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Structural features and *in silico* prediction of the biological properties of a pyrazole-based coordination complex

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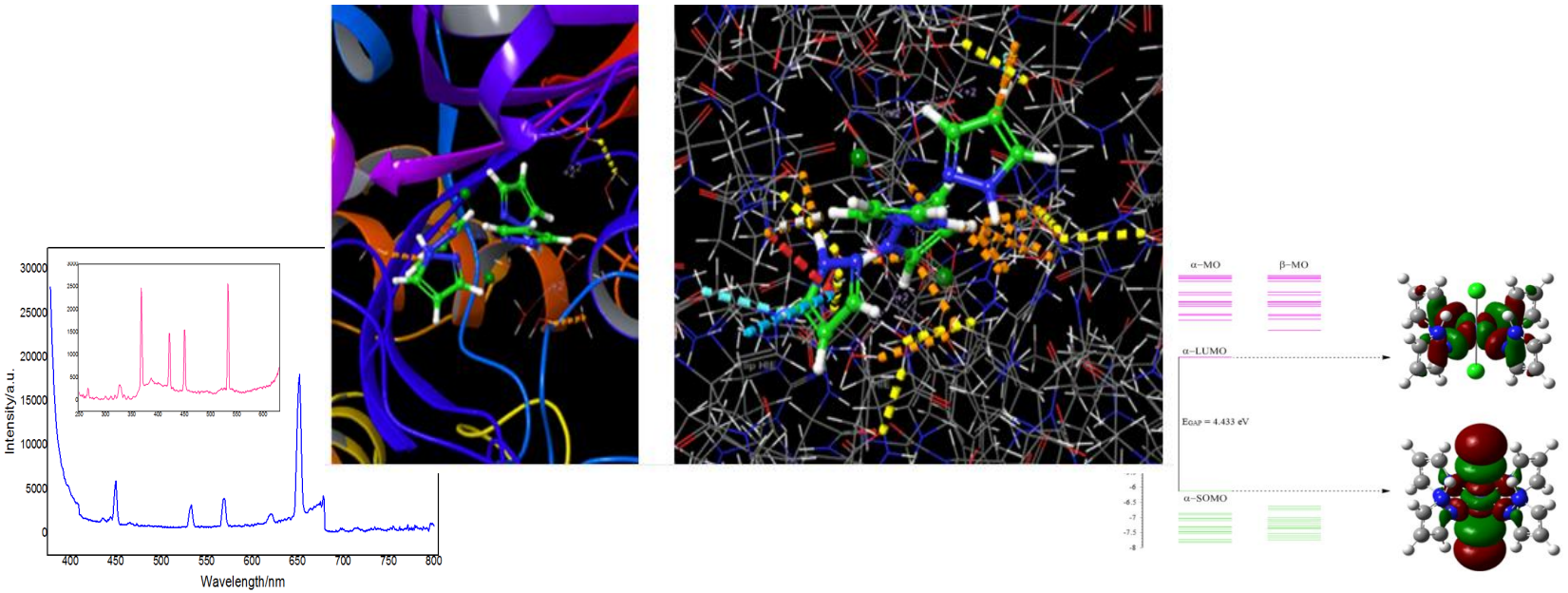
LASPI²A

Structural features and *in silico* prediction of the biological properties of a pyrazole-based coordination complex

Graphical Abstract



Abstract:
A pyrazole-based Co(II) complex, was synthesized and structurally characterized using single-crystal X-ray diffraction which showed that it crystallizes in the monoclinic *C*2/*c* space group with discrete [$CoPz_4Cl_2$] units held together *via* intra- and intermolecular hydrogen bonds. The structure was optimized, the MEP maps were obtained and the NLO properties estimated. Additionally, the optical properties were measured at room temperature by means of optical UV-visible absorption and photoluminescence spectroscopy, and the complex presented $\pi \rightarrow \pi^*$, $n \rightarrow \pi^*$, $d \rightarrow d$ and ligand-field transitions resulting in a predominant bright red photoluminescence. Furthermore, an *in silico* study was carried by estimating the binding ability of the cobalt complex with *Staphylococcus aureus* tyrosyl-tRNA synthetase and *Pyrococcus kodakaraensis* aspartyl-tRNA synthetase.

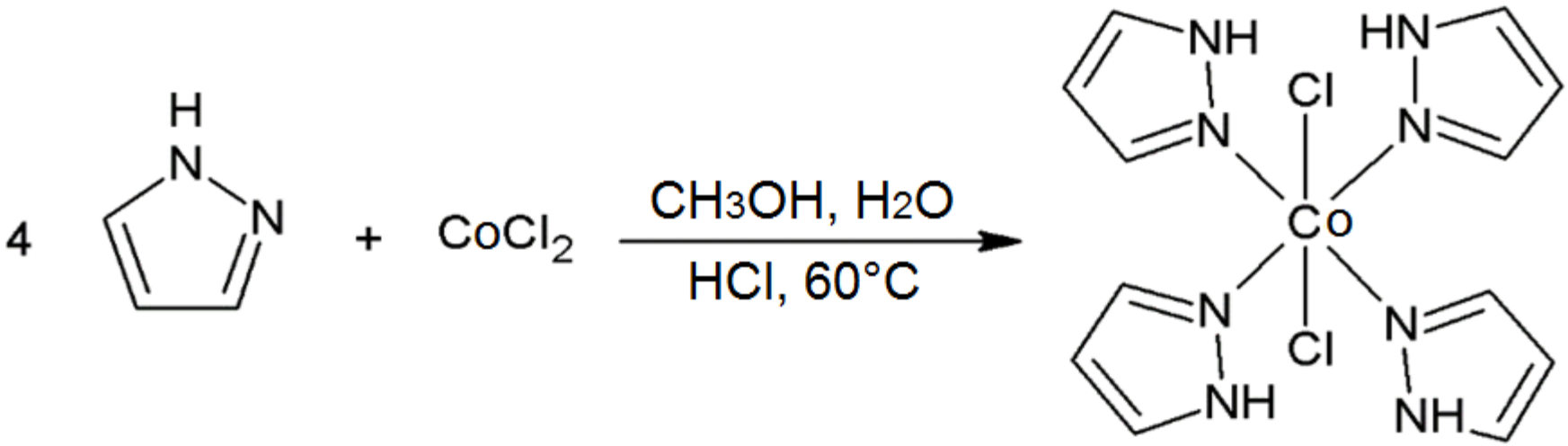
Keywords: Pyrazole-based complex, crystal structure, photoluminescence, *in silico* study, molecular docking.

Introduction

Pyrazole derivatives have been widely studied for their applications as analgesic [1], antibacterial [2], anti-hyperglycemic [3], anti-inflammatory [4], antipyretic [5], hypoglycaemic [6] and sedative hypnotic agents [18]. For instance, *celecoxib*, *rimonabant*, *fomepizole* and *sildenafil* were reported to be selective drugs [7]. In fact, *celecoxib* demonstrated an anti-inflammatory effect and inhibited cox-2 [8], whereas *rimonabant* is considered as a cannabixiod receptor and is used for obesity treatment. On the other hand, *Bindenafil* and *fomepizole* are known for inhibiting phosphodiesterase and alcohol dehydrogenase, respectively [9]. Additionally, some pyrazole derivatives have non-nucleoside HIV-1 reverse transcriptase inhibitory activities [10-13], their metallic complexes are active metallobiomolecules and have shown excellent antibacterial and antifungal efficiency [14-16]. In order to contribute to the enrichment of these systems study, we will discuss the synthesis of a pyrazole-based cobalt(II) complex [17] together with its structural and physical properties. Furthermore, an *in silico* study of the complex was performed in order to estimate its biological activity towards *Staphylococcus aureus* tyrosyl-tRNA synthetase and *Pyrococcus kodakaraensis* aspartyl-tRNA synthetase using molecular docking calculations.

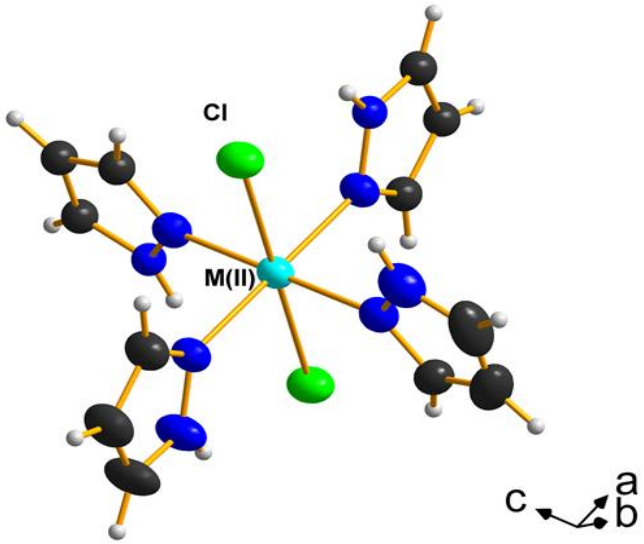
Results and discussion

Synthesis



Results and discussion

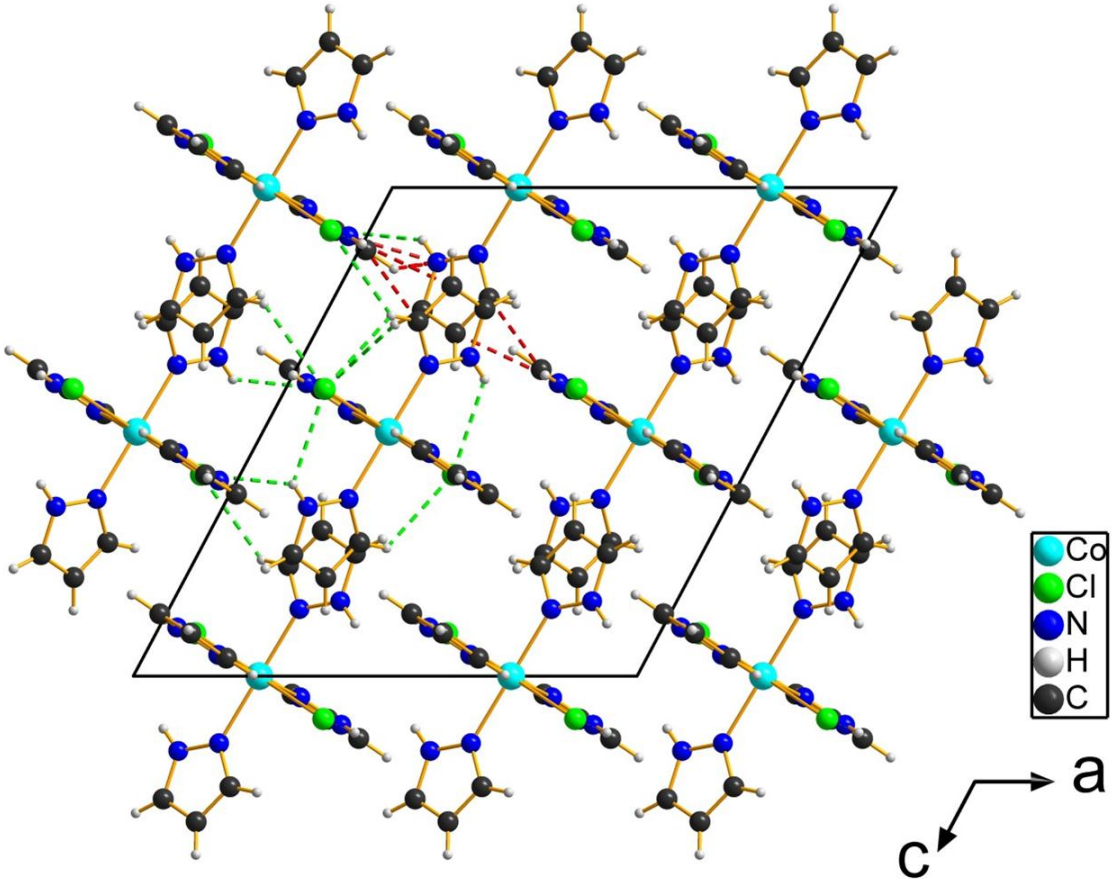
Crystal structure



Space Group	C2/c
a (Å)	13.6170(1)
b (Å)	9.2934(5)
c (Å)	14.9550(1)
β (°)	117.920(1)
$R[F^2 > 2\sigma(F^2)]$	0.0424
$wR(F^2)$	0.0952
$\Delta\rho_{max}$, $\Delta\rho_{min}$ (e $Å^{-3}$)	0.36, –0.30

Results and discussion

Crystal structure



Results and discussion

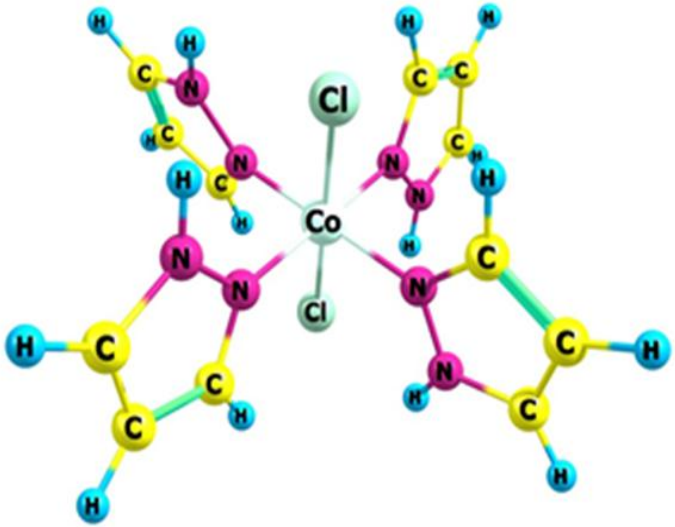
Crystal structure

D—H···A	D—H	H···A	D···A	D—H···A
N2—H2N···Cl1^{ii}	0.86	3.05	3.739 (3)	139
N4—H4N···Cl1	0.86	2.53	3.138 (2)	129
C3—H3···Cl1	0.93	2.74	3.324 (2)	121

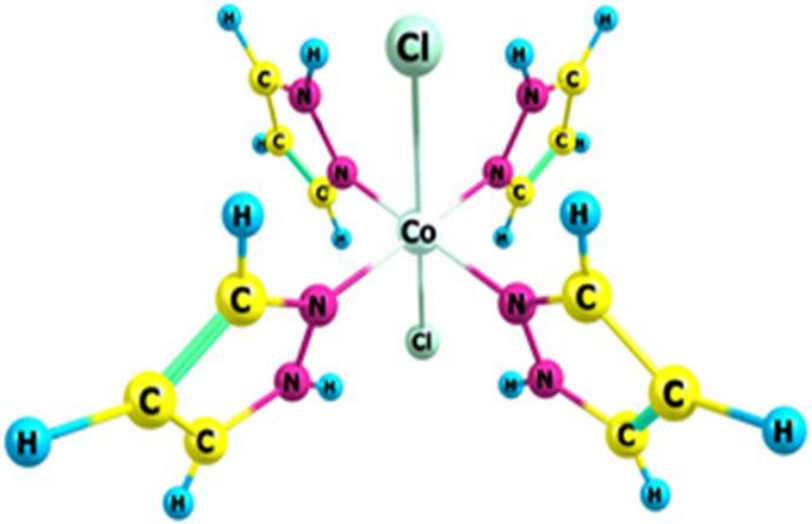
Results and discussion

Optimized structure

Quantum chemical calculations were performed by GaussView 5.0.9 [18] and Gaussian 09 AS64L-G09RevD.01 [19] programs, by using HF and B3LYP methods with 6-31+G(d)(LANL2DZ) mix basis sets in gas phase.



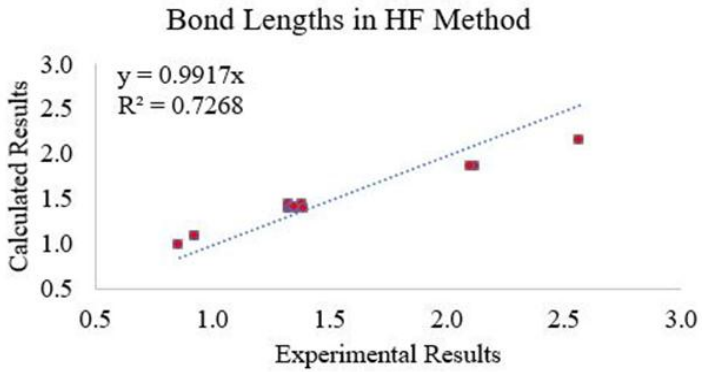
HF/6-31+G(d)(LANL2DZ)

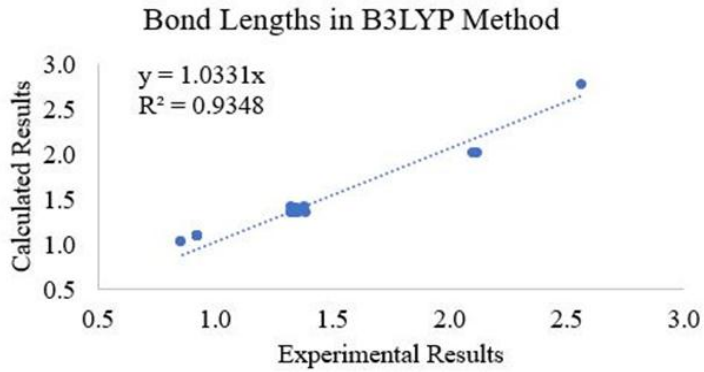


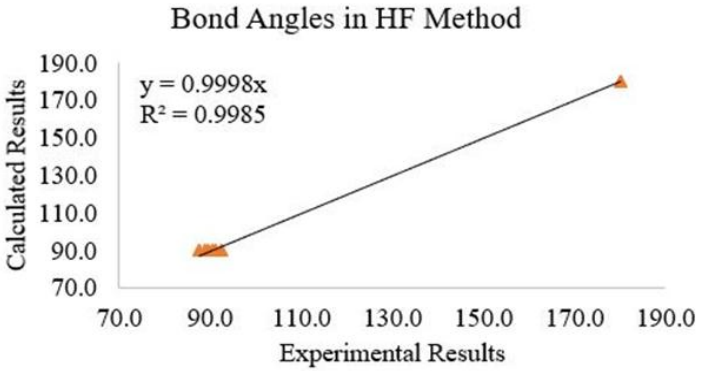
B3LYP/6-31+G(d)(LANL2DZ)

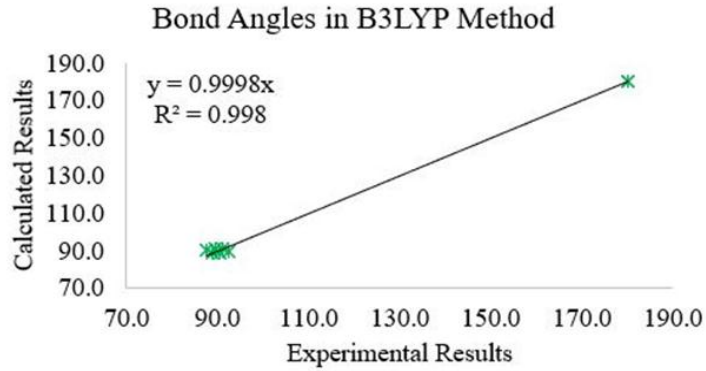
Results and discussion

Optimized structure



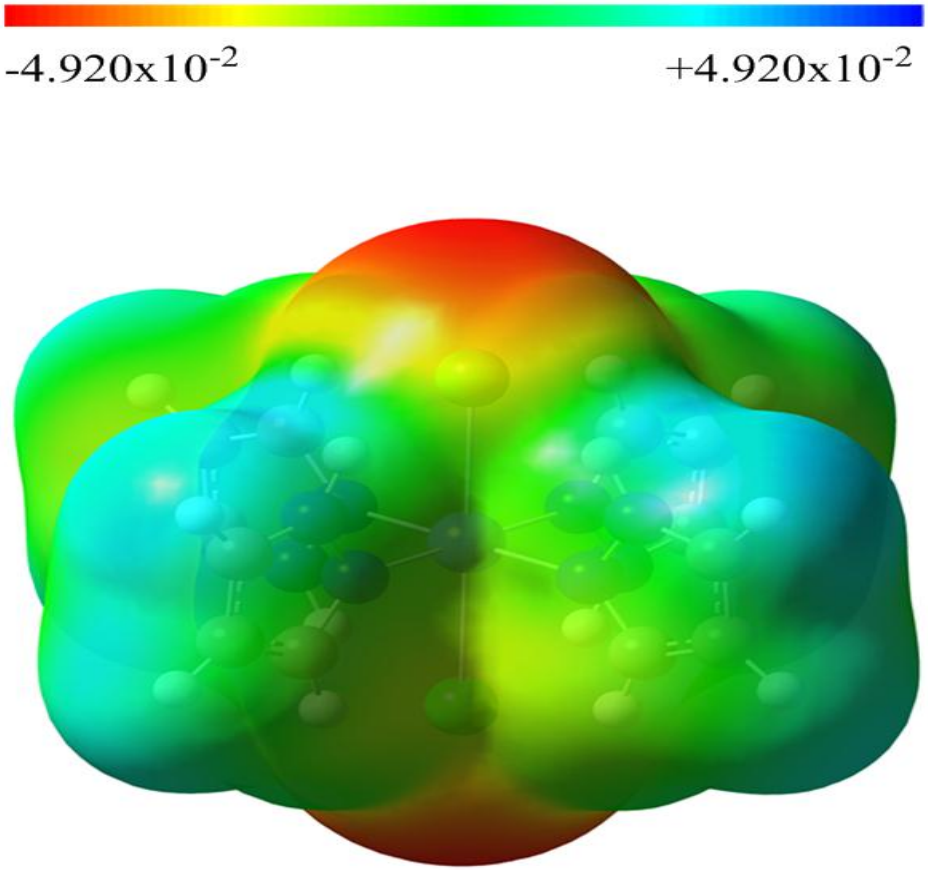






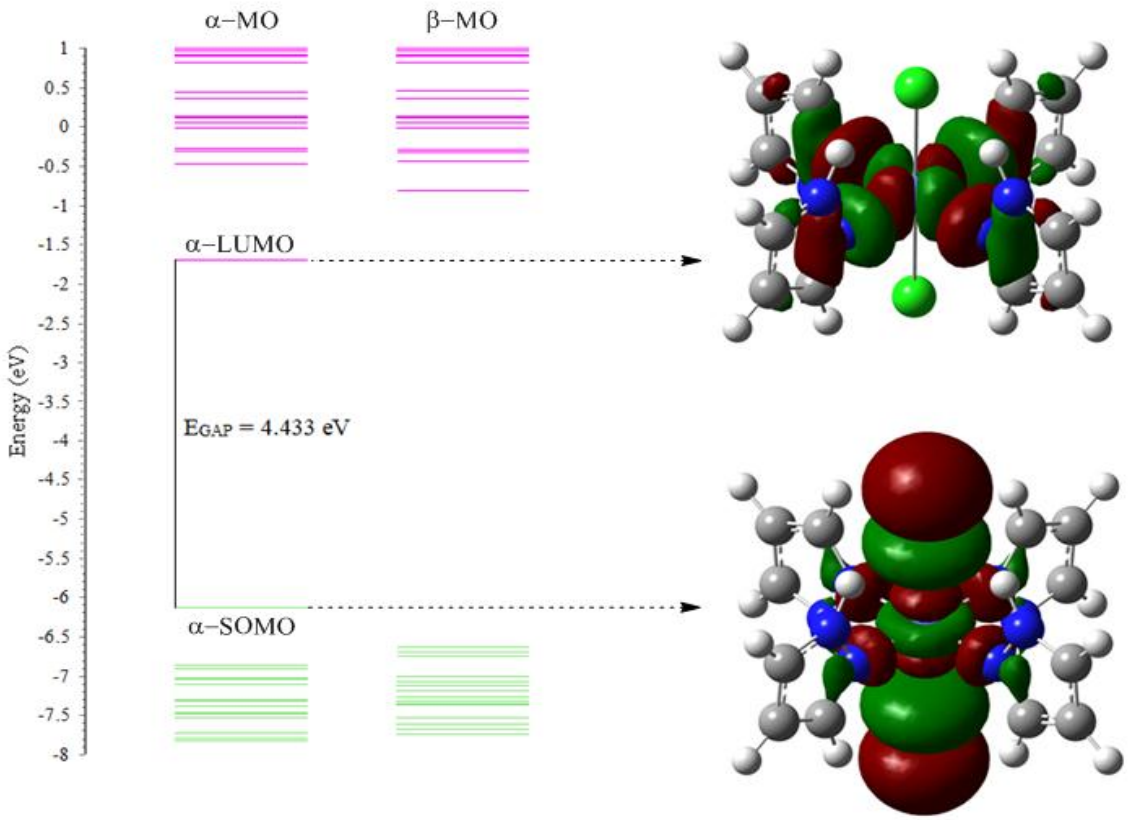
Results and discussion

MEP map



Results and discussion

SOMO and LUMO contour diagram



Results and discussion

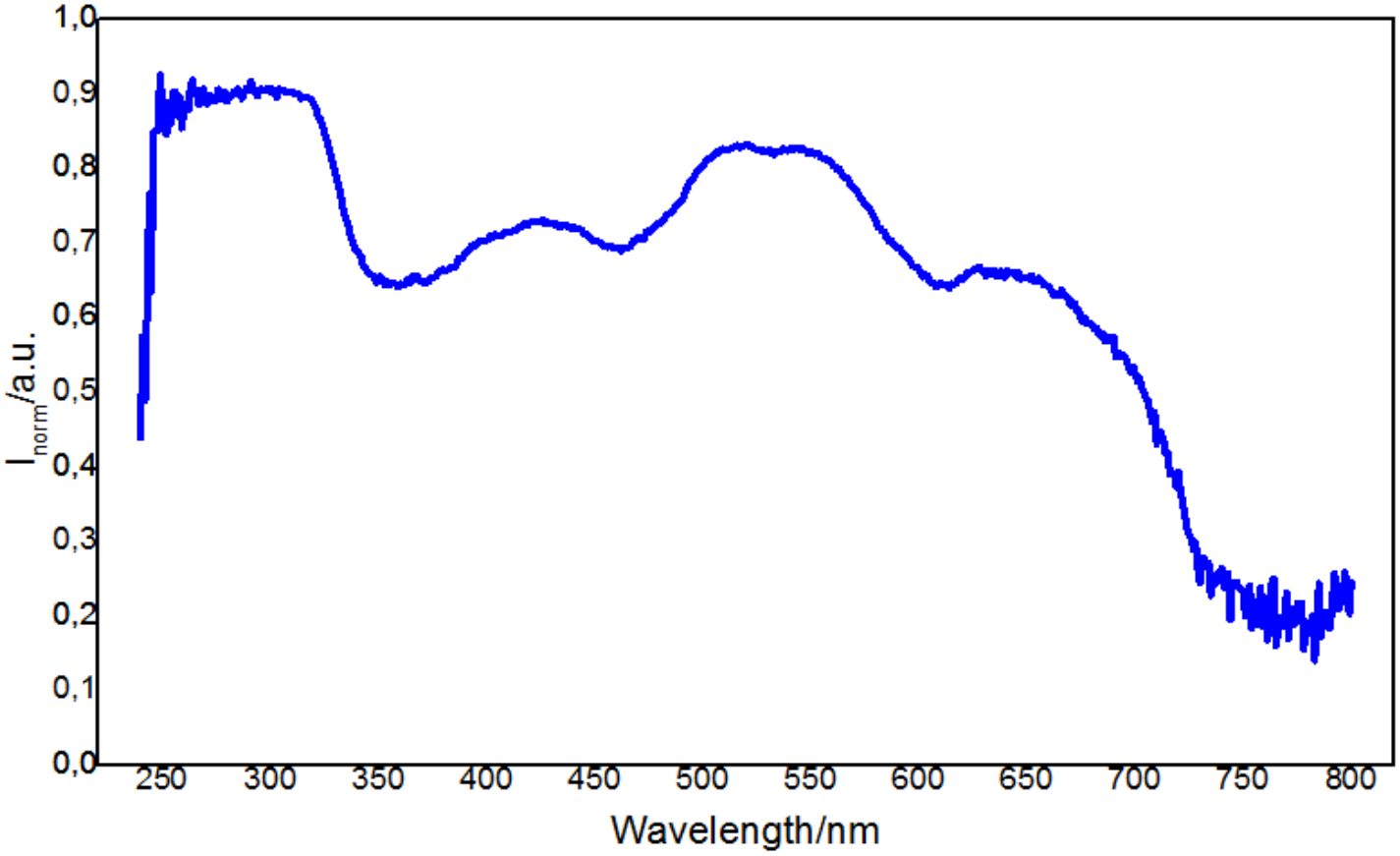
Estimated NLO properties

Compound	E_{HOMO}[a]	E_{LUMO}[a]	I[a]	A[a]	E_{GAP}[a]	η[a]
Co complex	-6.118	-1.685	6.118	1.685	4.433	2.216
Urea	-7.314	-0.372	7.314	0.372	6.942	3.471
Compound	σ[b]	σ_O[b]	χ[a]	CP[a]	ΔN_{Max}	α[c]
Co complex	0.451	0.226	3.902	-3.902	1.760	245.662
Urea	0.288	0.144	3.843	-3.843	1.107	32.505

[a] in eV [b] in eV^{-1} [c] in a.u.

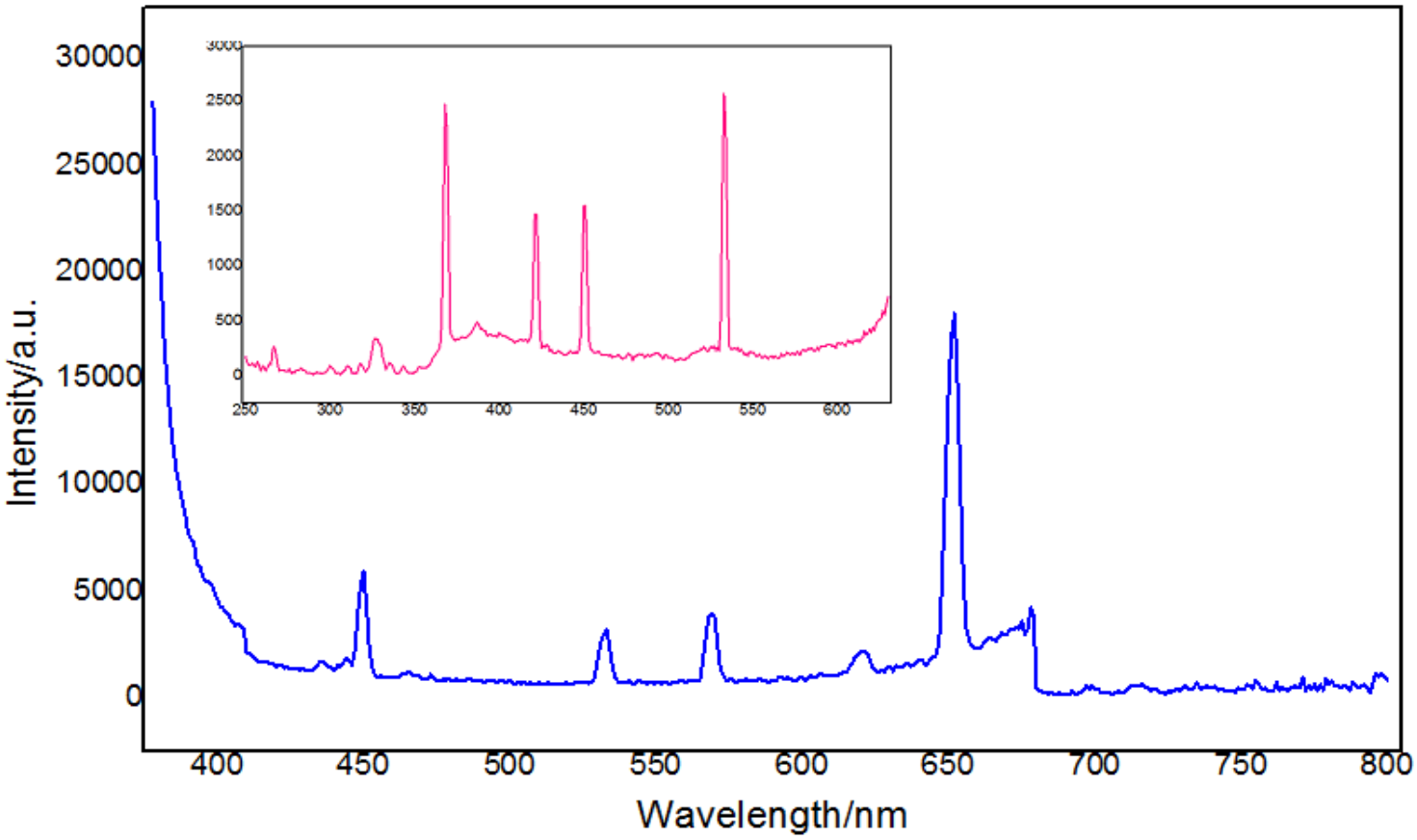
Results and discussion

Optical properties



Results and discussion

Photoluminescence properties



Results and discussion

Molecular docking

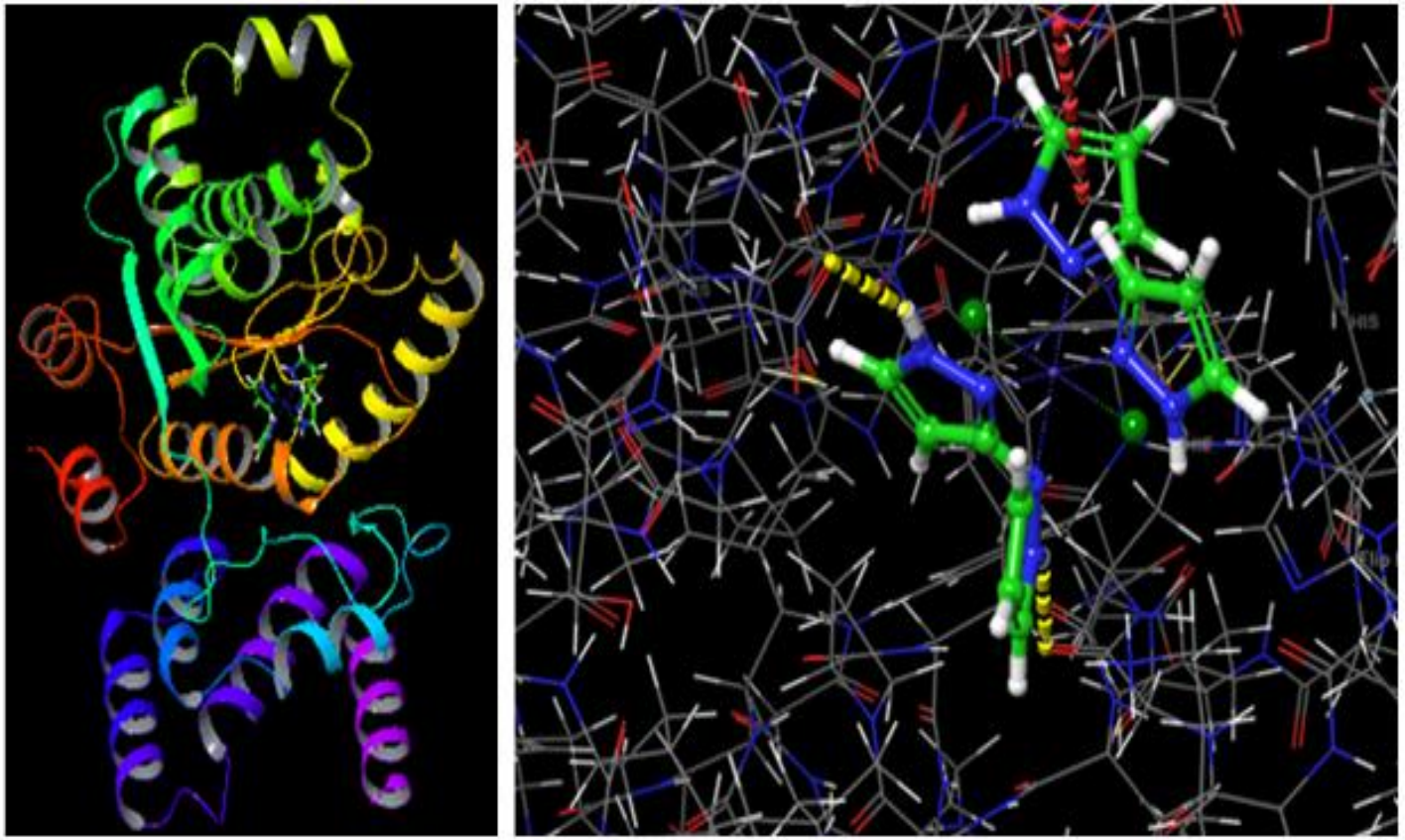
Molecular docking calculations were done against *Staphylococcus aureus* tyrosyl-tRNA synthetase and *Pyrococcus kodakaraensis* aspartyl-tRNA synthetase by using Maestro 12.2 program [20-25]. The related proteins were selected from protein data bank web tool (**1JIL** [26] and **1B8A** [27]).

Protein	Docking Score	van der Waals Energy	Coulomb Energy	Total Interaction Energy
1JIL	-2.690	-27.127	0.000	-27.127
1B8A	-3.072	-31.415	0.000	-31.415

Results and discussion

Molecular docking

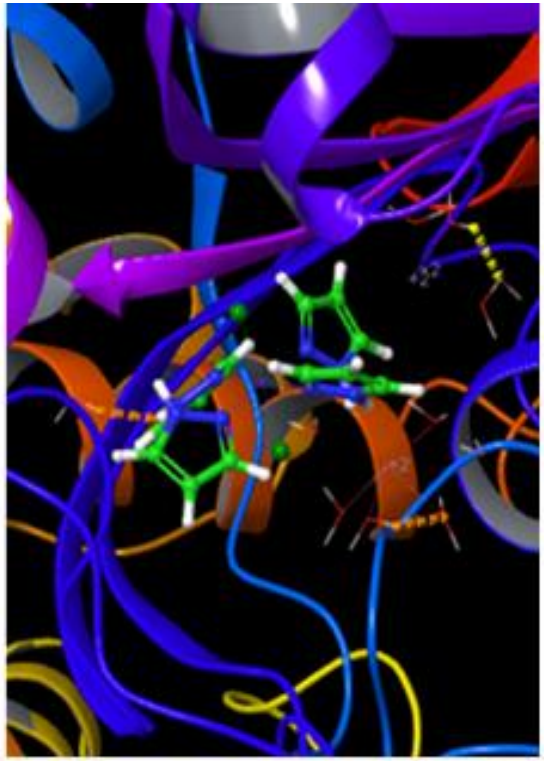
1JIL

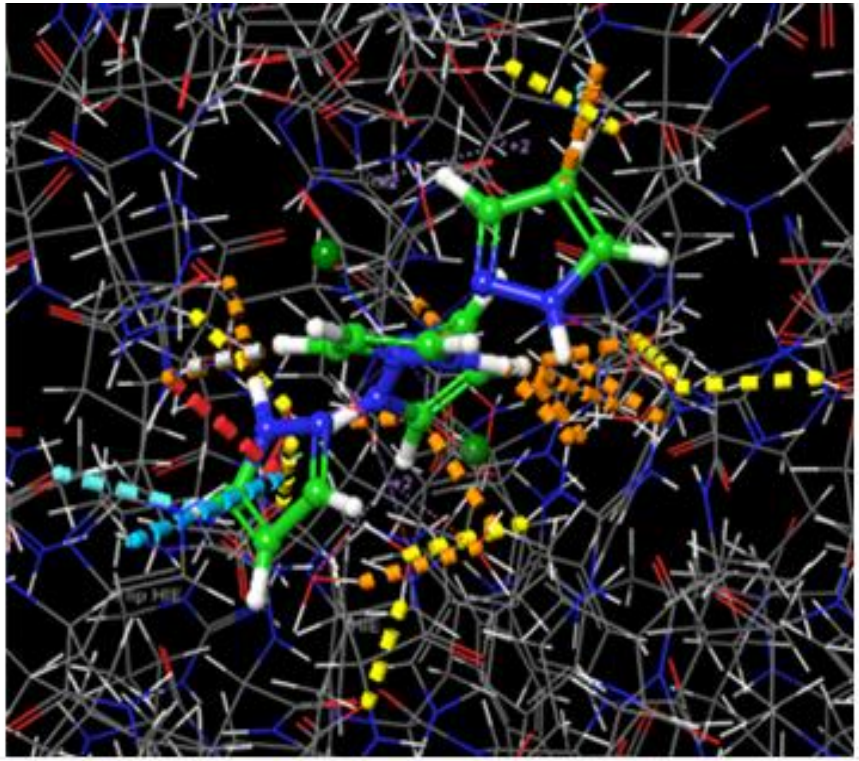


Results and discussion

Molecular docking

1B8A





Conclusions

The X-ray crystal structure of the pyrazole Co(II) complex showed the presence of weak inter- and intramolecular N—H···Cl and C—H···Cl hydrogen bonds. The optimized structure results showed a very good agreement with the experimental ones and the molecular electrostatic potential maps exhibited the complex active regions. The analysis of the optical properties of the cobalt complex investigated at room temperature using optical absorption UV-visible and photoluminescence spectroscopy showed its interesting photoluminescence behavior with a particular bright red relaxation. The estimated NLO properties suggested that the complex could be a candidate for NLO applications. On the other hand, the molecular docking calculations showed that the material displays an inhibition activity against *Pyrococcus kodakaraensis* aspartyl-tRNA synthetase.

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Acknowledgments

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