Electronic Supplementary Material (ESI) for New Journal of Chemistry. This journal is © The Royal Society of Chemistry and the Centre National de la Recherche Scientifique 2020

Electronic Supplementary Material

Studies of the stability, nucleophilic substitution reactions, DNA/BSA interactions, cytotoxic activity, DFT and molecular docking of some tetra- and penta-coordinated gold(III) complexes

Snežana Radisavljević,^{*a*}Ana ĐekovićKesić,^{*b*}Dušan Ćoćić,^{*a*}Ralph Puchta,^{*c,d,e*} Laura Senft,^{*c*}Milena Milutinović,^{*f*}Nevena Milojević^{*f*} and Biljana Petrović^{*1*}*

DNA-binding studies

Calculation of binding constant toDNA

In order to compare the binding strength of the complexes, the intrinsic binding constants $K_{\rm b}$ were calculated according to the changes in absorption at the MLCT band with increasing concentration of DNA. The binding constant of the complexes with DNA(in M⁻¹), may be calculated by the ratio of the slope to the y intercept in plots $\frac{[DNA]}{(\varepsilon_{\rm A} - \varepsilon_{\rm f})} vs.$ [DNA] (Inset in Figure 2), using the following equation(S1):^{s1}

$$\frac{[\text{DNA}]}{(\varepsilon_{\text{A}} - \varepsilon_{\text{f}})} = \frac{[\text{DNA}]}{(\varepsilon_{\text{b}} - \varepsilon_{\text{f}})} + \frac{1}{K_{\text{b}}(\varepsilon_{\text{b}} - \varepsilon_{\text{f}})}$$
(eq. S1)

where [DNA] is the concentration of DNA in base pairs, ε_f is the extinction coefficient for the unbound complex at the corresponding λ_{max} , $\varepsilon_A = A_{obsd}/[complex]$ and ε_b is the extinction coefficient for the complex in the fully bound form.

Stern-Volmer equation for EB competitive studies

The Stern-Volmer plots of DNA-EB illustrate that the quenching of EB bound to DNA by the compounds is in good agreement (R = 0.95)with the linear Stern-Volmer equation:

$$\frac{Io}{I} = 1 + K_{SV}[Q] \qquad (eq. S2)$$

where I and I₀ are the emission intensities in the presence and absence of gold(III) complexes, [Q] is the final concentration of the quencher, K_{sv} is the Stern-Volmer quenching constant.

Stern-Volmer equation for BSA studies

The values of the dynamic quenching constant (K_{SV} , M^{-1}) and the quenching rate constant (k_q , M^{-1} s⁻¹) for the interaction of gold(III) complexes with BSA, were calculated using the Stern-Volmer quenching equation:

$$\frac{Io}{I} = 1 + k_q \tau_0[Q] = 1 + K_{SV}[Q]$$
 (eq. S3)

where Io = the initial tryptophan fluorescence intensity of BSA, I = the tryptophan fluorescence intensity of BSA after the addition of complexes, k_q = the quenching rate constants of BSA, K_{SV} = the dynamic quenching constant, τ_o = the average lifetime of BSA without complexes, [Q] = the concentration of gold(III) complexes, $K_{SV} = k_q \tau_o$ and, taking as fluorescence lifetime (τ_o) of tryptophan in BSA at around 10⁻⁸ s.

Scatchard equation

Association binding constant (*K*) and number of binding sites per albumin (*n*) can be calculated using Scatchard equation, Eq. $(S4)^{s2}$:

$$\frac{\Delta I}{I_0} \div [Q] = nK - K \frac{\Delta I}{I_0}$$
 (eq. S4)

where *K* may be calculated from the slope in the Scatchard plots $\frac{\Delta I}{I_0} \div [Q]vs$. $\frac{\Delta I}{I_0}$ and *n* is given by the ratio of *y* intercept to the slope.

References

- S1. S. Yu-Min, W. Qiong, Y. Pei-Ju, L. Ni-Na, W. Liu-Fang and L. Ying-Mei, *J. Inorg.Biochem.*, 2006,**100**, 1685-1691.
- S2. S. S. Wu, W. B. Yuan, H. Y. Wang, Q. Zhang, M. Liu and K. B. Yu, *J Inorg. Biochem.*,2008, 102, 2026-2034.



Figure S1. ESI-MS spectrum of complex 1



Figure S2. ESI-MS spectrum of complex 2



Figure S3. IR spectrum of complex 1



Figure S4. IR spectrum of complex 2



Figure S5. UV-Vis spectra of complexes 1 and 2 in water over a 6hours period.

 $[\text{complex}] = 1 \times 10^{-4} \,\text{M}$



Figure S6. UV-Vis spectra of complexes 1 and 2 in Hepes buffer (pH=7.2) over a 6 hours

period. [complex] = 5×10^{-5} M



Figure S7. Kinetic traces for the substitution reactions of complex 1 with selected nucleophiles



Figure S8. Kinetic traces for the substitution reactions of complex 2 with selected nucleophiles



Figure S9. Pseudo-first order rate constants for the substitution reactions between complexes 1 and 2 with L-Met, as a function of nucleophile concentration and temperature, at pH = 7.2 (25 mM Hepes buffer) with the addition of 30 mM NaCl.



Figure S10. Pseudo-first order rate constants for the substitution reactions between complexes 1 and 2 with GSH, as a function of nucleophile concentration and temperature, at pH = 7.2 (25 mM Hepes buffer) with the addition of 30 mM NaCl.



Figure S11. Pseudo-first order rate constants for the substitution reactions between complexes 1 and 2 with 5'-GMP, as a function of nucleophile concentration and temperature, at pH = 7.2 (25 mM Hepes buffer) with the addition of 30 mM NaCl.



Figure S12. Fluorescence emission spectra (λ_{ex} = 527 nm) of the EB-DNA system (5×10⁻⁶ M EB, 5×10⁻⁶ M DNA) in the absence and in the presence of complexes **1** and **2** (1×10⁻⁴ M, 62.5µL per scan). Arrows show the intensity changes upon increasing the concentration of complex. Insert: Stern-Volmer quenching plot of DNA-EB.



Figure S13. Relative viscosity $(\eta/\eta_0)^{1/3}$ of CT-DNA (11 μ M) in buffer solution (25 mM Hepes, 30mM NaCl) in the presence of increasing amounts of complexes **1** and **2** (r).



Figure S14. Scatchard plots for complexes 1 and 2.



Figure S15. AIM plot of complex 2 with labels for bond critical points (BCP).



Figure S16.Laplacian of electron density presented in contour line map along 2N-1Au-3N plane (BCPs are presented as blue dots while bond paths are presented as brow lines).



Figure S17. The electron localization function (ELF) (upper) and localized orbital locator (LOL)

(lower) of **1**, **2**, **3** and **4** presented in color filed map along N-Au-N plane.



Figure S18. Grid data of electron density difference for complexes 1, 2 and 3 (isoval = 0.003).



Figure S19. Computational docking model illustrating interactions between investigated complexes and canonical B-DNA.



Figure S20. NCI plot for a representative conformation of complexes 1 and 2 docked in the canonical B-DNA, surfaces represent the non-covalent interactions according to the color bar (isoval = 0.3).



Figure S21. The effect of complexes **1** and **2** on the MDA-231 (top); HCT-116 (middle) and HaCaT (bottom) cell viability after 24 and 72 h of exposure. All values are mean, n=6; percentages of viable cells.

λ/nm	T/K	$10^{-4}C_L/M$	k_{obs1}/s^{-1}	kobs2/s-1
276	288	0.25	$6.165(6)^{a}$	$1.360(6)^{a}$
		0.5	7.595(5)	1.960(5)
		1	8.920(6)	2.450(6)
		1.5	10.230(6)	2.770(6)
		2	11.610(5)	3.565(5)
		2.5	12.580(6)	4.083(6)
	298	0.25	7 333(5)	2 070(5)
	270	0.25	8 770(5)	2.070(3)
		0.5	10,100(5)	2.633(3)
		1	10.100(6)	3.443(0)
		1.5	11.615(5)	4.160(5)
		2	13.057(5)	5.040(5)
		2.5	14.728(6)	6.145(6)
	308	0.25	8.465(6)	2.690(6)
		0.5	10.420(6)	3.030(6)
		1	12.010(6)	3,890(6)
		1.5	13.680(5)	4.910(5)
		2	15.000(5) 15.480(5)	5 900(5)
		25	16 990(6)	6 640(6)
		2.3	10.770(0)	0.0-0(0)

Table S1. Observed *pseudo*-first order rate constants (for the first and the second reaction steps) as a function of ligand concentration and temperature for the substitution reactions between complex **1** and Tu in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

^aNumber of runs in parenthesis.

λ/nm	T/K	10 ⁻⁴ C _L /M	kobs/s ⁻¹
255	200	0.05	0.407(5)3
255	288	0.25	$0.40/(5)^{a}$
		0.5	0.566(5)
		1	0.844(5)
		1.5	1.225(6)
		2	1.512(5)
		2.5	1.855(6)
	298	0.25	0.531(5)
		0.5	0.649(5)
		1	0.973(6)
		1.5	1.427(6)
		2	1.860(5)
		2.5	2.131(6)
	308	0.25	0.735(5)
		0.5	0.845(6)
		1	1.321(6)
		1.5	1.710(5)
		2	2.340(6)

Table S2. Observed *pseudo*-first order rate constants as a function of ligand concentration and temperature for the substitution reactions between complex **1** and 5'-GMP in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

λ/nm	T/K	10 ⁻⁴ C _L /M	kobs/s ⁻¹
280	288	0.25 0.5 1 1.5 2 2.5	0.455(5) 0.820(6) 1.128(5) 1.566(6) 2.100(5) 2.608(6)
	298	0.25 0.5 1 1.5 2 2.5	$\begin{array}{c} 0.700(6) \\ 1.087(5) \\ 1.527(6) \\ 1.997(5) \\ 2.532(5) \\ 2.943(6) \end{array}$
	308	$\begin{array}{c} 0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5 \end{array}$	$\begin{array}{c} 0.997(5) \\ 1.527(5) \\ 2.009(6) \\ 2.600(5) \\ 3.068(6) \\ 3.450(5) \end{array}$

Table S3. Observed *pseudo*-first order rate constants as a function of ligand concentration and temperature for the substitution reactions between complex **1** and GSH in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

λ/nm	T/K	10 ⁻⁴ C _L /M	kobs/s ⁻¹
295	288	$0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5$	0.560(6) 1.056(6) 1.524(5) 2.082(5) 2.571(5) 3.220(6)
	298	0.25 0.5 1 1.5 2 2.5	0.738(5) 1.360(6) 1.945(5) 2.470(6) 3.050(5) 3.643(5)
	308	$\begin{array}{c} 0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5 \end{array}$	0.930(5) 1.710(6) 2.530(5) 3.145(5) 3.455(6) 4.113(5)

Table S4. Observed *pseudo*-first order rate constants as a function of ligand concentration and temperature for the substitution reactions between complex **1** and L-Met in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2)

λ/nm	T/K	10 ⁻⁴ C _L /M	k_{obs1}/s^{-1}	kobs2/s-1
272	288	0.25	$8.715(5)^{a}$	2.520(5)
		0.5	9.320(5)	2.810(5)
		1	10.837(6)	3.437(6)
		1.5	12.370(5)	4.138(5)
		2	13.776(6)	4.910(6)
		2.5	15.417(5)	5.347(5)
	298	0.25	9.940(6)	3.493(6)
		0.5	11.495(6)	4.400(6)
		1	13.300(6)	5.090(6)
		1.5	14.870(6)	6.010(6)
		2	16.490(5)	6.830(5)
		2.5	18.080(5)	7.910(5)
	308	0.25	11.870(6)	4.260(6)
		0.5	13.530(5)	5.110(5)
		1	15.080(5)	6.133(5)
		1.5	17.450(6)	7.173(6)
		2	19.070(6)	7.950(6)
		2.5	20.860(5)	8.930(5)

Table S5. Observed *pseudo*-first order rate constants (for the first and the second reaction steps) as a function of ligand concentration and temperature for the substitution reactions between complex **2** and Tu in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

λ/nm	T/K	$10^{-4}C_L/M$	kobs/s ⁻¹
255	288	$0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5$	0.488(5) 1.010(6) 1.580(5) 1.980(6) 2.572(5) 3.143(5)
	298	0.25 0.5 1 1.5 2 2.5	0.810(6) 1.403(5) 2.010(5) 2.585(6) 3.158(5) 3.628(5)
	308	$\begin{array}{c} 0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5 \end{array}$	$1.205(6) \\ 1.906(6) \\ 2.680(6) \\ 3.230(5) \\ 3.988(5) \\ 4.650(5)$

Table S6. Observed *pseudo*-first order rate constants as a function of ligand concentration and temperature for the substitution reactions between complex **2** and 5'-GMP in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

λ/nm	T/K	10 ⁻⁴ C _L /M	kobs/s ⁻¹
294	288	$\begin{array}{c} 0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5 \end{array}$	0.835(5) 1.274(5) 1.867(6) 2.410(5) 3.020(5) 3.586(5)
	298	$\begin{array}{c} 0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5 \end{array}$	1.100(5) 1.620(5) 2.170(5) 2.910(6) 3.370(5) 4.090(6)
	308	$0.25 \\ 0.5 \\ 1 \\ 1.5 \\ 2 \\ 2.5$	1.270(5) 2.020(5) 2.690(6) 3.420(5) 4.240(5) 4.830(6)

Table S7. Observed *pseudo*-first order rate constants as a function of ligand concentration and temperature for the substitution reactions between complex **2** and GSH in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

λ/nm	T/K	$10^{-4}C_L/M$	kobs/s ⁻¹
294	288	0.25	1.202(5)
-		0.5	1.942(6)
		1	2.564(5)
		1.5	3.346(5)
		2	3.940(6)
		2.5	4.372(5)
		0.05	1 =00/=
	298	0.25	1.508(5)
		0.5	2.170(6)
		1	2.755(6)
		1.5	3.558(5)
		2	4.203(6)
		2.5	4.730(5)
		0.05	1 (00)(7)
	308	0.25	1.600(5)
		0.5	2.200(5)
		1	3.070(6)
		1.5	3.690(5)
		2	4.413(6)

Table S8. Observed *pseudo*-first order rate constants as a function of ligand concentration and temperature for the substitution reactions between complex **2** and L-Met in 25 mM Hepes buffer and 30 mM NaCl (pH=7.2).

Table S9. The effect of complexes **1** and **2** on MDA-231, HCT-116 and HaCaT cell lines viabilities, after 24 and 72 hours exposure. Results are expressed as absorbance.*p<0.05, treatment vs control.

Comular	Conc	MDA-MB-231		НСТ	HCT-116		HaCaT	
Complex	(µM)	24h	72h	24h	72h	24h	72h	
K (n=24)	0	0.89±0.03	2.10±0.16	0.79±0.11	1.54±0.24	1.25±0.25	2.22±0.38	
	0.1	1.01 ± 0.05	1.94 ± 0.32	0.62 ± 0.09	0.90 ± 0.34	1.30 ± 0.18	2.30 ± 0.20	
	1	0.84 ± 0.09	1.04 ± 0.33	0.44 ± 0.06	0.51 ± 0.05	1.09 ± 0.13	1.47 ± 0.07	
1	10	0.75 ± 0.03	0.86 ± 0.23	0.36 ± 0.03	0.22 ± 0.02	0.64 ± 0.09	0.22 ± 0.05	
\mathbf{I}	50	0.19 ± 0.01	0.18 ± 0.03	0.17 ± 0.02	0.19 ± 0.03	0.16 ± 0.01	0.17 ± 0.02	
(n=0)	100	0.19 ± 0.02	0.17 ± 0.02	0.18 ± 0.03	0.19±0.03	0.16 ± 0.01	0.18 ± 0.01	
	200	0.19 ± 0.01	0.18 ± 0.02	0.17 ± 0.02	0.19 ± 0.02	0.17 ± 0.02	0.18 ± 0.02	
	0.1	1.11±0.22	2.18±0.24	0.54 ± 0.03	0.52 ± 0.04	0.72 ± 0.04	2.31±0.13	
	1	1.11±0.06	1.19 ± 0.25	0.49 ± 0.05	0.24 ± 0.03	0.99 ± 0.06	1.41 ± 0.08	
2	10	0.97±0.19	1.14 ± 0.18	0.43 ± 0.07	0.22 ± 0.02	0.97 ± 0.07	0.65 ± 0.05	
(n-6)	50	0.65 ± 0.08	0.79 ± 0.14	0.27 ± 0.03	0.19 ± 0.03	0.95 ± 0.03	0.34 ± 0.03	
(11-0)	100	0.21 ± 0.01	0.21 ± 0.05	0.18 ± 0.01	0.20 ± 0.02	0.22 ± 0.04	0.19 ± 0.02	
	200	0.17 ± 0.02	0.18 ± 0.02	0.17 ± 0.02	0.20 ± 0.02	0.17 ± 0.01	0.19±0.01	

Table S10. The effect of complexes **1** and **2** on MDA-231, HCT-116 and HaCaT cell lines viabilities, after 24 and 72 hours exposure. Results are expressed as percentages of viable cells in treatment compared to control/untreated cells (100%).

Complay	Conc	MDA-N	MB-231	НСТ	HCT-116		HaCaT	
Complex	(µM)	24h	72h	24h	72h	24h	72h	
	0.1	114.32	92.33	78.36	58.28	103.82	103.59	
	1	94.28	49.59	56.02	33.25	87.49	66.36	
1	10	84.17	40.96	45.40	14.20	50.76	9.79	
(n-6)	50	21.04	8.45	21.79	12.18	13.15	7.87	
(II-0)	100	21.02	8.26	22.81	12.56	13.04	8.32	
	200	21.15	8.55	21.58	12.23	13.87	8.33	
	0.1	125.22	103.64	68.20	33.61	57.61	104.20	
	1	124.90	56.65	62.05	15.78	79.88	63.54	
2	10	109.43	54.37	54.81	14.31	77.52	29.17	
(n-6)	50	73.86	37.38	34.69	12.32	75.67	15.48	
(11-0)	100	23.97	9.96	22.55	12.97	17.81	8.55	
	200	19.72	8.36	21.75	12.70	13.32	8.62	

Table S11. Coefficient of correlation (R) between concentrations of complexes 1 and 2 and cytotoxic effect on MDA-231, HCT-116 and HaCaT cell lines after 24 and 72 hours incubation. Results are calculated upon percentages of viable cells.*significant correlation ($R \ge 0.70$)

			Coefficien	t of correlation	(R)		
Au-complex	MDA	-MB-231	НСТ	-116	HaC	HaCaT	
	24h	72h	24h	72h	24h	72h	
1	- 0.77*	-0.69	-0.72*	-0.55	-0.73*	-0.57	
2	- 0.92*	-0.80*	-0.87*	-0.46	-0.86*	-0.67	