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Ternary complexes of *cis*- and *trans*-$Pt(NH_3)_2Cl_2$ (*cis*-, *trans*-DDP) with 9-methylguanine (9-MeG), the dipeptides glycylglycine (glygly), glycyl-L-alanine (glyala), glycyl-L-2-aminobutyric acid (gly-2-aba), glycyl-L-norvaline (glynval), glycyl-L-norleucine (glynleu), and of *trans*-$Pt(NH_3)_2Cl_2$ with Na-L-acetylhistidine

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Abstract

The reactions of *cis*- and *trans*-$[(NH_3)_2Pt(9\text{-MeG})X]Y$ ($X=Cl$, H_2O; $Y=Cl$, NO_3, BPh_4) with the dipeptides glygly, glyala, gly-2-aba, glynval and glynleu, and of *trans*-$[(NH_3)_2Pt(9\text{-MeG})X]Y$ with the sodium salt of Na-L-acetyl-histidine in aqueous solutions, produced the analytically pure ternary complexes *cis*- and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(glygly)]Y_n$, ($n=1$, 2) (**1A**, **1B**), *cis*- and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(glyala)]Y_n$, (**2A**, **2B**), *cis*- and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(gly\text{-}2\text{-}aba)]Y_n$ (**3A**, **3B**), *cis*- and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(glynval)]Y_n$ (**4A**, **4B**), *cis*- and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(glynleu)]Y_n$ (**5A**, **5B**) and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(achis\text{-}N_1,N_3)](NO_3)$. These were characterized in the solid state with elemental analysis, IR, ^1H NMR and ^{195}Pt NMR spectra. 9-MeG retains its N_7 coordination in the ternary complexes. Hydrophobic intramolecular ligand–ligand interactions were detected in the *cis*-ternary systems with ^1H NMR spectra, between 9-MeG and the dipeptides, increasing with the length of the aliphatic side chain of the latter. These were much weaker in the *trans* series, and might be of intermolecular nature. The *trans*-$[(NH_3)_2Pt(9\text{-MeG})(achis\text{-}N_1)]NO_3$ and *trans*-$[(NH_3)_2Pt(9\text{-MeG})(achis\text{-}N_3)](NO_3)$ contained achis coordinated through the N_1 and N_3 atoms in a ratio of 0.8.

Keywords: Platinum complexes; Amino acid complexes; Peptide complexes

1. Introduction

The simplest models of DNA–Pt–protein crosslinks known to take place in vivo with both *cis* and *trans*-DDP [1–4] and possibly related to the toxicity of the antitumor drug *cis*-DDP [5] are the ones containing Pt(II), amino acids–peptides (proteins) and nucleobases–nucleotides (DNA).

Recently, we prepared and studied such ternary complexes containing amino acids–peptides with increasing aliphatic side chain and nucleobases–nucleosides [6–16]. Hydrophobic (aliphatic–aromatic) ligand–ligand interactions were detected in these systems, increasing with the aliphatic side chain of the amino acids–peptides [9,10].

Continuing our studies on similar systems, we report here on ternary complexes of *cis*- and *trans*-DDP of the general formulae *cis*- and *trans*-$[(NH_3)_2Pt(dipeptide)(9\text{-MeG})]Y_n$ ($n=1, 2$), where dipeptide is glygly (**1A**), glyala (**2A**), gly-2-aba (**3A**), glynval (**4A**), glynleu (**5A**), for the *cis* analogues, and (**1B**), (**2B**), (**3B**), (**4B**) and (**5B**) for the *trans* analogues correspondingly, and $Y=BPh_4^-, NO_3^-, Cl^-$. The properties of the complexes of the two series are also compared.

On the other hand, histidine residues in Zn-finger proteins interact with DNA through a hydrogen bridge involving their N_3 atoms and guanine N_7 atoms [17]. Replacing this weak hydrogen bridge by a metal with square planar coordination like Pt(II) could result in

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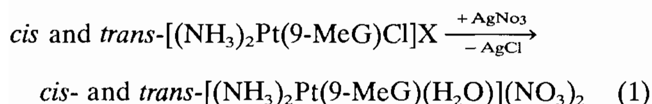
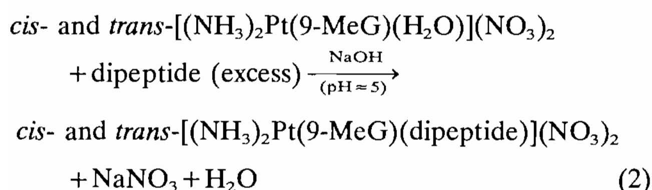
a stronger bonding between the protein and DNA. As a good model for such a bonding we also prepared and studied the ternary complex *trans*-$[(NH_3)_2Pt(9\text{-}MeG)(achis)](NO_3)$.

2. Results and discussion

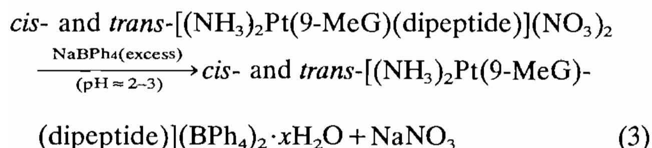
The reactions for the preparation of the two series of complexes started with the mononucleobase derivative [18,19], as follows:



$$cis \text{ and } trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)Cl]X \xrightarrow[-AgCl]{+AgNo_3} cis\text{- and } trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(H_2O)](NO_3)_2 \quad (1)$$



$$cis\text{- and } trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(H_2O)](NO_3)_2 + \text{dipeptide (excess)} \xrightarrow[(pH \approx 5)]{NaOH} cis\text{- and } trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(\text{dipeptide})](NO_3)_2 + NaNO_3 + H_2O \quad (2)$$



$$cis\text{- and } trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(\text{dipeptide})](NO_3)_2 \xrightarrow[(pH \approx 2\text{–}3)]{NaBPh_4(excess)} cis\text{- and } trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(\text{dipeptide})](BPh_4)_2 \cdot xH_2O + NaNO_3 \quad (3)$$

$NaBPh_4$ was used for precipitation of the complexes. Depending on pH, one or two BPh_4^- ions were retained by the complexes with subsequent ionization of the terminal carboxylate group of the peptides. For the spectroscopic IR and ^1H NMR studies however, NO_3^- or Cl^- salts were also used.

Elemental analyses and other data of the isolated complexes are given in Table 1.

2.1. IR spectra

Characteristic IR frequencies of the compounds are listed in Table 2. In the 3000–3500 cm^{-1} region, the overlap of the various νNH, νOH and νCH of the peptides, the nucleobase 9-MeG, the ammonia molecules, and waters of hydration prevent the recognition of each individual absorption. A massive absorption is observed near 2300–2500 cm^{-1} in the deuterated complexes. Attempted assignments are given in Table 2.

In the region below 1700 cm^{-1} however, deuteration experiments in combination with other similar literature studies [9,14,15,20], give us good indications for the binding sites of Pt(II) with both ligands. The use of the chloride salts of the complexes, though not very pure analytically, containing small amounts of $NaNO_3$, permits the clear observation of this region. Thus, the intense absorption with maxima at about 1680, 1630 and 1600 cm^{-1}, and the individual medium intensity band at 1540 cm^{-1} for all the complexes are assigned as follows. The near 1680 cm^{-1} strong band is due to the νC=O of the protonated carboxylate group of the peptide [9,21] and not removed upon deuteration. The near 1630 cm^{-1} band is due to the free δNH_2 of the coordinated 9-MeG, shifted to near 1200 cm^{-1} in the deuterated derivatives [14,15]. The near 1600 cm^{-1} band is assigned to the deprotonated carboxylate (νC=O) frequency of the coordinated peptide, coupled with ring stretchings (νC=N, νC=C) [14,15,20]. Finally, the near 1540 cm^{-1} band is due to the coordinated terminal amino group of the dipeptide, shifted also to about 1200 cm^{-1} upon deuteration (NH/ND = 1.33).

The coordination of 9-MeG to Pt(II) should be through the N_7 atom as in the starting complexes [14,15,18,20] because (i) the νC=O frequency of the carbonyl group at the 6 position of 9-MeG is not removed, implying retention of the N_1–H protonation, and (ii) the 9-MeG ring breathing motion occurring at

Table 1
Elemental analysis of the complexes

Compound	C (%)	N (%)	H (%)	Pt (%)	Yield (%)	pH of isolation
1A·$3H_2O$	56.5(56.1)[a]	12.1(12.9)	5.7(5.4)	17.8(18.0)	15	2.5
2A·$5H_2O$	49.5(49.0)	11.7(12.2)	4.6(4.6)	17.1(17.0)	12	2.5
3A·$6H_2O$	53.5(53.2)	13.0(13.0)	5.2(5.0)	15.2(16.0)	10	2.5
4A·$5H_2O$	49.0(49.4)	9.7(9.9)	5.9(5.6)	15.0(15.3)	12	2.5
5A·$6H_2O$	48.8(49.0)	9.5(9.2)	6.1(5.9)	14.7(14.5)	12	2.5
1B·$4H_2O$[b]	44.5(44.2)	13.7(13.8)	5.6(5.7)	21.3(21.9)	15	3.8
2B·$6H_2O$	54.5(54.2)	9.9(10.4)	5.9(4.8)	15.2(15.0)	13	2.5
3B·$6H_2O$	55.4(55.3)	9.7(9.3)	5.8(5.3)	15.0(14.5)	11	2.5
4B·$5H_2O$[c]	21.7(21.7)	19.7(19.5)	4.6(3.9)	24.9(25.4)	10	3.5
5B·$6H_2O$	48.8(49.1)	9.5(9.8)	6.1(5.9)	14.7(14.0)	12	2.5

[a]The number in parentheses is the experimental value.
[b]This compound contains only one BPh_4^- ion, with deprotonated peptide.
[c]This compound is the nitrate (NO_3^-) salt.

Table 2
Characteristic IR frequencies of the complexes

Compounds	νNH_2 9-MeG + peptide	$\nu CH(CH_2,CH_3)$ 9-MeG + peptide	δNH_2 9-MeG	δNH_2 peptide	$\nu_{asym}C=O$ 9-MeG + peptide	$\nu_{asym}COO^-$ peptide	Ring breathing	Ring stretchings
cis-[$(NH_3)_2Pt(9\text{-}MeG)Cl$]Cl	3900sbr	2920sh	1628s		1690s		620m	1580s, 1500m
trans-[$(NH_3)_2Pt(9\text{-}MeG)Cl$]Cl	3250sbr	2920sh	1640ssh		1670s		625m	1580s, 1500m
1A	3245msh	2980sh, 2940sh	1640s	1540m	1680m	1608s	640w	1580msh, 1495m
2A	3240sbr	2920sh	1630sh	1550msh	1688s, 1680s	1600msh	630w	1590msh, 1500m
3A	3277sbr	2961sh	1632s	1559msh	1637sh	1595s	638wsh	1595s, 1498m
3A deuterated	2855sbr	2918sh, 2860sh	1202sbr	1202sbr	1672sh	1587s	640w	1587m, 1500w
4A	3250sbr	2910sh	1630sh	1550msh	1680s	1615msh	630w	1600s, 1500w
5A	3293sbr	2928sh, 2910sh	1632s	1559msh	1670s	1620s	634w	1600s, 1498w
1B	3269sbr	2936sh	1630ssh	1559msh	1685s	1605ssh	634w	1587s, 1498m
2B	3264sbr	2930sh, 2917sh	1620sh	1551msh	1688s	1600ssh	627w	1583s, 1497m
3B	3247sbr	2921s	1641s, 1622s	1553msh	1680s	1600s	626w	1588s, 1497m
3B deuterated	2895sbr	2918sh, 2860sh	1202sbr	1202sbr	1674sh	1587s	640w	1587m, 1500w
4B	3283sbr	2459m, 2919m	1657s	1588msh	1685s	1602s	639w	1582s, 1503m
5B	3275sbr	2951sh, 2932sh	1649s	1555s	1680s	1632s	629w	1582s, 1500m

w = weak, m = medium, s = strong, vs = very strong, br = broad, sh = shoulder.

about 650 cm^{-1} in the free guanine derivatives is shifted near 620–630 cm^{-1} in the ternary complexes [14,22,23].

2.2. ^1H NMR spectra

The ^1H NMR spectra of the ternary complexes and anionic forms of the various dipeptides are given in Table 3. The H_8 proton of 9-MeG shifts upfield by 0.03–0.09 ppm (see Table 3) on passing from the starting 1:1 *cis* complex to the ternary ones and by 0.02–0.04 ppm from the analogous *trans* complex to the corresponding ternary ones. This proves the retention of the N_7 coordination of the base in the ternary complexes in solution, as expected [14,15,20]. The slightly larger upfield shifts in the *cis* compared to the *trans* series is a first indication for the stronger hydrophobic ligand–ligand interactions in the former case.

The N_7 coordination of 9-MeG and the lack of coordination to Pt(II) of the terminal carboxylate group of the peptides are also substantiated from the ^1H NMR chemical shifts as functions of pD of the protons of the ternary complex *trans*-[$(NH_3)_2Pt(9\text{-}MeG)(glynval)$]($NO_3$) and the free peptide glynval from pD 1.3 to 13.95 (see Fig. 1).

Values of $pK_1 \approx 3.2$ and $pk_2 \approx 7.6$ were found for the free peptide, glynval, corresponding to the deprotonation of carboxylate and the amino groups, respectively. These values agree with the literature data [19,24,25]. For the complexed peptide in the ternary complexes, on the other hand, the values of $pk_1 \approx 3.1$ and $pk_2 \approx 8.8$ are also estimated and assigned to the carboxylate and the N_1 site of 9-MeG, respectively. The pk_2 value of 8.8 for the N_1–H of 9-MeG is only about 1 logarithmic unit lower than that of the free base [26]. It is found around 8.2 in other Pt(II) complexes [27–29]. The smaller lowering of p*k* in the present case may be due to the inductive effect of the bulky aliphatic side chain group of the peptide [30].

The positive difference in the chemical shifts of the terminal methyl groups of the free dipeptides (anionic forms) minus the ones of the Pt(II)–amino-coordinated and carboxylate deprotonated dipeptides ($\Delta\delta = \delta$(peptide anion) $-\ \delta$(complex)) versus the dipeptides has been used as a measure of the strength of aromatic–aliphatic (nucleobase–peptide) ligand–ligand interactions in aqueous solutions [14,15,31,32]. Also the positive value of the difference in the chemical shifts of the various protons of the dipeptide glynval in the zwitterionic form minus the ones of the ternary complexes ($\Delta\delta = \delta$(peptide zwitterion) $-\ \delta$(complex)) measures the strength of the hydrophobic interactions for the various ligand protons [14,15,31,32]. The results are shown in Fig. 2 and Table 4. The glygly is not included in Fig. 2(a) showing downfield shifts (no ligand–ligand interactions).

Table 3
^{1}H NMR chemical shifts of the compounds (ppm)

Compound	pD	Nucleobase protons		Peptide protons						$\Delta\delta CH_{term}$ = δ(peptide) − δ(complex)
		H(8)	N–CH_3	N-term. gly −CH_2−	αCH	C-term. amino acid βCH	γCH	δCH	εCH	
Glygly	4.7			3.8573s	3.8295s					
1A	3.5	8.1520s	3.7500s	4.1350s	4.0850s					
1B	3.1	8.25715s	3.7233s	4.0057s	3.8838s					
Glyala	4.6			3.8204s	4.1846q	1.3550d				
	12.6			3.3179s	4.1611q	1.3391d				
2A	4.5	8.2038s	3.8563s	4.0811s	4.3512q	1.2790d				0.0601
	3.5	8.2118s	3.8575s	4.0823s	4.4200q	1.2808d				
2B	4.3	8.2400s	3.7451s	3.9805s	4.2935q	1.3791d				−0.0400
	3.1	8.2461s	3.7500s	3.9822s	not obs.	1.3802d				
Gly-2-aba	4.5			3.8448s	4.1130q	1.7616m	0.9127t			
	12.5			3.3413s	4.1094q	1.7372m	0.8962t			
3A	4.6	8.1648s	3.7967s	3.9985s	not obs.	1.6641m	0.7125t			0.1837
	3.0	8.1777s	3.8016s	4.0172s	not obs.	1.6738m	0.7241t			
3B	4.8	8.2295s	3.7400s	4.0105s	not obs.	1.7512m	0.9027t			−0.0065
	4.0	8.2411s	3.7482s	4.0236s	not obs.	1.7645m	0.9132t			
Glynval	6.3			3.8325s	4.1891q	1.7120m	1.3582m	0.8969t		
	12.6			3.3323s	4.1685q	1.7048m	1.3309m	0.8904t		
4A	5.3	8.1534s	3.7621s	3.9554s	4.1200q	1.7116m	1.3562m	0.6924t		0.1980
4B	4.0	8.2510s	3.7627s	3.8501s	4.1661q	1.7141m	1.3580m	0.8967t		
	4.8	8.2561s	3.7256s	3.8402s	4.1702q	1.7106m	1.3412m	0.8953t		−0.0049
Glynleu	4.6			3.8323s	4.1546q	1.7376m		1.2996m	0.8682t	
	12.5			3.3314s	4.1579q	1.7091m		1.3054m	0.8660t	
5A	4.8	8.2085s	3.7806s	3.9927s	4.1100q	1.7285m		1.2530m	0.6505t	0.2155
	3.0	8.2128s	3.7880s	3.9942s	not obs.	1.7316m		1.2835m	0.6571t	
5B	5.0	8.2187s	3.7418s	3.8656s	4.1490q	1.7319m		1.2719m	0.8670t	−0.0010
	3.8	8.2396s	3.7476s	3.8713s	not obs.	1.7339m		1.2876m	0.8691t	

s: singlet, d: doublet, t: triplet, q: quartet, m: multiplet, dd: doublet doublet.

Table 4
Chemical shifts of the various protons of nval, in glynval, in *cis*- and *trans*-[$(NH_3)_2$Pt(9-MeG)(glynval)](NO_3)

Amino acid protons	Nval zwitterion	Chemical shifts 4A	4B	Δδ $\delta_{pept}-\delta_{cis}$	$\delta_{pept}-\delta_{trans}$	$\delta_{trans}-\delta_{cis}$
α	4.1891	4.1200	4.1702	0.0691	0.0189	0.0502
β	1.7210	1.7116	1.7106	0.0094	0.0104	−0.0010
γ	1.3582	1.3562	1.3412	0.0020	0.0170	−0.0015
δ	0.8969	0.6924	0.8953	0.2045	0.0016	0.2029

The ligand–ligand interactions were always weaker in the *trans* series of complexes [6,9,10,13,15] compared to the *cis* series. The same is also true in the present system, e.g. in the *cis* series of complexes Δδ (ppm) is always positive, starting with glyala and increasing gradually to glynleu, Fig. 2(a). In the *trans* series however, Δδ (ppm) is always negative, showing the absence of such interactions. Here again however the negative values decrease, approaching zero, with increasing aliphatic side chain of the peptides. The situation is similar to the *cis*- and *trans*-[$(NH_3)_2$Pt(nucl)-(amac)](NO_3) series [14,15] and may be intramolecular in the *cis* and intermolecular in the *trans* complexes.

Comparing the strength of the ligand–ligand interactions ($\Delta\delta > 0$) of the various protons in the ternary complexes of glynval, again the α protons of nval, near the bonding sites, are the most upfield shifted compared to the others, except the terminal methyl in the *cis* series, and more in the *cis* than the *trans* series [9,13,15] (Fig. 2(b)). This is also seen in Table 4 (Δδ (ppm) $= \delta_{trans} - \delta_{cis}$) which is positive for the α and δ protons and near zero for the β and γ protons. The terminal methyl group (δ proton) for glynval is the most upfield shifted of all, in the *cis* complex, in agreement with Fig. 2(a).

Finally, the reaction of *trans*-[$(NH_3)_2$Pt(9-MeG)-(H_2O)]$(NO_3)_2$ with the sodium salt Na-L-acetylhistidine

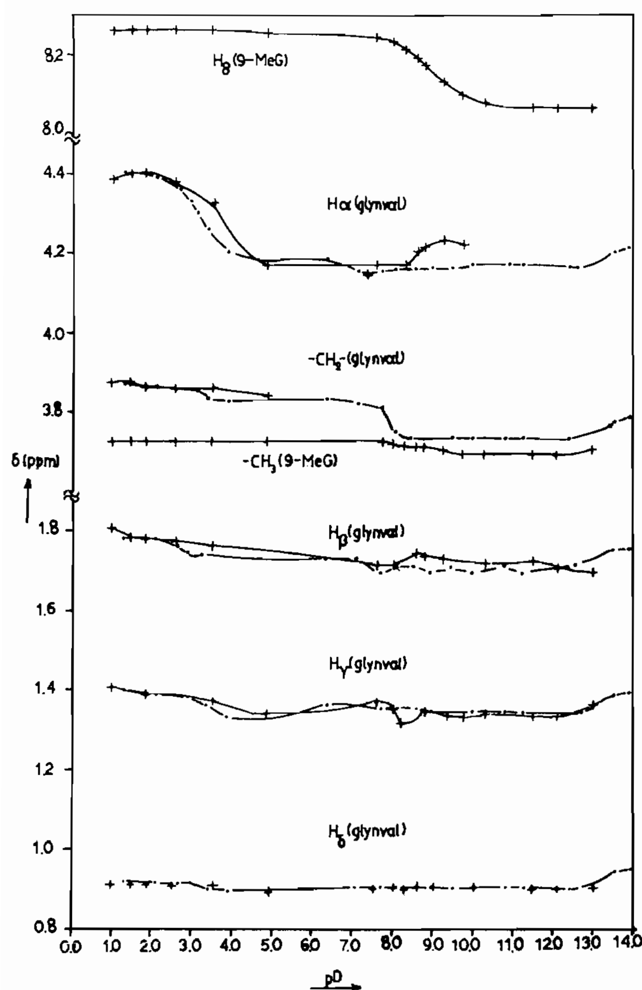
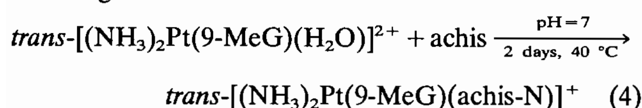


Fig. 1. pD dependence of the ^{1}H NMR chemical shifts of resonances of glynval (●) and *trans*-$[(NH_3)_2Pt(9\text{-}MeG)(glynval)](NO_3)$ (+).

(achis) was attempted at constant pH = 7 in 1:2 metal:ligand ratio.



$$trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(H_2O)]^{2+} + \text{achis} \xrightarrow[2\ \text{days},\ 40\ °C]{pH=7} trans\text{-}[(NH_3)_2Pt(9\text{-}MeG)(\text{achis-N})]^{+} \quad (4)$$

The ^{1}H NMR spectrum of the crude product shows, besides the free ligand in excess, two sets of peaks assigned to the *trans*-$[(NH_3)_2Pt(9\text{-}MeG)(\text{achis-}N_1)](NO_3)$ and *trans*-$[(NH_3)_2Pt(9\text{-}MeG)(\text{achis-}N_3)](NO_3)$ species containing N_1 and N_3 bonded histidine, respectively (see Fig. 3). The methine resonance of achis in the first N_1 bonded to Pt(II) complex is slightly upfield shifted ($\Delta\delta = 0.1$ ppm) compared to that of the free amino acid, while that of the second N_3 bonded complex is downfield shifted ($\Delta\delta = 0.6$ ppm).

Metal coordination of N_3 achis is expected to hinder the rotation around the CH_2-CH bond, while coordination at N_1 has little effect, being relatively remote from this bond [33]; this may explain this difference in chemical shifts. Another reason might be the possible existence of hydrogen bonding between the amide hydrogen of the N_3 coordinated achis with the O_6 of guanine (see Fig. 4). The assignment of the imidazole protons to the two isomers was based on a 2D-COSY spectrum.

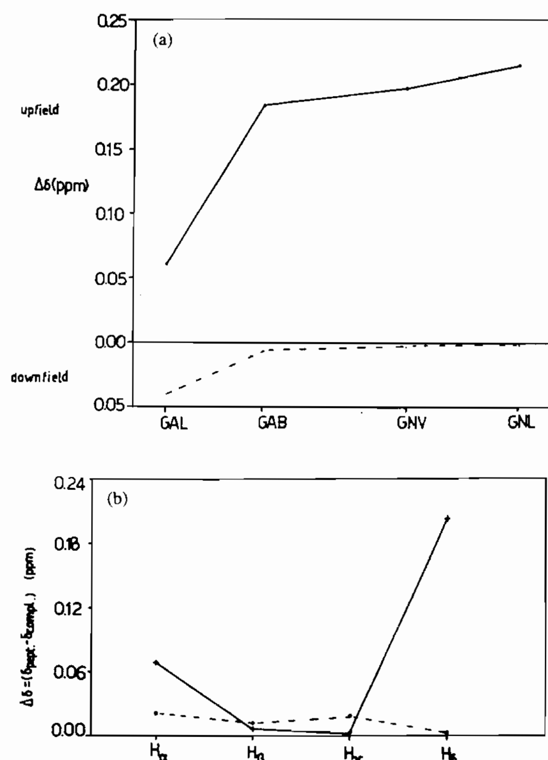


Fig. 2. (a) Plot of $\Delta\delta$ (ppm) = δ(peptide) − δ(complex) of the terminal methyl groups of the anionic forms of the $-NH_2$ *cis* (solid line) and *trans* (dotted line) coordinated peptides, as a function of the peptides. (b) Plot of the difference $\Delta\delta$ (ppm) = δ(peptide) − δ(complex) of the free zwitterionic forms of the dipeptide glynval and its *cis* (solid line) and *trans* (dotted line) complexed forms, as a function of the various nval protons. Abbreviations: GAL = glyala, GAB = gly-2-aba, GNV = glynval, GNL = glynleu.

Finally, the ^{195}Pt NMR spectrum confirms the two N_1 and N_3 coordinated achis by showing two partially overlapping peaks at −2470 and −2493 ppm [34]. The ratio of N_1 to N_3 coordinated achis species is 0.8, similar to the ratio of the two tautomers of free achis [35] (Scheme 1), as integration of the ^{1}H NMR spectra showed.

3. Experimental

3.1. Materials

The L-amino acids used for the preparation of the dipeptides and t-BOC-gly were purchased from Aldrich Chemical Company and used without further purification. *Cis*- and *trans*-DDP were prepared from K_2PtCl_4 (Degussa A.G. Germany) according to the published methods [36–38]. The dipeptides were synthesized according th the known method of coupling via DCC

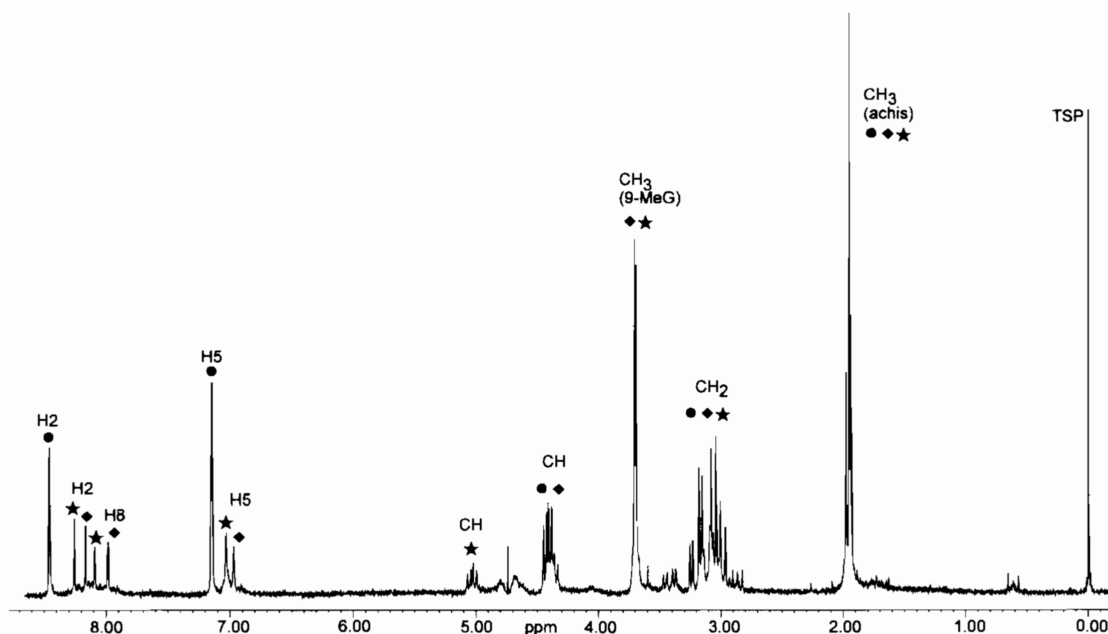


Fig. 3. ^1H NMR spectrum of the reaction of *trans*-[$(NH_3)_2Pt$(9-MeG)(H_2O)]$(NO_3)_2$ with Na-L-acetylhistidine (D_2O, pD = 6.8). ♦, *trans*-[$(NH_3)_2Pt$(9-MeG)(achis-N_1)](NO_3); ★, *trans*-[$(NH_3)_2Pt$(9-MeG)(achis-N_3)](NO_3); ●, Na-L-acetylhistidine.

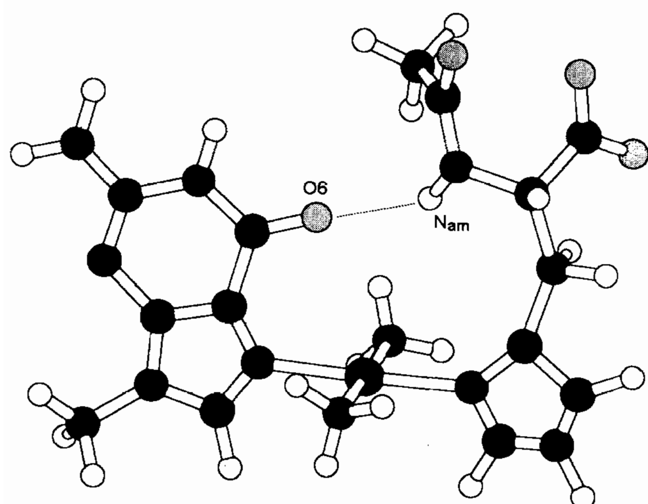
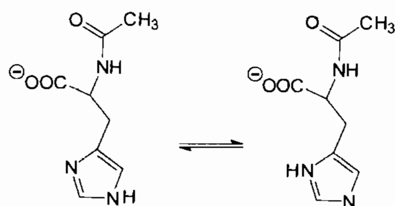


Fig. 4. Ball–stick model of *trans*-[$(NH_3)_2Pt$(9-MeG)(achis-N_3)](NO_3).



Scheme 1. The two tautomeric forms of Na-acetyl-L-histidine.

with 1-hydroxybenzotriazole and were all analytically pure and had IR and ^1H NMR spectra consistent with their structure. The complexes *cis*-[$(NH_3)_2Pt$(9-MeG)Cl](NO_3) and *trans*-[$(NH_3)_2Pt$(9-MeG)Cl](NO_3) were also prepared according to published methods [15,18,19].

3.2. Methods

The elemental analyses were carried out in the Analytical Laboratory of the University of Dortmund. The IR spectra were recorded on Perkin–Elmer model 580 and 880 spectrophotometers in the region 4000–200 cm^{-1} in KBr pellets or Nujol mulls. The ^1H NMR spectra were recorded on AM-300 and AM-220 Brucker spectrometers (0.1 M; D_2O; TSP as internal standard). The pD values were measured with a glass electrode and obtained by adding 0.4 units to the meter reading.

3.3. Preparation of the complexes

0.5 mmol of the binary *cis*- or *trans*-[$(NH_3)_2Pt$(9-MeG)Cl]Cl complex and 0.5 mmol of solid $AgNO_3$ were stirred in 5 ml of water at room temperature for one day without sunlight. The AgCl formed was centrifuged and after filtration the solution was allowed to react for 2 days with 2 mmol of the corresponding dipeptide at 30 °C, by keeping the pH of the solution nearly constant, to about 5. The solution was then evaporated to dryness, redissolved in 3 ml of H_2O, centrifuged, and after filtration it was passed through a Sepharose CM-fast flow column (cation exchanger) as already described [15]. The fractions were evaporated to dryness and contained also $NaNO_3$ or NaCl. They were isolated in an analytically pure form, as BPh_4^- or NO_3^- salts, as follows. The solid was dissolved in a minimum volume of water and a concentrated solution of $NaBPh_4$ was added dropwise. The resulting precipitates were filtered, washed with water, and dried over $CaCl_2$ and P_4O_{10} in vacuum. For the NO_3^- salts, the

BPh_4^- salts were dissolved in acetone and small amounts of $LiNO_3$ were added. The resulting precipitate was filtered, washed with acetone and ether, and dried in vacuum over $CaCl_2$ and P_4O_{10}. The final yields of the complexes were 10–15%.

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