
	N2...C4	1	0.006	0.020	-		3.37	-	-
	O6...N1	4	0.002	0.007	-		3.80÷3.88	-	-
	N1H...O6	8	0.038	0.098÷0.099	10.49÷10.66 [6.52]		2.81÷2.82	1.78	169.9÷172.6
	N2H...N7	8	0.035÷0.036	0.075÷0.076	8.26÷8.49		2.90÷2.91	1.88÷1.89	167.8÷168.3
(G4) ₂ (planar)	O6...N1	4	0.003	0.011	-	151.96	3.56÷3.57	-	-
	N2...C4	4	0.006	0.021	-		3.27÷3.28	-	-
	N2...N7	3	0.006	0.024	-		3.27	-	-
	N3...N2	1	0.006	0.024	-		3.27	-	-
	N3...N7	4	0.006	0.023	-		3.32	-	-
	C2...C5	4	0.006	0.020	-		3.26	-	-
	N1H...O6	8	0.038÷0.039	0.099÷0.101	10.58÷11.15 [6.52÷6.75]		2.80÷2.81	1.76÷1.78	171÷171.2
	N2H...N7	8	0.034÷0.035	0.074÷0.075	7.96÷8.31		2.91÷2.92	1.89÷1.90	167.2÷167.9
(G4) ₂ ·Na ⁺ (fully optimized)	O6...N1	8	0.005	0.022	-	153.82	3.27÷3.29	-	-
	O6...O6	8	0.004÷0.005	0.017÷0.018	-		3.32÷3.36	-	-
	O6...Na ⁺	8	0.006÷0.010	0.031÷0.058	-		2.59÷2.80	-	-
	N2...C5	8	0.006	0.020	-		3.40÷3.41	-	-
	C2...N7	8	0.006	0.022÷0.023	-		3.20÷3.21	-	-
	N1H...O6	8	0.035÷0.036	0.092÷0.094	9.45÷9.87 [5.85÷6.07]		2.83÷2.84	1.81÷1.82	164.1÷165.7
	N2H...N7	8	0.039÷0.040	0.077÷0.078	9.41÷9.75		2.87÷2.88	1.84÷1.85	172.5÷173.4
(G4) ₂ ·Na ⁺ (planar)	C2...N7	4	0.006	0.022÷0.023	-	154.51	3.23÷3.24	-	-
	N2...C5	8	0.006	0.021	-		3.39÷3.40	-	-
	O6...N1	8	0.005÷0.006	0.018÷0.019	-		3.35÷3.36	-	-
	N3...N7	4	0.006	0.023	-		3.34	-	-
	O6...Na ⁺	8	0.006÷0.009	0.029÷0.051	-		2.63÷2.83	-	-
	N1H...O6	8	0.035÷0.036	0.092÷0.094	9.47÷9.83 [5.85÷6.07]		2.83÷2.84	1.81÷1.82	163.9÷165.3
	N2H...N7	8	0.040	0.077÷0.078	9.58÷9.78		2.87÷2.88	1.84	173.4÷174.2
(G4) ₂ ·K ⁺ (fully optimized)	O6...K ⁺	8	0.012÷0.013	0.060÷0.064	-	141.12	2.81÷2.84	-	-
	O6...N1	4	0.004	0.017	-		3.39÷3.40	-	-
	N2...C5	8	0.006	0.019	-		3.40÷3.42	-	-
	C2...N7	8	0.006	0.021	-		3.25	-	-
	N1H...O6	8	0.034÷0.035	0.092÷0.093	9.22÷9.42 [5.62÷5.65]		2.84÷2.85	1.82÷1.83	167.4÷167.8
	N2H...N7	8	0.036	0.074	8.30÷8.37		2.92	1.89	171.1÷171.5

X4 (fully optimized)	N1H...O6	4	0.036	0.096	9.99÷10.02 [6.07]	81.62 [49.92]	2.82	1.80	167.2÷167.4
	N7H...O2	4	0.037÷0.038	0.095÷0.096	10.38÷10.43 [6.30÷6.52]		2.82	1.78	173.8÷174.0
X4 (planar)	N1H...O6	4	0.042	0.103	12.01÷12.02 [7.42]	81.10 [50.36]	2.77	1.74	167.6÷167.7
	N7H...O2	4	0.032	0.086	8.24 [5.17]		1.89	1.86	179.3
X4·Na ⁺ (fully optimized)	O6...Na ⁺	4	0.018	0.117÷0.119	-	77.16 [47.68]	2.35÷2.36	-	-
	N1H...O6	4	0.035	0.094	9.48÷9.53 [5.85]		2.83	1.82	163.8÷164.2
	N7H...O2	4	0.036	0.092	9.77÷9.80 [6.07]		2.84	1.80	173.7÷174.2
X4·K ⁺ (fully optimized)	O6...K ⁺	4	0.013÷0.014	0.066÷0.068	-	78.46 [48.34]	2.79÷2.80	-	-
	N1H...O6	4	0.034	0.093	9.12÷9.23 [5.62]		2.84÷2.85	1.83	166.2÷166.4
	N7H...O2	4	0.037÷0.038	0.095	10.37÷10.50 [6.30÷6.52]		2.81÷2.82	1.78÷1.79	172.4÷173.1
(X4) ₂ (fully optimized)	O2...N3	4	0.004÷0.005	0.018	-	174.23 [107.73]	3.36	-	-
	N3...C5	4	0.007	0.022	-		3.30÷3.31	-	-
	N1...C6	4	0.006	0.021	-		3.26	-	-
	N3...N7	4	0.007	0.027	-		3.24	-	-
	N7...O2	4	0.007	0.028	-		3.15	-	-
	N1H...O6	8	0.042÷0.044	0.103÷0.106	11.99÷12.80 [7.42÷7.87]		2.75÷2.77	1.72÷1.74	168.2÷170.6
	N7H...O2	8	0.034÷0.035	0.091÷0.092	9.33÷9.44 [5.62÷5.85]		2.85	1.81÷1.82	174.5÷178.0
(X4) ₂ (planar)	C2...C5	4	0.007	0.021	-	174.04 [107.04]	3.24÷3.25	-	-
	O6...N1	4	0.002÷0.003	0.009÷0.010	-		3.63÷3.66	-	-
	N3...N7	4	0.006	0.025	-		3.30	-	-
	N7...O2	4	0.006	0.024	-		3.19	-	-
	O2...N3	3	0.006	0.023	-		3.24	-	-
	O6...N3	1	0.006	0.023	-		3.24	-	-
	N1H...O6	8	0.044÷0.046	0.106÷0.109	12.79÷13.63 [7.87÷8.32]		2.73÷2.75	1.70÷1.72	169÷169.3
(X4) ₂ ·Na ⁺ (fully optimized)	N7H...O2	8	0.032÷0.033	0.086÷0.089	8.24÷8.85 [5.17÷5.40]	174.77 [107.04]	2.87÷2.89	1.83÷1.86	177.6÷178.0
	O6...N1	7	0.002÷0.003	0.009÷0.010	-		3.63÷3.66	-	-
	O2...N3	3	0.006	0.023	-		3.24	-	-
	C2...C5	3	0.007	0.021	-		3.24÷3.25	-	-
	N3...N7	4	0.006	0.025	-		3.30	-	-
	N1...C6	4	0.007	0.026	-		3.14	-	-
	O6...O6	3	0.005÷0.006	0.022	-		3.21÷3.23	-	-
	O6...Na ⁺	8	0.007÷0.008	0.037÷0.045	-		2.67÷2.75	-	-
(X4) ₂ ·Na ⁺ (planar)	N1H...O6	8	0.042÷0.044	0.102÷0.105	11.89÷12.86 [7.42÷7.87]	174.32 [107.70]	2.74÷2.77	1.72÷1.75	165.4÷165.6
	N7H...O2	8	0.034÷0.036	0.089÷0.092	9.15÷9.74 [5.62÷6.07]		2.84÷2.86	1.81÷1.83	178.5÷178.9
	C2...C5	4	0.007	0.022	-		3.24	-	-
	N1...C6	4	0.007	0.024	-		3.18÷3.19	-	-
	O6...N1	4	0.003	0.013	-		3.48	-	-
	N3...N7	4	0.006÷0.007	0.026	-		3.27÷3.28	-	-
	N7...O2	4	0.006	0.024÷0.025	-		3.19	-	-
	O6...O6	4	0.005÷0.006	0.022	-		3.21÷3.23	-	-
	O6...Na ⁺	8	0.002	0.042÷0.045	-		2.67÷2.70	-	-
(X4) ₂ ·K ⁺ (fully optimized)	N1H...O6	8	0.042÷0.044	0.102÷0.105	11.79÷12.86 [7.42÷7.87]	157.07 [96.68]	2.74÷2.77	1.72÷1.75	165.4÷165.6
	N7H...O2	8	0.034÷0.036	0.089÷0.092	9.15÷9.74 [5.62÷6.07]		2.84÷2.86	1.81÷1.83	178.5÷178.9
	O2...N3	4	0.004	0.018	-		3.35÷3.36	-	-
	N3...C5	4	0.006	0.021	-		3.35	-	-
	N1...C6	2	0.006	0.021	-		3.27	-	-
	N1...C5	2	0.006	0.021	-		3.27	-	-
	C4...N7	4	0.006	0.024	-		3.21	-	-
	N7...O2	4	0.006	0.026	-		3.17	-	-
(X4) ₂ ·K ⁺ (fully optimized)	O6...K ⁺	8	0.012÷0.013	0.058÷0.062	-		2.82÷2.85	-	-
	N1H...O6	8	0.038÷0.040	0.099÷0.101	10.64÷11.45		2.78÷2.80	1.76÷1.78	166.4÷167.5

					[6.52÷6.97]				
	N7H···O2	8	0.032÷0.034	0.087÷0.089	8.26÷8.93 [5.17÷5.62]		2.87÷2.89	1.83÷1.86	174.3÷178.8

Note: ^a Number of times a particular interaction occurs in a structure; ^b Ranges (from minimal to maximal value) for the electron density and the Laplacian of the electron density at the bond critical point (BCP or (3,-1) critical point), atomic units; ^c Energy range (in kcal/mol) for H-bonds determined by EML formula (4). The values in brackets indicate alternative energy values for the NH···O hydrogen bonds calculated by formula $E_{\text{NH}\cdots\text{O}} = -2.03 + 225 \cdot \rho$ (see Computational methodology section and Ref. 60). ^d Sum (in kcal/mol) of all the H-bond energies in a complex. For xanthine complexes containing only H-bonds of the NH···O type, the sum of the alternative energies (in brackets) was calculated; ^e Range (in Å) for the distance between atoms A and B in the case of hydrogen bonds AH···B. For van der Waals A···B contacts, this is the distance between two interacting atoms A and B. ^f Range (in Å) for the distance between hydrogen (H) and acceptor (B) atoms in the case of hydrogen bonds AH···B. ^g Range for the H-bond angle AHB (for H-bonds), degrees.

Table S5. NBO analysis of H-bonds in model Gua- and Xan-containing DNA quadruplex structures. The geometries were optimized at the BLYP-D3 level of theory in TURBOMOLE. NBO analysis was performed at the same level of theory in Gaussian 09. All characteristics are calculated as average values for each H-bond type.

Complex	H-bond	N ^a	E ₂ ^b	CT ^c	Q _A ^d	Q _H ^d	Q _B ^d
G4 (fully optimized)	N1H...O6	4	16.49	0.053	-0.559	0.448	-0.659
	N2H...N7	4	15.62	0.052	-0.750	0.430	-0.472
G4 (planar)	N1H...O6	4	15.94	0.052	-0.560	0.448	-0.657
	N2H...N7	4	15.87	0.052	-0.750	0.430	-0.472
G4·Na ⁺ (fully optimized)	N1H...O6	4	12.35	0.045	-0.549	0.447	-0.679
	N2H...N7	4	16.86	0.055	-0.745	0.430	-0.469
G4·K ⁺ (fully optimized)	N1H...O6	4	13.73	0.047	-0.549	0.446	-0.671
	N2H...N7	4	15.25	0.052	-0.741	0.428	-0.455
(G4) ₂ (fully optimized)	N1H...O6 (T1)	4	16.60	0.054	-0.565	0.449	-0.660
	N2H...N7 (T1)	4	16.07	0.054	-0.760	0.430	-0.470
	N1H...O6 (T2)	4	16.97	0.054	-0.565	0.449	-0.659
	N2H...N7 (T2)	4	15.90	0.053	-0.753	0.432	-0.471
(G4) ₂ (planar)	N1H...O6 (T1)	4	18.18	0.056	-0.566	0.450	-0.658
	N2H...N7 (T1)	4	15.86	0.053	-0.759	0.431	-0.469
	N1H...O6 (T2)	4	16.81	0.054	-0.564	0.450	-0.659
	N2H...N7 (T2)	4	15.09	0.051	-0.756	0.431	-0.472
(G4) ₂ ·Na ⁺ (fully optimized)	N1H...O6 (T1)	4	14.91	0.052	-0.557	0.451	-0.658
	N2H...N7 (T1)	4	18.45	0.059	-0.757	0.430	-0.471
	N1H...O6 (T2)	4	14.18	0.051	-0.555	0.451	-0.667
	N2H...N7 (T2)	4	19.00	0.060	-0.755	0.430	-0.470
(G4) ₂ ·Na ⁺ (planar)	N1H...O6 (T1)	4	15.02	0.052	-0.557	0.451	-0.659
	N2H...N7 (T1)	4	18.91	0.060	-0.756	0.431	-0.471
	N1H...O6 (T2)	4	14.22	0.051	-0.555	0.451	-0.670
	N2H...N7 (T2)	4	19.40	0.061	-0.755	0.430	-0.470
(G4) ₂ ·K ⁺ (fully optimized)	N1H...O6 (T1)	4	12.46	0.047	-0.546	0.452	-0.602
	N2H...N7 (T1)	4	16.03	0.053	-0.752	0.432	-0.456
	N1H...O6 (T2)	4	12.62	0.047	-0.546	0.452	-0.605
	N2H...N7 (T2)	4	16.08	0.053	-0.752	0.432	-0.455
X4 (fully optimized)	N1H...O6	4	15.56	0.051	-0.574	0.451	-0.628
	N7H...O2	4	16.69	0.054	-0.455	0.458	-0.657
X4 (planar)	N1H...O6	4	19.91	0.058	-0.574	0.449	-0.626
	N7H...O2	4	13.82	0.047	-0.455	0.459	-0.656
X4·Na ⁺ (fully optimized)	N1H...O6	4	13.55	0.047	-0.563	0.448	-0.658
	N7H...O2	4	16.22	0.053	-0.453	0.458	-0.646
X4·K ⁺ (fully optimized)	N1H...O6	4	12.81	0.046	-0.573	0.444	-0.664
	N7H...O2	4	16.87	0.055	-0.460	0.456	-0.628
(X4) ₂ (fully optimized)	N1H...O6 (T1)	4	19.15	0.058	-0.581	0.452	-0.625
	N7H...O2 (T1)	4	15.34	0.050	-0.458	0.459	-0.660
	N1H...O6 (T2)	4	21.09	0.060	-0.579	0.451	-0.626
	N7H...O2 (T2)	4	15.55	0.051	-0.464	0.462	-0.655
(X4) ₂ (planar)	N1H...O6 (T1)	4	22.77	0.064	-0.583	0.452	-0.624
	N7H...O2 (T1)	4	14.43	0.049	-0.455	0.459	-0.660
	N1H...O6 (T2)	4	21.07	0.060	-0.578	0.451	-0.625

Complex	H-bond	N ^a	E ₂ ^b	CT ^c	Q _A ^d	Q _H ^d	Q _B ^d
(X4) ₂ (planar)	N7H...O2 (T2)	4	13.58	0.047	-0.464	0.462	-0.656
(X4) ₂ ·Na ⁺ (fully optimized)	N1H...O6 (T1)	4	18.71	0.057	-0.572	0.452	-0.647
	N7H...O2 (T1)	4	15.79	0.051	-0.455	0.458	-0.651
	N1H...O6 (T2)	4	18.69	0.057	-0.571	0.452	-0.632
	N7H...O2 (T2)	4	16.51	0.053	-0.463	0.460	-0.649
(X4) ₂ ·Na ⁺ (planar)	N1H...O6 (T1)	4	19.96	0.059	-0.574	0.452	-0.642
	N7H...O2 (T1)	4	16.12	0.052	-0.455	0.458	-0.651
	N1H...O6 (T2)	4	18.35	0.056	-0.568	0.452	-0.638
	N7H...O2 (T2)	4	15.42	0.051	-0.464	0.461	-0.648
(X4) ₂ ·K ⁺ (fully optimized)	N1H...O6 (T1)	4	14.57	0.049	-0.569	0.453	-0.591
	N7H...O2 (T1)	4	13.33	0.047	-0.461	0.457	-0.642
	N1H...O6 (T2)	4	15.76	0.052	-0.569	0.450	-0.600
	N7H...O2 (T2)	4	14.67	0.050	-0.467	0.460	-0.638

Note: ^a Number of times a particular H-bond occurs in a structure; ^b Stabilization energy for the LP→BD* interaction (defined by formula (3) in the manuscript), where the LP – lone pair(s) of the H-bond acceptor atom, BD* is the anti-bonding orbital of the H-bond donating group; ^c Charge transfer to the anti-bonding orbital corresponding to the H-bond donor group; ^d Natural charges of the donor (A), hydrogen (H), and acceptor (B) atoms involved in the H-bond AH...B.

Notations T1 and T2 refer to different tetrads in the (B4)₂ complexes.

Table S6. Parameters and energies of the H-bonds and ion-base coordination contacts at the B3LYP-D/6-31++G(d,p) level of theory. The geometries were optimized in Gaussian 09. QTAIM and the NBO analyses were performed in the AIMAll and Gaussian 09 programs, using BLYP-D/6-31++G(d,p) wavefunctions and geometries. All characteristics are calculated as average values for each type of non-covalent contact.

Complex	Interaction	N ^a	ρ^b	$\Delta\rho^b$	E_{HB}^c	$d_{A...B}^d$	$d_{H...B}^e$	AHB ^f	E_2^g	C_{ij}^h
G4·Na ⁺	N1H...O6	4	0.033	0.099	7.66	2.83	1.82	166.0	21.24	2.681
	N2H...N7	4	0.036	0.089	7.35	2.89	1.86	172.2	23.69	2.820
	O6...Na ⁺	4	0.020	0.121	-	2.32	-	-	-	2.236
G4·K ⁺	N1H...O6	4	0.028	0.087	6.57	2.90	1.87	175.3	16.94	3.822
	N2H...N7	4	0.023	0.058	4.57	3.04	2.05	164.4	12.38	7.476
	O6...K ⁺	4	0.023	0.105	-	2.59	-	-	-	2.381
X4·Na ⁺	N1H...O6	4	0.038	0.117	8.90	2.78	1.76	166.0	25.27	2.780
	N7H...O2	4	0.035	0.107	7.99	2.82	1.79	175.0	24.31	4.180
	O6...Na ⁺	4	0.017	0.104	-	2.37	-	-	-	3.083
X4·K ⁺	N1H...O6	4	0.036	0.111	8.40	2.80	1.78	167.0	24.14	3.108
	N7H...O2	4	0.036	0.109	8.12	2.81	1.78	175.3	24.30	4.037
	O6...K ⁺	4	0.014	0.061	-	2.79	-	-	-	5.604

Note: ^a Number of times a particular interaction occurs in a structure; ^b The electron density and the Laplacian of electron density values at the bond critical point (3,-1), a.u.; ^c The H-bond energy calculated by the EML formula (4), kcal/mol; ^d The distance between atoms A and B in the case of the hydrogen bond AH...B, Å. For ion-base contacts, this is the distance between the O6 atom of Gua/Xan and the metal ion; ^e The distance between the hydrogen (H) and the H-bond acceptor atom (B), Å; ^f The H-bond angle AH...B, degrees; ^g The stabilization energy for the LP→BD* interaction (defined by formula (3) in the manuscript), where the LP – lone pair(s) of the H-bond acceptor atom, BD* is the anti-bonding orbital of the H-bond donating group, kcal/mol; ^h Compliance constant, Å/mDyn.

Table S7. NPA charges calculated for atoms A and B, involved in van der Waals contacts A⋯B in (B4)₂ complexes. All characteristics are calculated as average values for each type of van der Waals contact.

Complex	Interaction	N ^a	Q _A	Q _B
(G4) ₂	C2⋯C5	4	0.552	-0.093
	N3⋯N7	4	-0.532	-0.471
	N2⋯N7	4	-0.752	-0.469
	N2⋯C4	1	-0.760	0.316
	O6⋯N1	4	-0.660	-0.565
(G4) ₂ (planar)	O6⋯N1	4	-0.564	-0.658
	N2⋯C4	4	-0.759	0.317
	N2⋯N7	3	-0.757	-0.469
	N3⋯N2	1	-0.469	-0.757
	N3⋯N7	4	-0.531	-0.472
	C2⋯C5	4	0.556	-0.091
(G4) ₂ ·Na ⁺ (fully optimized)	O6⋯N1	8	-0.668	-0.557
	O6⋯O6	8	-0.658	-0.668
	N2⋯C5	8	-0.755	-0.085
	C2⋯N7	8	0.556	-0.471
(G4) ₂ ·Na ⁺ (planar)	C2⋯N7	4	0.555	-0.470
	N2⋯C5	8	-0.756	-0.084
	O6⋯N1	8	-0.557	-0.662
	N3⋯N7	4	-0.526	-0.471
(G4) ₂ ·K ⁺	O6⋯N1	4	-0.606	-0.546
	N2⋯C5	8	-0.752	-0.078
	C2⋯N7	8	0.555	-0.470
(X4) ₂	O2⋯N3	4	-0.660	-0.517
	N3⋯C5	4	-0.528	-0.070
	N1⋯C6	4	-0.581	0.583
	N3⋯N7	4	-0.528	-0.464
	N7⋯O2	4	-0.458	-0.655
(X4) ₂ (planar)	C2⋯C5	4	0.721	-0.564
	O6⋯N1	4	-0.624	-0.656
	N3⋯N7	4	-0.527	-0.578
	N7⋯O2	4	-0.455	-0.524
	O2⋯N3	3	-0.659	-0.656
	O6⋯N3	1	-0.660	-0.464
(X4) ₂ ·Na ⁺ (fully optimized)	O6⋯N1	7	-0.632	-0.572
	O2⋯N3	3	-0.651	-0.512
	C2⋯C5	3	0.722	-0.066
	N3⋯N7	4	-0.522	-0.463
	N1⋯C6	4	-0.572	0.583
	O6⋯O6	3	-0.632	-0.632
(X4) ₂ ·Na ⁺ (planar)	C2⋯C5	4	0.723	-0.065
	N1⋯C6	4	-0.574	0.585
	O6⋯N1	4	-0.642	-0.568
	N3⋯N7	4	-0.522	-0.464
	N7⋯O2	4	-0.455	-0.648
	O6⋯O6	4	-0.642	-0.638
(X4) ₂ ·K ⁺	O2⋯N3	4	-0.642	-0.514

Complex	Interaction	N ^a	Q _A	Q _B
	N3...C5	4	-0.527	-0.068
	N1...C6	2	-0.569	0.578
	N1...C5	2	-0.569	0.579
	C4...N7	4	0.306	-0.467
	N7...O2	4	-0.461	-0.638

Note: ^a Number of times a particular van der Waals contact occurs in a structure.