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Structure and Dynamics of Solvation Shells of Copper(II) Complexes with N,O-Containing Ligands

Mikhail S. Bukharov,[†] Valery G. Shtyrlin,*[,†] Georgy V. Mamin,[‡] Siegfried Stapf,[§] Carlos Mattea,[§] Anvar Sh. Mukhtarov,[†] Nikita Yu. Serov,[†] and Edward M. Gilyazetdinov[†]

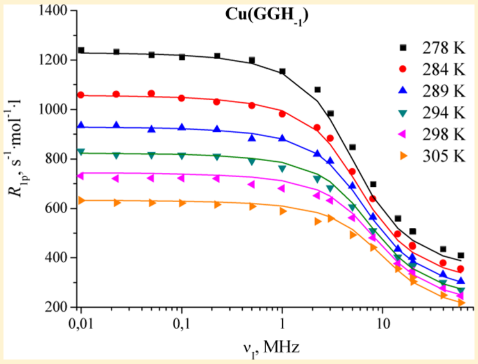
[†] A.M. Butlerov Chemistry Institute, Kazan Federal University, Kremlevskaya St. 18, 420008, Kazan, Russian Federation

[‡] Institute of Physics, Kazan Federal University, Kremlevskaya St. 18, 420008 Kazan, Russian Federation

[§] Fachgebiet Technische Physik II/Polymerphysik, Institute of Physics, Technische Universität Ilmenau, P.O. Box 100 565, 98684 Ilmenau, Germany

S *Supporting Information*

ABSTRACT: EPR, NMR relaxation methods, and DFT calculations were jointly used to investigate the structural and dynamical characteristics of solvation shells of copper(II) complexes with iminodiacetic acid, glycylglycine, and glycyglycylglycine in comparison with the copper(II) bis-glycinate studied previously. A strong *trans* influence of deprotonated peptide nitrogen was revealed in EPR spectra parameters of copper(II) complexes with oligopeptides. With models of the experimental NMRD data and literature X-ray structural information, it was suggested that only one water molecule coordinates in axial position of copper(II) complexes with glycine and di- and triglycine ($Cu(Gly)_2$, $Cu(GGH_{-1})$, and $Cu(GGGH_{-2})^-$), and the copper ion in these complexes is pentacoordinated, while in the iminodiacetate complex, Cu(IDA), both apical positions can be occupied by solute molecules. The obtained structural results were confirmed by DFT calculations of structures of studied compounds using different functionals and basis sets. It was shown that the donor ability of equatorial ligands and *trans* influence have an effect on the characteristics of the axial water bond. With increasing donor strength of equatorial ligands, pentacoordination of copper(II) complexes in water solutions becomes more preferable.



■ INTRODUCTION

Coordination number of copper(II) in its complexes in solutions is a debatable question for the past several years. This is especially true for the copper(II) aqua ion. Earlier, it was generally accepted that copper(II) is hexacoordinated in water solution. This statement was mainly based on crystallographic data.[1−3] However, the work of Pasquarello et al.[4] has made this statement questionable. On the basis of neutron diffraction studies and molecular dynamics simulations the authors[4] have concluded that copper(II) is 5-fold coordinated in aqua ion. The work[4] has become a "trigger" for many other articles in this field (theoretical and experimental). Some of them confirm 5-fold coordination of copper(II) or existence of several structures (see refs 5−17 and references therein), and other ones[18−23] support the traditional point of view. It is interesting to note that 5-fold coordination of Cu(II) was obtained in a supramolecular sandwich consisting of two crown ether molecules and a trigonal-bipyramidal $[Cu(H_2O)_5]^{2+}$ complex.[24] Also, it should be mentioned that for a copper(II) tetra-imidazole complex the elongated square-pyramidal structure with very weak second axial water interaction was found by EXAFS and MXAN methods.[25] However, at present, the debates about copper(II) coordination sphere in solutions are not finished.

On the basis of EPR and NMRD (nuclear magnetic relaxation dispersion) data as well as DFT computations in our previous work[26] we have shown that in the copper(II) bis-complexes with 9 amino acids only one water molecule is presented in axial position. If two water molecules are taken into simulation of the copper(II) bis-glycinate ($Cu(Gly)_2$) NMRD data, the structural parameters obtained under simulation do not agree with those found by the EXAFS method.[27]

In the present work we continue our methodology developed in a previous article[26] in combination with EPR, NMRD, and quantum-chemical computations to investigate hydration sphere characteristics of copper(II) mono-complexes with N,O-containing ligands: iminodiacetic acid ($IDAH_2$), glycylglycine (GGH), and glycylglycylglycine (GGGH). For the special experimental conditions used, the following coordination of nitrogens in equatorial planes of the complexes is realized: in Cu(IDA) one imino nitrogen is coordinated, in $Cu(GGH_{-1})$ one amino and one deprotonated peptide nitrogen are present, and in $Cu(GGGH_{-2})^-$ one amino and two deprotonated peptide nitrogens are coordinated. The results obtained are

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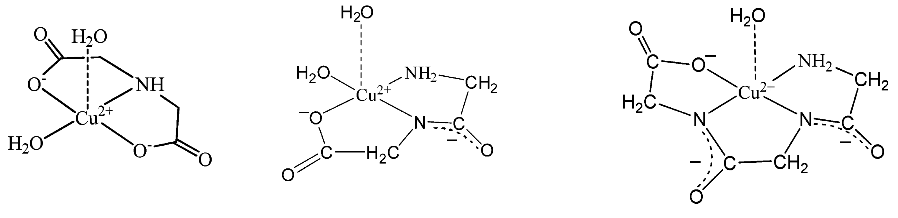


Cu(IDA) Cu(GGH$_{-1}$) Cu(GGGH$_{-2}$)$^-$

Figure 1. Simplified structures of the complexes studied.

compared with previous data[26] for Cu(Gly)$_2$ in which two amino groups are bonded equatorially. The main objective of the study was to reveal and interpret the dependence of hydration sphere parameters of the copper(II) complexes on number and nature of equatorially coordinated groups.

■ EXPERIMENTAL SECTION AND COMPUTATIONAL DETAILS

Reagents. Copper(II) nitrate of analytical grade, iminodiacetic acid recrystallized from water solution, glycylglycine recrystallized from water−ethanol solution, and glycyglycylglycine from Reanal were used to prepare solutions. The pH was adjusted by adding HNO_3 (analytical grade) and KOH (Chemapol). Potassium nitrate (analytical grade) recrystallized from water solution was used to create 1.0 M salt background.

The metal concentration in studied solutions was set to 5−10 mM. Such concentrations allow one to decrease spin−lattice relaxation times (T_1) and avoid a contribution from spin exchange. The pH values and the 3−5% ligands excess were chosen so as to maximize the accumulation degrees (>98%) of the copper(II) complexes studied and to avoid theirs hydrolysis: the pH values at 293 K were 5.30, 6.90, and 7.95 for the iminodiacetate, glycylglycinate, and glycylglycylglycinate systems, respectively. Calculations of concentrations of all species presented in the studied solutions were performed with the STALABS computer program[28] using reported equilibrium constants.[29−32]

Structures of the studied complexes are given in Figure 1.

Methods. Measurements of the pH values were carried out with a Titrando 907 automatic titrator from Metrohm.

A Bruker ESP 300 spectrometer was used to obtain X-band EPR spectra in the 277−324 K temperature range. Two thin tubes (1 mm outer diameter) with sample were placed inside a single 5 mm diameter tube to record the spectra. Temperature was regulated with a Bruker variable temperature controller by the nitrogen gas flow. The temperature accuracy was ±1 K, and it was checked by a thermocouple put inside the outer tube.

The EPR spectra were simulated with the modified program[33] in fast motion regime and with the EasySpin software package[34] in slow motion limit. The isotropic g_0 factors, hyperfine coupling constants A_0, super hyperfine coupling constants A_0^N, and rotational correlation times τ_R were obtained by the simulations. In the slow motion limit, the g_0 and A_0 values were found as an average of anisotropy values, $^1/_3(2g_\perp + g_\|)$ and $^1/_3(2A_\perp + A_\|)$, respectively, to compare corresponding parameters with those obtained in fast motion limit. Anisotropy spin-Hamiltonian parameters needed for simulation of the EPR spectra were taken from literature data.[35−37]

^{1}H nuclear magnetic relaxation dispersion (NMRD) measurements were performed on a Stelar Spinmaster FFC2000 field-cycling NMR relaxometer (0.01−20 MHz, Stelar s.r.l., Mede, Italy) and on the Bruker Minispec systems (20, 40, and 60 MHz for Cu(II)-diglycine system) in the temperature range 278−319 K with an accuracy of ±0.5 K. Before measurements all solutions were blown by argon for the oxygen removal and next shut hermetically. A routine based on the Solomon−Bloembergen equations and the Hwang and Freed equations (see below) was used to fit the NMRD profiles. The diamagnetic contribution found with blank saline solution was subtracted from measured spin−lattice relaxation rates

$$\frac{1}{T_{1p}} = \frac{1}{T_1} - \frac{1}{T_{1d}} \qquad (1)$$

where T_1 is the spin−lattice relaxation time of the sample solution, $1/T_{1d}$ is the diamagnetic contribution to the relaxation rate, and $1/T_{1p}$ is the paramagnetic contribution.

The structures of the studied compounds with 1 or 10 water molecules were optimized in the GAMESS program package[38] using the DFT method[39] with three parameter Becke exchange functional[40] and the Lee−Yang−Parr correlation functional[41] (B3LYP); also, the B3LYP functional with Coulomb-attenuating method (CAM-B3LYP)[42] has been used as well as all-electron TZVP[43] (valence triple-ζ + polarization), TZP[44,45] (triple-ζ + polarization), and aug-cc-pVTZ[46] (correlation consistent valence triple-ζ + polarization + diffuse) basis sets. Polarizable continuum model (C-PCM)[47] was used to account for solvent effects. Ten water molecules in the initial structures were placed by three schemes. In the first scheme (5−5 scheme) five water molecules were placed on each side of the equatorial plane. One of these five molecules was put in axial position and others near equatorial ligands to form hydrogen bonds with them and the axial water molecule. In other words in this initial structure there are two axial water molecules. The second scheme (6−4a) is similar to the 5−5 scheme, but opposite to it six water molecules were placed on one side of equatorial plane and only four water molecules on the other one. The third scheme (6−4b scheme) is the same as the 6−4a scheme, but four water molecules on the second side of the equatorial plane were arranged in the shape of a square (thus, only one water molecule is coordinated in axial position). Such disposition of opposite water molecules has been first obtained by us previously[26] on the example of the *cis*-Cu(Gly)$_2$·44H$_2$O structure. The initial structures of the third scheme lead to best local energy minima in comparison with the others in all cases except the Cu(IDA) complex where all three schemes considered give nearly the same optimized energies (see Figure 4). It also should be noted that even by using the first and second schemes only one water molecule is remained in apical position with short enough axial bond distance in all final optimized structures. The local energy minimum was defined with the 10^{-4} or 10^{-6} Hartree optimization tolerance. All energy minima have been tested for the absence of imaginary frequencies.

■ RESULTS AND DISCUSSION

EPR. To get reliable parameters by the NMR relaxation method it is necessary to obtain some values by another method. EPR gives the chance to determine rotational correlation times of complexes in order to use them later for fitting NMRD data. Experimental and simulated EPR spectra of the copper(II) complexes with IDAH$_2$, GGH, and GGGH at 295 K are presented in Figure 2. Parameters of the spectra are given in Table 1 for 295 K with corresponding data for the Cu(Gly)$_2$ *cis* and *trans* isomers from ref 26.

Parameters obtained for the complexes studied are similar to those found by other authors.[48−54]

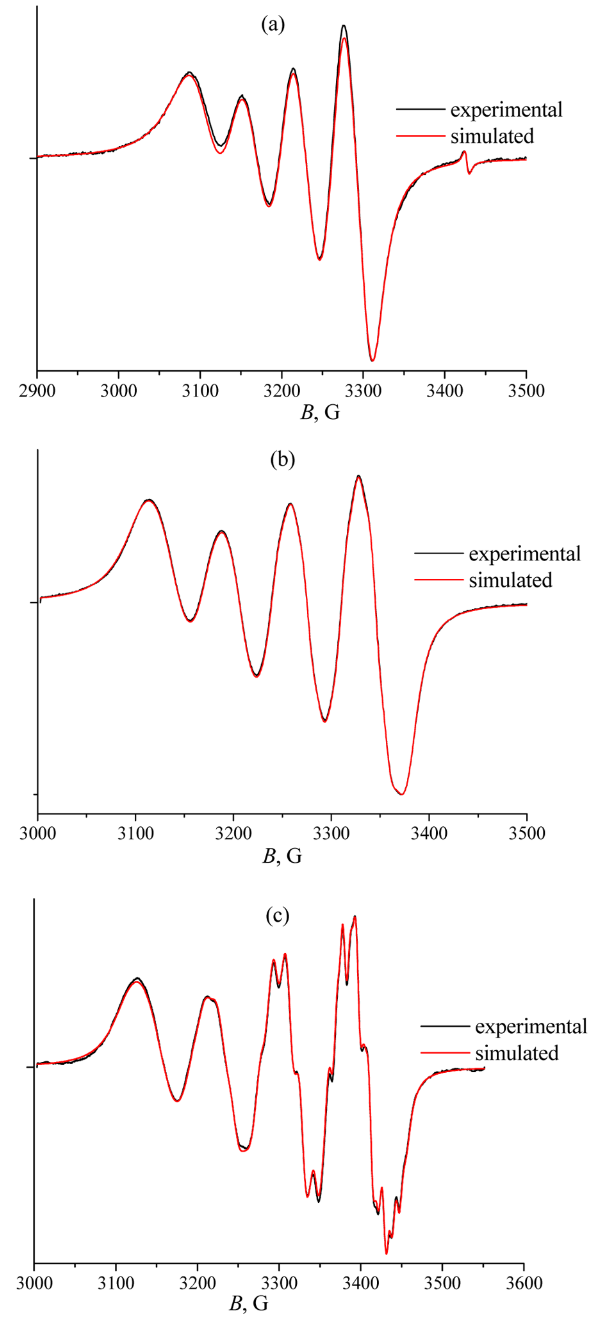


Figure 2. Experimental and simulated EPR spectra of (a) Cu(IDA) at 1.0 M KNO_3, pH 5.30, $C_{Cu(II)}$ = 5.00 mM, C_{IDAH2} = 5.20 mM; (b) $Cu(GGH_{-1})$ at 1.0 M KNO_3, pH 6.90, $C_{Cu(II)}$ = 4.81 mM, C_{GGH} = 5.01 mM; (c) $Cu(GGGH_{-2})^-$ at 1.0 M KNO_3, pH 7.95, $C_{Cu(II)}$ = 4.81 mM, C_{GGGH} = 5.01 mM; T = 295 K.

In the $Cu(GGH_{-1})$ complex one deprotonated peptide nitrogen and one amino nitrogen coordinate in the equatorial plane and give ligand hyperfine splitting 14.2 and 11.8 G, respectively (Table 1). In the case of the $Cu(GGGH_{-2})^-$ complex two deprotonated peptide nitrogens and one amino nitrogen have ligand hyperfine coupling constants of 17.1, 14.7, and 8.6 G, respectively (Table 1). The smaller hyperfine splitting of the amino nitrogen in the copper(II) tripeptide complex is due to the strong *trans* influence of the deprotonated peptide group (*trans* influence in the copper(II) complexes was discovered previously[31,55]). Disposition of a strong donor (like deprotonated peptide nitrogen) opposite to the amino group (Figure 1) results in a weaker bond between copper(II) and the amino nitrogen. *Vice versa*, the amino group also exerts the same influence on the deprotonated peptide nitrogen so two deprotonated peptide nitrogens in the triglycine complex have different A_0^N values. The same effect is also observed for the *trans* isomer of $Cu(Gly)_2$ in comparison with the *cis* one.[26] Overall, the metal–ligand bond strength and *trans* influence are increased in the following order: imino nitrogen, amino nitrogen, deprotonated peptide nitrogen (cf., refs 55 and 56).

Table 1. EPR Spectra Parameters of the Cu(IDA), $Cu(Gly)_2$, $Cu(GGH_{-1})$, and $Cu(GGGH_{-2})^-$ Complexes on the 1.0 M KNO_3 Background (T = 295 K)[a]

complex	g_0	A_0, G	A_0^N, G	τ_R, 10^{-11} s
Cu(IDA)	2.1462(4)	60.2(4)	11(1)	3.2(2)
$Cu(Gly)_2$				
trans isomer[26]	2.1285	63.4	8.9, 8.9	3.4
cis isomer[26]	2.1277	74.2	10.5, 10.5	3.4
$Cu(GGH_{-1})$	2.1232(2)	67.7(2)	14.2(3), 11.8(4)	3.4(2)
$Cu(GGGH_{-2})^-$	2.0993(2)	82.1(3)	17.1(2), 14.7(2), 8.6(2)	4.3(1)

[a] Numbers in parentheses denote errors in last digits.

Rotational motion of complexes modulates EPR line shapes due to Zeeman and hyperfine anisotropies. So by simulation of EPR spectra it is possible to determine rotational correlation times τ_R of complexes. From temperature dependences of τ_R, the activation energies $E_{a(rot)}$ of rotational motion (as a whole molecule), τ_0 coefficients, and hydrodynamic radii r_h of complexes were found by Arrhenius law (eq 2) and Stokes–Einstein eq 3:

$$\tau_R = \tau_0 \exp(E_{a(rot)}/RT) \tag{2}$$

$$\tau_R = \frac{4\pi\eta r_h^3}{3kT} \tag{3}$$

Here η is the viscosity, k is the Boltzmann constant, and T is the temperature. The obtained parameters are presented in Table 2.

NMRD. Usually three processes can contribute to experimental NMRD profiles: inner sphere, second sphere, and outer sphere relaxation (see, e.g., refs 57 and 58). Inner sphere contribution is due to protons of water molecules coordinated to metal ion and is well-described by the Solomon–Bloembergen equations[59,60] for dipole–dipole (dd) and contact (con) relaxation mechanisms:

$$\frac{1}{T_{1p}} = \frac{[C_M]}{[C_H]}\frac{q}{T_{1M} + \tau_M} \tag{4}$$

$$\left(\frac{1}{T_{1M}}\right)_{dd} = \frac{2}{15}\gamma_I^2 g_e^2 \mu_B^2 S(S+1) r^{-6} \times \left(\frac{7\tau_C}{1+\omega_S^2\tau_C^2} + \frac{3\tau_C}{1+\omega_I^2\tau_C^2}\right) \tag{5}$$

$$\left(\frac{1}{T_{1M}}\right)_{con} = \frac{2}{3}S(S+1)\left(\frac{A}{\hbar}\right)^2 \frac{\tau_C}{1+\omega_S^2\tau_C^2} \tag{6}$$

Here, τ_M is the lifetime of the bound protons, $[C_M]$ and $[C_H]$ are the concentrations of paramagnetic ion and solvent protons

Table 2. Comparison of the NMRD Best Fitting Parameters Obtained for the Copper(II) Complexes with Iminodiacetic Acid, Glycine, Glycylglycine, and Glycylglycylglycine[a]

complex	r_1, Å $1H_2O/2H_2O$	r_{eq}, Å $1H_2O/2H_2O$	τ_0, 10^{-13} s	$E_{a(rot)}$, kJ/mol	$E_{a1(ex)}$, kJ/mol	k_1, 10^9 s^{-1} (298 K)	r_2, Å	d, Å	r_h, Å
Cu(IDA)	3.1/3.1	2.63/2.81	0.25(4)	17.5(4)	16.6	4.5	4.0	3.8	3.2
$Cu(Gly)_2$[26]	3.1 ($1H_2O$)		0.69	15.2	16.6	4.5	4.0	3.8	3.2
$Cu(GGH_{-1})$	3.1/3.1	2.82/3.16	0.43(2)	16.5(3)	16.6	4.5	4.1	3.8	3.3
	3.1/3.1	2.80/3.09	0.43(2)	16.5(3)	15.4	7.5	4.1	3.8	3.3
$Cu(GGGH_{-2})^-$	3.3/3.7		0.24(4)	18.7(4)	16.6	4.5	4.1	4.0	3.6
	3.2/3.6		0.24(4)	18.7(4)	15.4	7.5	4.1	4.2	3.6

[a] r_1 is the distance between copper(II) and axial water protons. r_{eq} is the distance between copper(II) and equatorial water protons; r_2 is the distance between copper(II) and protons of the second c.s. water molecules. $E_{a2(ex)}$ = 12.5 kJ/mol for all complexes (τ_{M2} [298 K] = 5 ps). Calculating errors of r_1, r_2, d, and r_h are about 0.1 Å, and calculating errors of r_{eq} are about 0.05 Å.

(111 mol/dm^3), respectively, q is the number of exchangeable protons in the first coordination sphere of the metal, γ_I is the nuclear gyromagnetic ratio, μ_B is the Bohr magneton, S is the electron spin, ω_S and ω_I are the electron and nuclear Larmor precession frequencies, respectively, g_e is the electronic g-factor, r is the proton−metal ion distance, and A is the electron−nuclear hyperfine coupling constant. Correlation time τ_C is defined as

$$\tau_C^{-1} = \tau_R^{-1} + \tau_M^{-1} + \tau_S^{-1} \tag{7}$$

where τ_S is the electronic spin relaxation time. For protons, the contact part of inner sphere relaxation can be neglected.

The second sphere contribution is calculated by the same equations as for inner sphere relaxation.

Temperature dependences of protons lifetimes ($\tau_{Mi} = k_i^{-1}$) are usually described by the Eyring equation:

$$\tau_{Mi} = A_i/T \exp(E_{ai(ex)}/RT) \tag{8}$$

Here i = 1, 2 for the inner and second coordination sphere, respectively. In this work the initial τ_{Mi} values were fixed as for $Cu(Gly)_2$[26] because glycine, iminodiacetic acid, diglycine, and tryglicine have a similar nature. It should be noted that r_2 and d values obtained for studied compounds are close to values found for $Cu(Gly)_2$, confirming the possibility of borrowing some parameters.

The outer sphere contribution is due to protons of water molecules diffused near the complex. As for copper(II) complexes with amino acids[26] we used equations for translationally modulated outer sphere relaxation:[61−63]

$$\left(\frac{1}{T_1}\right)_{os} = \frac{32}{405}\pi\frac{N_A[C_M]\hbar^2\gamma_I^2\gamma_S^2 S(S+1)}{1000d(D_M + D_L)}\{7J(\omega_S) + 3J(\omega_I)\} \tag{9}$$

$$J(\omega) = \mathrm{Re}\left\{\frac{1 + 1/4z}{1 + z + 4/9z^2 + 1/9z^3}\right\}$$

where

$$z = \sqrt{\left(i\omega\tau_D + \frac{\tau_D}{\tau_S}\right)} \qquad \tau_D = \frac{d^2}{D_M + D_L}$$

N_A is the Avogadro's number, d is the distance of closest approach between the solvent protons and paramagnetic ion, D_M and D_L are the diffusion coefficients of the paramagnetic species and solvent molecule, respectively, and τ_D is the diffusion correlation time. The values of the $D_M + D_L$ sum were taken as for $Cu(Gly)_2$[26] for all complexes studied.

Because of many variables involved in simulation it is useful to obtain some of them by another method or to fix theirs on the basis of theoretical assumptions. As mentioned above rotational correlation times were found by EPR and were used in fitting NMRD profiles. As a number of protons of the second coordination sphere (c.s.) water molecules (q_2) and distance r_2 are correlated we fixed the q_2 parameter. We supposed that the second c.s. water molecules can be located on the 8 faces of the distorted copper(II) octahedron (i.e., n_2 = 8 and q_2 = 16).[26] The number of the second c.s. water molecules in complexes studied will be checked by MD calculations in our later works. It should be noted that eight second c.s. water molecules were also found for copper(II) tetra-imidazole complex by EXAFS and MXAN methods.[25]

Figure 3 shows experimental and simulated NMRD profiles for solutions of the copper(II) complexes studied (left column) and NMRD profiles with different contributions at single temperature (right column). Best fitting parameters are presented in Table 2.

The equatorial plane of $Cu(GGGH_{-2})^-$ is fully occupied only by the $GGGH_{-2}^{3-}$ ligand. In the case of $Cu(GGH_{-1})$ and Cu(IDA) one water molecule is coordinated in equatorial position, and its protons give an additional contribution to the observed relaxivity. So, first NMRD profiles of $Cu(GGGH_{-2})^-$ were fitted to simplify simulation of the $Cu(GGH_{-1})$ and Cu(IDA) experimental data.

Because of correlation of some parameters the simulations were carried out by successive variation of two sets of parameters, (r_1, d) and (r_1, r_2, $E_{a2(ex)}$). As the number of axial water molecules and r_1 value are correlated we fixed the number of axial waters (one or two) and obtained the r_1 values.

Using r_1 value, one can calculate the smallest distance between copper(II) and the oxygen of the axial water, compare this distance with literature data, and therefore estimate the number of axial water molecules. At a given r_1 value the smallest $r_{Cu\text{-}Oax}$ value is realized if hydrogens of axial water are pointing outward (Scheme 1). Then, the $r_{Cu\text{-}Oax}$ value can be calculated by means of the cosine theorem for Cu−O−H triangle.

In accordance with crystallographic data[64] for sodium glycylglycylglycinate cuprate(II) monohydrate, the axial position of metal ion is occupied by the nitrogen atom of the adjacent ligand at a distance of 2.57 Å. So the length of the axial bond with oxygen in copper(II) glycylglycylglycinate may be approximately 2.6 Å. In this case the longest distance between copper(II) and protons of axial water can be estimated as ~3.3 Å (using cosine theorem for Cu−O−H triangle, see Scheme 1). As can be seen from Table 2 the r_1 value obtained for only one axial water molecule in $Cu(GGGH_{-2})^-$ agrees with this estimation.

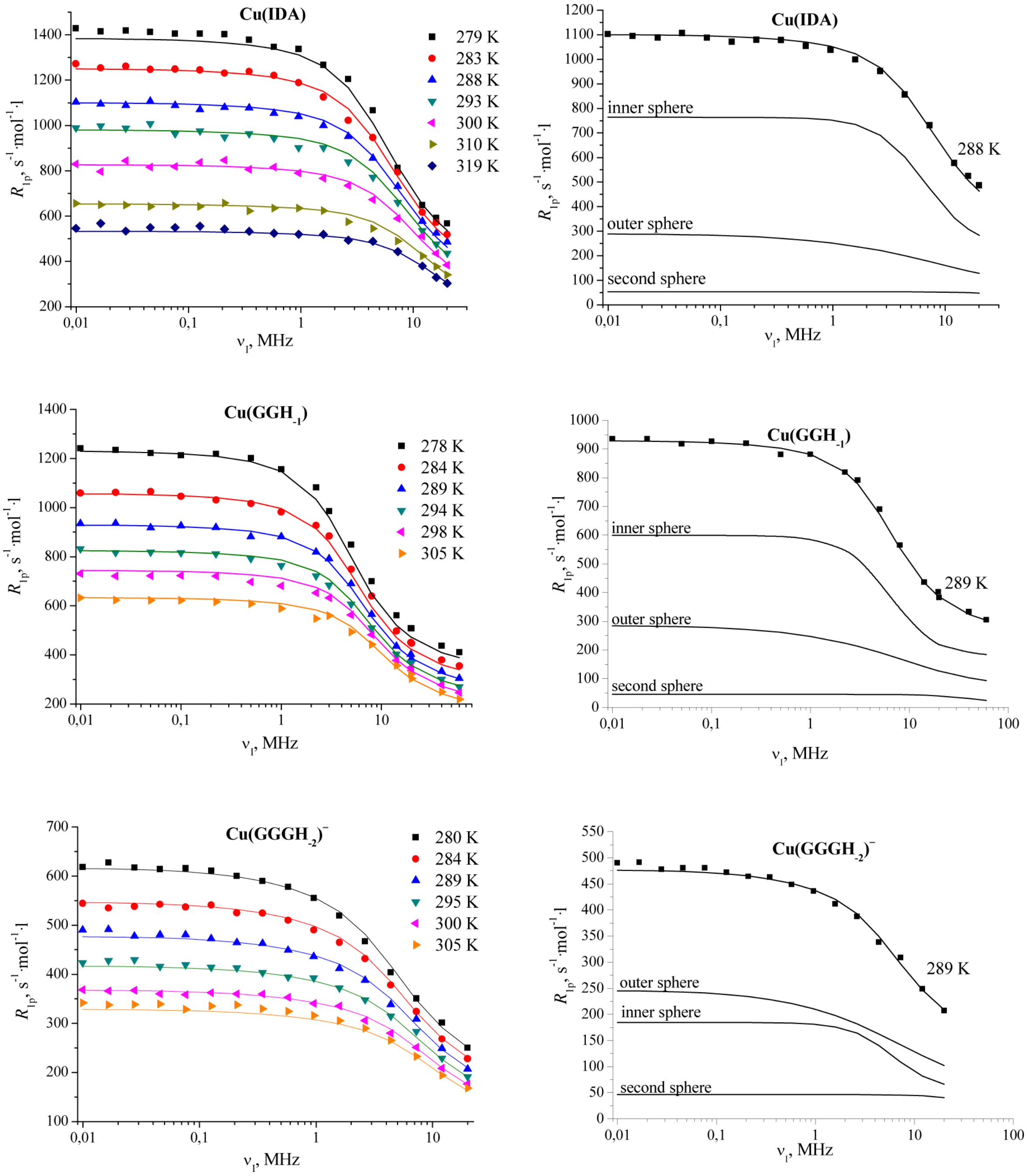
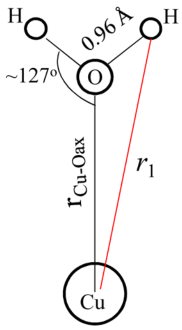


Figure 3. Experimental and simulated NMRD profiles of copper(II) complexes with $IDAH_2$, GGH, and GGGH. The abscissa is $\nu_I = \omega_I/2\pi$. $R_{1p} = T_{1p}^{-1}/C_M$ is the molar relaxivity, where C_M is the metal concentration: C_M = 9.94 mM for Cu(IDA) and $Cu(GGGH_{-2})^-$, and C_M = 5.01 mM for $Cu(GGH_{-1})$.

There is one way to decrease r_1 obtained under fitting NMRD data: to increase the exchange rate constant k_1 of the axial water molecule. In this work we chose the initial exchange rate constant $k_1(298\text{ K}) = 4.5 \times 10^9$ s^{-1} obtained for a copper(II) aqua ion.[4] It is possible to get r_1 = 3.3 Å for 2 axial H_2O molecules in $Cu(GGGH_{-2})^-$ by using $k_1 = 18.3 \times 10^9$ s^{-1} and d = 4.9 Å. However, such a value of k_1 is 4 times more than that for the copper(II) aqua ion and seems to be unrealistic. Also, d = 4.9 Å is even greater than for a bigger copper(II) complex with lysine (d = 4.1 Å, see ref 26). Thus, on the basis of NMRD data it should be concluded that in water solution only one water molecule coordinates in axial position of the $Cu(GGGH_{-2})^-$ complex and copper(II) is pentacoordinated. It also should be noted that in the above-mentioned copper(II) glycylglycylglycinate crystal[64] the copper(II) ion has 5-fold coordination.

To confirm our conclusion we have also investigated a copper(II) complex with glycyglycine in which one equatorial position is occupied by a water molecule. Contributions of axial water protons and equatorial water protons have almost identical profiles, and it is not possible to separate them under simulation (one can obtain r_1 for any value of r_{eq}). So the r_1 value was fixed on the basis of crystallographic data[65] according to which the distance between copper(II) and axial water oxygen of $Cu(GGH_{-1})$ equals 2.3 or 2.39 Å. It can be assumed that in solution $r_{Cu\text{-}Oax} \approx 2.4$ Å for $Cu(GGH_{-1})$. Then

Scheme 1. Schematic Representation of Copper(II) and Axial Water Disposition



the maximum r_1 value can be estimated to be 3.1 Å. This r_1 value was further used to simulate experimental NMRD profiles. Also, parameters of the second c.s. (r_2, $E_{2(ex)}$) obtained for $Cu(GGGH_{-2})^-$ were used to fit NMRD data of the $Cu(GGH_{-1})$ complex. We have considered two possible ways under simulation (1 axial H_2O and 2 axial H_2O) and found the averaged distance between copper(II) and protons of equatorial water molecule r_{eq} (Table 2).

According to the estimations,[66] the distance between copper(II) and water protons in aqua ion complex equals 2.7 or 2.8 Å for five and six water molecules in the first coordination sphere, respectively. In other words this distance belongs to the approximate range 2.7–2.8 Å. As can be seen from Table 2, the r_{eq} value obtained for only one axial water molecule in $Cu(GGH_{-1})$ agrees with the range 2.7–2.8 Å obtained for Cu(II) aqua ion. Such a comparison is not rigorous but gives an argument in favor of pentacoordination of copper(II) in the $Cu(GGH_{-1})$ complex also.

At simulation of NMRD data for the Cu(IDA) complex we have used the r_2, $E_{a1(ex)}$, and k_1 parameters obtained for $Cu(Gly)_2$. The r_1 value was estimated from crystallographic data[67] as well. We again have found r_{eq} values depending on the number of axial water molecules (Table 2). In this case we could not differentiate between penta- or hexacoordinated complexes because r_{eq} values of both structures agree with the Cu(II) aqua ion results.

Thus, we can say that pentacoordination of copper(II) complexes in water solutions is favored rather at the equatorial bonding of a larger number of stronger donor groups. It should be mentioned that previously[68,69] ligand exchange reactivity of copper(II) bis-chelates was explained with the assumption of pentacoordination in solutions.

We emphasize that the second c.s. of all compared complexes is described by about the same values of the r_2, $E_{a2(ex)}$, and τ_{M2} parameters (Table 2).

The r_1 distances between copper(II) and axial protons obtained are changed in the row $Cu(Gly)_2 \approx Cu(GGH_{-1}) < Cu(GGGH_{-2})^-$ in accordance with the $r_{Cu\text{-}Oax}$ distances in crystals of these complexes (Table 3). This may be explained by higher donor ability of two deprotonated peptide groups. Equatorial coordination of such groups decreases charge of metal ion and results in weaker bond between copper(II) and the axial water molecule. Higher donor strength of the ligands in the $Cu(GGGH_{-2})^-$ complex is confirmed by the short-wave shift of the absorption maximum in the electronic spectrum of $Cu(GGGH_{-2})^-$ (λ_{max} = 555 nm)[32] relative to $Cu(Gly)_2$ (λ_{max} = 620 nm)[70] and $Cu(GGH_{-1})$ (λ_{max} = 640 nm)[31] (see also discussion in ref 55). The decrease of g_0-factor in the row $Cu(IDA) > Cu(Gly)_2 > Cu(GGH_{-1}) > Cu(GGGH_{-2})^-$ (Table 1) reflects also an increase of the ligand field strength and metal–ligand bond covalence (see, e.g., refs 71 and 72).

Some confirmation of influence of ligand donor ability on axial coordination can be obtained by the DFT method. Optimized structures and total energies (in atomic units, au) of studied compounds with 10 H_2O at the CAM-B3LYP/TZVP level are presented on Figure 4 (all optimized structures with B3LYP functional and other basis sets are given in Supporting Information). It should be noted that the CAM-B3LYP functional leads to lower energies of optimized structures and shorter distances between copper(II) and axial water molecules versus the B3LYP functional. At the same time transition from TZVP basis set to TZP and aug-cc-pVTZ basis sets results in growth of the copper(II)–axial water distance (see Figures S1–S4 and Table 3). As can be seen from Figure 4 and Table 3, an increase of the number and donor strength of equatorial nitrogens leads to a longer distance between copper(II) and the axial water molecule.

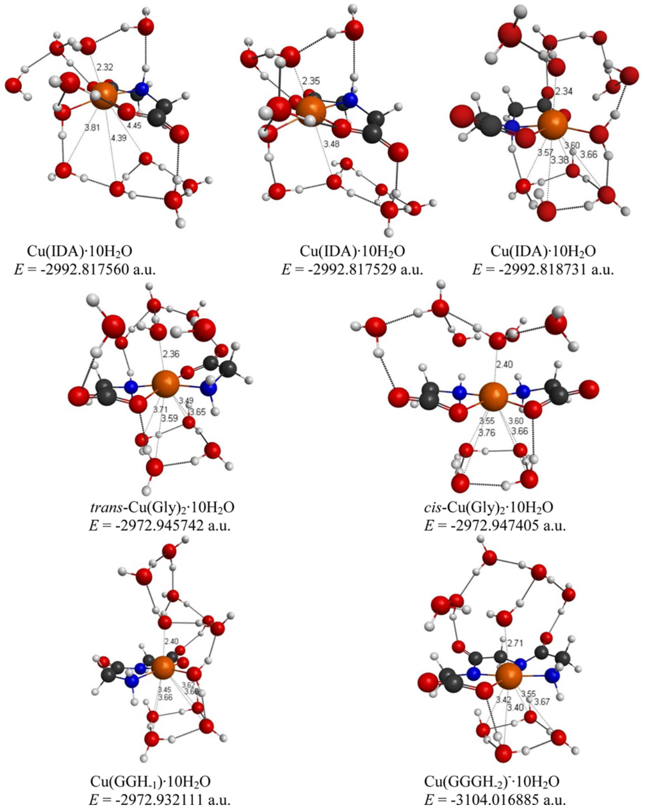
From Table 3 it can be seen that the r_{Ow} distance obtained by structure optimization is smaller for *trans*-$Cu(Gly)_2$ (Table 3) than for the *cis* structure. This effect can be explained by the *trans* influence of two opposite amino groups. As has been mentioned above, the disposition of two strong donor groups opposite to each other reduces the strength of their binding with the metal ion. As a result, the *trans* influence decreases the effect of equatorial amino groups on weakening metal bonds with axial water molecules.

■ CONCLUSIONS

In this work the copper(II) complexes with iminodiacetic acid, glycylglycine, and glycylglycyglycine were investigated by combined EPR and NMR relaxation methods. The *trans* influence of a deprotonated peptide nitrogen was observed in spectral parameters of olygopeptide complexes. On the basis of NMRD results and in comparison with structural data the

Table 3. Copper(II)−Oxygen of Axial Water Molecule (r_{Ow}) and Copper(II)−Hydrogens of Axial Water Molecule (r_{H1w}, r_{H2w}) Distances in Structures Optimized on the B3LYP/aug-cc-pVTZ, B3LYP/TZVP, and CAM-B3LYP/TZVP Levels Using the C-PCM Model with a Different Number of Water Molecules in the Solvation Shell

	B3LYP/aug-cc-pVTZ with C-PCM and 1H_2O		B3LYP/TZVP with C-PCM and 1H_2O		CAM-B3LYP/TZVP with C-PCM and 1H_2O		CAM-B3LYP/TZVP with C-PCM and 10H_2O		cryst data
complex	r_{Ow}/Å	r_{H1w}, r_{H2w}/Å	r_{Ow}/Å	r_{H1w}, r_{H2w}/Å	r_{Ow}/Å	r_{H1w}, r_{H2w}/Å	r_{Ow}/Å	r_{H1w}, r_{H2w}/Å	r_{ax}/Å
Cu(IDA)	2.46	3.04, 3.08	2.37	2.98, 3.01	2.31	2.92, 2.95	2.34	2.88, 2.97	2.38[67]
trans-$Cu(Gly)_2$	2.49	3.05, 3.17	2.43	2.99, 3.10	2.36	2.92, 3.05	2.36	2.91, 2.93	
cis-$Cu(Gly)_2$	2.56	2.83, 3.21	2.48	2.89, 3.10	2.40	2.83, 3.14	2.40	2.91, 2.99	2.40[73]
$Cu(GGH_{-1})$	2.54	3.06, 3.06	2.47	3.00, 3.01	2.39	2.94, 2.95	2.40	2.98, 3.09	2.3–2.39[65]
$Cu(GGGH_{-2})^-$	4.17	4.34, 4.94	4.17	4.35, 4.96	4.13	4.32, 4.92	2.71	3.03, 3.40	2.57[64]



Cu(IDA)·10H_2O E = -2992.817560 a.u.
Cu(IDA)·10H_2O E = -2992.817529 a.u.
Cu(IDA)·10H_2O E = -2992.818731 a.u.
trans-Cu(Gly)$_2$·10H_2O E = -2972.945742 a.u.
cis-Cu(Gly)$_2$·10H_2O E = -2972.947405 a.u.
Cu(GGH$_{-1}$)·10H_2O E = -2972.932111 a.u.
Cu(GGGH$_{-2}$)$^-$·10H_2O E = -3104.016885 a.u.

Figure 4. Structures and total energies of studied copper(II) complexes optimized in GAMESS program package at CAM-B3LYP/TZVP level using the C-PCM model to account for solvent effects.

pentacoordination of copper(II) in complexes with GGH$_{-1}^{2-}$ and GGGH$_{-2}^{3-}$ was suggested. In these complexes only one water molecule is coordinated in axial position. However, in the case of the Cu(IDA) complex the structures with one or two axial water molecules are possible. A greater axial water−copper(II) distance was obtained for the Cu(GGGH$_{-2}$)$^-$ complex in comparison with Cu(Gly)$_2$ and Cu(GGH$_{-1}$). This effect was explained by higher donor ability of deprotonated peptide groups and confirmed by EPR parameters and DFT calculations of the Cu(IDA), Cu(Gly)$_2$, Cu(GGH$_{-1}$), and Cu(GGGH$_{-2}$)$^-$ structures. On the other hand DFT calculations of *cis* and *trans* isomers of Cu(Gly)$_2$ have shown that the effect of ligand donor ability on axial coordination can be reduced by the *trans* influence of opposing strong donor groups of ligands. Overall, pentacoordination of copper(II) complexes in water solutions is rather favored at the equatorial bonding of a larger number of stronger donor groups.

■ ASSOCIATED CONTENT

S Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acs.inorgchem.5b01467.

Optimized structures of studied compounds with one H_2O molecule at B3LYP/TZVP, B3LYP/TZP, B3LYP/aug-cc-pVTZ, and CAM-B3LYP/TZVP levels (Figures S1, S2, S3, and S4, respectively), and atomic coordinates for all optimized structures (Tables S1−S27) (PDF)

■ AUTHOR INFORMATION

Corresponding Author

*E-mail: Valery.Shtyrlin@gmail.com.

Notes

The authors declare no competing financial interest.

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■ REFERENCES

(1) Beevers, C. A.; Lipson, H. *Proc. R. Soc. London, Ser. A* **1934**, *146*, 570−582.
(2) Mani, N. V.; Ramaseshan, S. *Z. Kristallogr.* **1961**, *115*, 97−109.
(3) Hathaway, B. J. In *Comprehensive Coordination Chemistry*; Wilkinson, G., Ed.; Pergamon: Oxford, 1987; Vol. 5, Chapter 53, pp 533−774.
(4) Pasquarello, A.; Petri, I.; Salmon, P. S.; Parisel, O.; Car, R.; Tòth, È.; Powell, D. H.; Fischer, H. E.; Helm, L.; Merbach, A. E. *Science* **2001**, *291*, 856−859.
(5) Benfatto, M.; D'Angelo, P.; Della Longa, S.; Pavel, N. V. *Phys. Rev. B: Condens. Matter Mater. Phys.* **2002**, *65*, 174205-1−174205-5.
(6) Blumberger, J.; Bernasconi, L.; Tavernelli, I.; Vuilleumier, R.; Sprik, M. *J. Am. Chem. Soc.* **2004**, *126*, 3928−3938.
(7) Frank, P.; Benfatto, M.; Szilagyi, R. K.; D'Angelo, P.; Della Longa, S.; Hodgson, K. O. *Inorg. Chem.* **2005**, *44*, 1922−1933.
(8) Amira, S.; Spångberg, D.; Hermansson, K. *Phys. Chem. Chem. Phys.* **2005**, *7*, 2874−2880.
(9) Chaboy, J.; Muñoz-Páez, A.; Merkling, P. J.; Sànchez Marcos, E. *J. Chem. Phys.* **2006**, *124*, 064509-1−064509-9.
(10) Frank, P.; Benfatto, M.; Hedman, B.; Hodgson, K. O. *Inorg. Chem.* **2008**, *47*, 4126−4139.
(11) O'Brien, J. T.; Williams, E. R. *J. Phys. Chem. A* **2008**, *112*, 5893−5901.
(12) de Almeida, K. J.; Murugan, N. A.; Rinkevicius, Z.; Hugosson, H. W.; Vahtras, O.; Ågren, H.; Cesar, A. *Phys. Chem. Chem. Phys.* **2009**, *11*, 508−519.
(13) Smirnov, P. R.; Trostin, V. N. *Russ. J. Gen. Chem.* **2009**, *79*, 1591−1599.
(14) Liu, X.; Lu, X.; Meijer, E. J.; Wang, R. *Phys. Chem. Chem. Phys.* **2010**, *12*, 10801−10804.
(15) Zitolo, A.; Chillemi, G.; D'Angelo, P. *Inorg. Chem.* **2012**, *51*, 8827−8833.
(16) Bowron, D. T.; Amboage, M.; Boada, R.; Freeman, A.; Hayama, S.; Dìaz-Moreno, S. *RSC Adv.* **2013**, *3*, 17803−17812.
(17) Muñoz-Páez, A.; Sànchez Marcos, E. *Reference Module in Chemistry, Molecular Sciences and Chemical Engineering, Comprehensive Inorganic Chemistry II*, 2nd ed.; Elsevier: New York, 2013; Vol. 9, *Theory and Methods*, pp 133−159.
(18) Persson, I.; Persson, P.; Sandström, M.; Ullström, A. S. *J. Chem. Soc., Dalton Trans.* **2002**, 1256−1265.
(19) Rode, B. M.; Schwenk, C. F.; Hofer, T. S.; Randolf, B. R. *Coord. Chem. Rev.* **2005**, *249*, 2993−3006.
(20) Moin, S. T.; Hofer, T. S.; Weiss, A. K. H.; Rode, B. M. *J. Chem. Phys.* **2013**, *139*, 014503-1−014503-10.
(21) Xiang, J. Y.; Ponder, J. W. *J. Comput. Chem.* **2013**, *34*, 739−749.
(22) van Duin, A. C. T.; Bryantsev, V. S.; Diallo, M. S.; Goddard, W. A.; Rahaman, O.; Doren, D. J.; Raymand, D.; Hermansson, K. *J. Phys. Chem. A* **2010**, *114*, 9507−9514.
(23) Xiang, J. Y.; Ponder, J. W. *J. Chem. Theory Comput.* **2014**, *10*, 298−311.
(24) Shivaiah, V.; Das, S. K. *Angew. Chem.* **2006**, *118*, 251−254.
(25) Frank, P.; Benfatto, M.; Hedman, B.; Hodgson, K. O. *Inorg. Chem.* **2012**, *51*, 2086−2096.

(26) Bukharov, M. S.; Shtyrlin, V. G.; Mukhtarov, A. Sh.; Mamin, G. V.; Stapf, S.; Mattea, C.; Krutikov, A. A.; Il'in, A. N.; Serov, N. Yu. *Phys. Chem. Chem. Phys.* **2014**, *16*, 9411−9421.

(27) D'Angelo, P.; Bottari, E.; Festa, M. R.; Nolting, H.-F.; Pavel, N. V. *J. Phys. Chem. B* **1998**, *102*, 3114−3122.

(28) Krutikov, A. A.; Shtyrlin, V. G.; Spiridonov, A. O.; Serov, N. Yu.; Il'yin, A. N.; Gilyazetdinov, E. M.; Bukharov, M. S. *J. Phys.: Conf. Ser.* **2012**, *394*, 012031-1−012031-6.

(29) *Stability Constants of Metal-Ion Complexes. Part B. Organic Ligands*; Perrin, D. D., Ed.; Pergamon Press: Oxford, U.K., 1979.

(30) Yatsimirskii, K. B.; Kriss, E. E.; Gvjazdovskaja, V. L. *Stability Constants of Metal Complexes with Bioligands*; Naukova Dumka: Kiev, 1979. (in Russian).

(31) Shtyrlin, V. G.; Gogolashvili, E. L.; Zakharov, A. V. *J. Chem. Soc., Dalton Trans.* **1989**, 1293−1297.

(32) Ilakin, V. S.; Shtyrlin, V. G.; Zakharov, A. V.; Konkin, A. L. *Russ. J. Gen. Chem.* **2002**, *72*, 349−357.

(33) Garipov, R. R.; Shtyrlin, V. G.; Safin, D. A.; Zyavkina, Yu. I.; Sokolov, F. D.; Konkin, A. L.; Aganov, A. V.; Zakharov, A. V. *Chem. Phys.* **2006**, *320*, 59−74.

(34) Stoll, S.; Schweiger, A. *J. Magn. Reson.* **2006**, *178*, 42−55.

(35) Tabbì, G.; Giuffrida, A.; Bonomo, R. P. *J. Inorg. Biochem.* **2013**, *128*, 137−145.

(36) Deshpande, S. V.; Sharma, R. K.; Srivastava, T. S. *Inorg. Chim. Acta* **1983**, *78*, 13−17.

(37) Szabò-Plànka, T.; Peintler, G.; Rockenbauer, A.; Gyõr, M.; Varga-Fàbiàn, M.; Institòrisz, L.; Balàzspiri, L. *J. Chem. Soc., Dalton Trans.* **1989**, 1925−1932.

(38) Schmidt, M. W.; Baldridge, K. K.; Boatz, J. A.; Elbert, S. T.; Gordon, M. S.; Jensen, J. H.; Koseki, S.; Matsunaga, N.; Nguyen, K. A.; Su, S.; Windus, T. L.; Dupuis, M.; Montgomery, J. A. *J. Comput. Chem.* **1993**, *14*, 1347−1363.

(39) Kohn, W.; Becke, A. D.; Parr, R. G. *J. Phys. Chem.* **1996**, *100*, 12974−12980.

(40) Becke, A. D. *J. Chem. Phys.* **1993**, *98*, 5648−5652.

(41) Lee, C. T.; Yang, W. T.; Parr, R. G. *Phys. Rev. B: Condens. Matter Mater. Phys.* **1988**, *37*, 785−789.

(42) Yanai, T.; Tew, D. P.; Handy, N. C. *Chem. Phys. Lett.* **2004**, *393*, 51−57.

(43) Schäfer, A.; Huber, C.; Ahlrichs, R. *J. Chem. Phys.* **1994**, *100*, 5829−5835.

(44) Feller, D. *J. Comput. Chem.* **1996**, *17*, 1571−1586.

(45) Schuchardt, K. L.; Didier, B. T.; Elsethagen, T.; Sun, L.; Gurumoorthi, V.; Chase, J.; Li, J.; Windus, T. L. *J. Chem. Inf. Model.* **2007**, *47*, 1045−1052.

(46) Balabanov, N. B.; Peterson, K. A. *J. Chem. Phys.* **2005**, *123*, 064107-1−064107-15.

(47) Cossi, M.; Rega, N.; Scalmani, G.; Barone, V. *J. Comput. Chem.* **2003**, *24*, 669−681.

(48) Kittl, W. S.; Rode, B. M. *J. Chem. Soc., Dalton Trans.* **1983**, 409−414.

(49) Deshpande, S. V.; Sharma, R. K.; Srivastava, T. S. *Inorg. Chim. Acta* **1983**, *78*, 13−17.

(50) Bonomo, R. P.; Calì, R.; Cucinotta, V.; Impellizzeri, G.; Rizzarelli, E. *Inorg. Chem.* **1986**, *25*, 1641−1646.

(51) Szabó-Plánka, T.; Peintler, G.; Rockenbauer, A.; Gyõr, M.; Varga-Fábián, M.; Institórisz, L.; Balázspiri, L. *J. Chem. Soc., Dalton Trans.* **1989**, 1925−1932.

(52) Pogni, R.; Baratto, M. C.; Busi, E.; Basosi, R. *J. Inorg. Biochem.* **1999**, *73*, 157−165.

(53) Szabó-Plánka, T.; Rockenbauer, A.; Korecz, L. *Magn. Reson. Chem.* **1999**, *37*, 484−492.

(54) Nagy, N. V.; Szabó-Plánka, T.; Rockenbauer, A.; Peintler, G.; Nagypál, I.; Korecz, L. *J. Am. Chem. Soc.* **2003**, *125*, 5227−5235.

(55) Shtyrlin, V. G.; Zyavkina, Y. I.; Gilyazetdinov, E. M.; Bukharov, M. S.; Krutikov, A. A.; Garipov, R. R.; Mukhtarov, A. S.; Zakharov, A. V. *Dalton Trans.* **2012**, *41*, 1216−1228.

(56) Prenesti, E.; Daniele, P. G.; Prencipe, M.; Ostacoli, G. *Polyhedron* **1999**, *18*, 3233−3241.

(57) Chen, J. W.; Auteri, F. P.; Budil, D. E.; Belford, R. L.; Clarkson, R. B. *J. Phys. Chem.* **1994**, *98*, 13452−13459.

(58) Chen, J. W.; Belford, R. L.; Clarkson, R. B. *J. Phys. Chem. A* **1998**, *102*, 2117−2130.

(59) Solomon, I. *Phys. Rev.* **1955**, *99*, 559−565.

(60) Bloembergen, N. *J. Chem. Phys.* **1957**, *27*, 572−573.

(61) Polnaszek, C. F.; Bryant, R. G. *J. Chem. Phys.* **1984**, *81*, 4038−4045.

(62) Hwang, L.-P.; Freed, J. H. *J. Chem. Phys.* **1975**, *63*, 4017−4025.

(63) Bennett, H. F.; Brown, R. D., III; Koenig, S. H.; Swartz, H. M. *Magn. Reson. Med.* **1987**, *4*, 93−111.

(64) Freeman, H. C.; Schoone, J. C.; Sime, J. G. *Acta Crystallogr.* **1965**, *18*, 381−392.

(65) Strandberg, B.; Lindqvist, I.; Rosenstein, R. *Z. Kristallogr.* **1961**, *116*, 266−289.

(66) Bertini, I.; Luchinat, C.; Parigi, G. *Adv. Inorg. Chem.* **2005**, *57*, 105−172.

(67) Román-Alpiste, M. J.; Martín-Ramos, J. D.; Castineiras-Campos, A.; Bugella-Altamirano, E.; Sicilia-Zafra, A. G.; Gonzáles-Pérez, J. M.; Niclós-Gutiérrez, J. *Polyhedron* **1999**, *18*, 3341−3351.

(68) Shtyrlin, V. G.; Zakharov, A. V.; Evgen'eva, I. I. *Zh. Neorg. Khim.* **1983**, *28*, 435−441.

(69) Zakharov, A. V.; Shtyrlin, V. G. *Rapid Ligand Exchange Reactions*; KSU: Kazan, 1985 (in Russian).

(70) Shtyrlin, V. G.; Zilberman, Ya. E.; Zakharov, A. V.; Evgen'eva, I. I. *Zh. Neorg. Khim.* **1982**, *27*, 2291−2295.

(71) Kivelson, D.; Neiman, R. *J. Chem. Phys.* **1961**, *35*, 149−155.

(72) Kon'kin, A. L.; Shtyrlin, V. G.; Zabirov, N. G.; Aganov, A. V.; Zapechelnyuk, L. E.; Zakharov, A. V. *Zh. Neorg. Khim.* **1996**, *41*, 1156−1167.

(73) Freeman, H. C.; Snow, M. R.; Nitta, I.; Tomita, K. *Acta Crystallogr.* **1964**, *17*, 1463−1470.