



Reactivity of 12-tungstophosphoric acid and its inhibitor potency toward Na^+/K^+ -ATPase: A combined ^{31}P NMR study, *ab initio* calculations and crystallographic analysis

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ABSTRACT

Influence of 12-tungstophosphoric acid (WPA) on conversion of adenosine triphosphate (ATP) to adenosine diphosphate (ADP) in the presence of Na^+/K^+ -ATPase was monitored by ^{31}P NMR spectroscopy. It was shown that WPA exhibits inhibitory effect on Na^+/K^+ -ATPase activity. In order to study WPA reactivity and intermolecular interactions between WPA oxygen atoms and different proton donor types (D = O, N, C), we have considered data for WPA based compounds from the Cambridge Structural Database (CSD), the Crystallographic Open Database (COD) and the Inorganic Crystal Structure Database (ICSD). Binding properties of Keggin's anion in biological systems are illustrated using Protein Data Bank (PDB). This work constitutes the first determination of theoretical Bader charges on polyoxotungstate compound via the Atom In Molecule theory. An analysis of electrostatic potential maps at the molecular surface and charge of WPA, resulting from DFT calculations, suggests that the preferred protonation site corresponds to WPA bridging oxygen. These results enlightened WPA chemical reactivity and its potential biological applications such as the inhibition of the ATPase activity.

1. Introduction

Polyoxometalates (POMs) are a class of metal-oxygen cluster compounds with unique structural and physicochemical properties [1]. They have attracted great attention for many years due to their strong acidity and redox properties, which have led to their broad applications in industry as homogeneous and heterogeneous catalysts [2–5]. POMs are generally nontoxic to normal cells and exhibit *in vitro*, and *in vivo* biological activities [1,6–10]. Such activities include highly selective inhibition of enzyme functions, *in vitro* and *in vivo* antitumoral [11–15], antiviral [16] and antiretroviral activities [17] against human immunodeficiency virus (HIV) infections.

Biomedical importance of POMs, as confirmed by numerous studies is mostly based on their interactions with proteins [10,14,18–21]. These studies illustrate the importance of noncovalent interactions between POM and peptides. Negative charge of POMs is thought to be one of the key features for their interactions with proteins, as POMs are

binding primarily to the positively charged protein region [22]. It is consistent with the experimental results obtained by Zhang et al. indicating that the binding of POM to proteins may cause the protein molecule to undergo an unfolding process [23].

Among the POMs, 12-tungstophosphoric acid ($\text{H}_3\text{PW}_{12}\text{O}_{40}$ abbreviated WPA) occupies a special position. It is recognized as a promising catalyst in biomass fuel production [24–25]. The anion has also various biological properties [26–33], including inhibition of ATPase. Primary structure of WPA is the Keggin unit, which is composed of a central PO_4^{3-} tetrahedron surrounded by 12 WO_6 octahedra as a polyanion ($\text{PW}_{12}\text{O}_{40}^{3-}$) with three negative charges that are neutralized by three protons. Fig. 1 represents the anion structure. According to a representation of oxygen octahedron (Fig. 1b), 4 oxygen types can be defined; 4 central oxygen atoms (Oa), 12 oxygen atoms that bridge two tungsten atoms sharing a central oxygen atom (edge-sharing Oc), 12 oxygen atoms that bridge tungsten atoms not sharing a central oxygen atom (Ob) and 12 terminal oxygen atoms (Od) bound to a single

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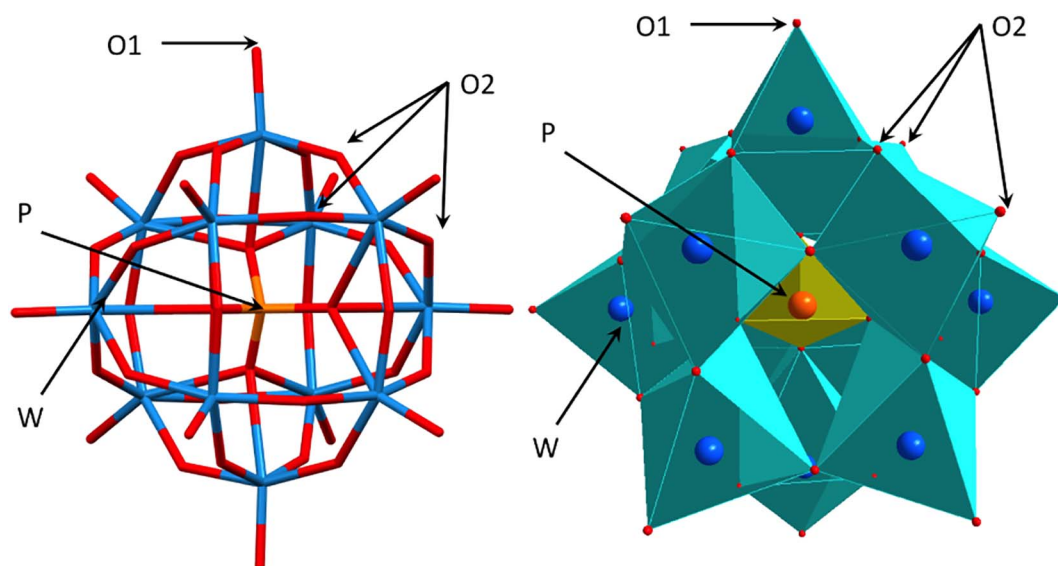


Fig. 1. Chemical structure and atom labeling of WPA a) wireframe bond style b) oxygen octahedral representation.

tungsten atom. However, a precise analysis of the WPA geometry shows that there is no significant difference (as deduced from classical X-ray diffraction) between Ob and Oc oxygen atoms in terms of bond lengths and bond angles. It remains than in solution the accessibility of the Ob and Oc oxygen atoms could be distinguished as demonstrated by Lopez et al. via molecular dynamic simulations [34]. Therefore, two types of “external” oxygen atoms, those which are accessible to a noncovalent interaction, will be used, according to their tungsten coordination: O1x (bonded to only one tungsten atom) and O2x (shared between two tungsten atoms). They will be referred to as O1 and O2 in this paper (Fig. 1a). Oxygen atoms of a WPA anion are attractive sites, and can therefore form intermolecular hydrogen bonds. These interactions bear a particular importance because they are responsible for their biological actions toward viral enzymes or viral cell envelopes.

Precise proton positions and acid strength of tungstophosphoric acid, which are essential for understanding of the nature of the catalytic sites and reactivity, are still under active debate in the community. Kozhevnikov et al. [35] concluded from ^{17}O NMR spectroscopy that the protons are located on the terminal oxygen atoms (O1). Ganapathy et al. [36] reached a similar conclusion based on the results from $^1\text{H}/^{31}\text{P}$ and $^{31}\text{P}/^1\text{H}$ Rotational Echo Double Resonance (REDOR) NMR experiments and density functional theory (DFT) based quantum chemical calculations of the proton affinity for a single proton. ^{31}P NMR analysis and DFT calculations indicated that the trimethylphosphine oxide complexes are associated with protons located at three different terminal oxygen (O1) sites of the WPA polyanion [37]. Solid-state NMR technique [38] was used to argue that the anhydrous protons reside on the bridging oxygen atoms. The most energetically favorable site for the acidic proton in anhydrous heteropolyacids was determined by quantum chemical calculations to be a bridging oxygen atom [39]. DFT calculations, which considered the position of all three protons, indicated that the energy preference for either oxygen type is small and that protons are likely to be distributed among all oxygen types [40]. REDOR NMR experiments combined with quantum chemical DFT calculations demonstrated that acidic protons in anhydrous WPA are localized on both bridging (O2) and terminal (O1) atoms of the Keggin unit [41].

Recently, we found that WPA exhibits potential bioactivities, especially the inhibition of Na^+/K^+ -ATPase [31]. In a number of enzyme reactions involving phosphates, the most direct method for monitoring interaction between WPA and enzyme and identification of generated chemical species is ^{31}P NMR spectroscopy [42–44]. The possibility of readily distinguishing and assigning each phosphorus atom of

adenosine triphosphate (ATP) and adenosine diphosphate (ADP) by ^{31}P NMR was early recognized and demonstrated in 1960 [45]. Therefore we applied ^{31}P NMR to follow ATPase activity in the presence of WPA.

The understanding of the interaction, between WPA and enzyme (ATPase), at a molecular level is essential for the interpretation and the development of potent compounds with selective enzymatic affinity. In order to understand the reactivity of WPA, the $\text{OH}\cdots\text{O}$, $\text{NH}\cdots\text{O}$ and $\text{CH}\cdots\text{O}$ interactions between different organic parts and WPA were analyzed using the Cambridge Structural Data Base (CSD) [46], Crystallographic Open Database (COD) [47] as well as the Inorganic Crystal Structure Database (ICSD) [48] or the Protein Data Bank (PDB) [49]. This analysis was performed according to the oxygen atom type (O1 or O2). Consequently, it explains the interaction of organic molecules with Keggin anion through hydrogen bonding. Hydrogen bonds, weak interactions and their environment have a well-documented geometry in the crystalline state. CSD provides a large amount of experimental data that allows a better description of hydrogen bonds geometry [50–53]. This method has already been applied to different POMs compounds such as decavanadate [54] and functionalized hexavanadate [55].

The aim of this paper is a contribution to a better understanding of the WPA anion reactivity and its inhibitor potency toward Na^+/K^+ -ATPase. These interactions have been studied through a combined approach using both theoretical and experimental tools. We have investigated the action of the ATPase inhibitor WPA on the breakdown of extracellular ATP. The influence of WPA binding to Na^+/K^+ -ATPase activity in conversion of ATP to ADP is supported by an analysis of ^{31}P NMR spectroscopy data. To achieve this goal, a theoretical analysis of various interactions of WPA, has been provided, with an emphasis on the changes of bonding nature depending on the oxygen position in the molecules (O1 or O2). Binding properties of Keggin anion in a biological system are illustrated using the PDB. A more efficient and elegant method to predict ligand binding sites involves the use of DFT calculations and the subsequent determination of the electrostatic potential (EP) values at the molecular surface of WPA.

2. Materials and methods

2.1. Chemicals

All chemicals were of analytical grade. Na^+/K^+ -ATPase from porcine cerebral cortex and ATP were purchased from Sigma Chemicals Co. (Germany), as well as some chemicals for assay medium (magnesium chloride and Tris-HCl). WPA was prepared according to the literature

[56] and the structure confirmed by powder X-ray diffraction and infrared spectroscopy. Synthesized WPA was recrystallized prior to use and heated about 10 min at 80 °C in order to get stable acid hexahydrate (WPA·6H₂O).

2.2. Medium for ³¹P NMR experiment

The standard assay medium for common investigation of Na⁺/K⁺-ATPase activity was used in our ³¹P NMR experiment. The medium contained (in mmol/L): 50 Tris–HCl (pH 7.4), 100 NaCl, 20 KCl, 5 MgCl₂, 2 ATP and 125 mgL^{−1} SPM proteins (i.e. 290 mgL^{−1} commercial porcine cerebral cortex proteins) in a final volume of 5 mL. After preincubation for 10 min at 37 °C in the absence (referred hereafter as control solution) or in the presence (referred hereafter as probe solution) of investigated WPA compound, the reaction was initiated by addition of ATP. Concentration of WPA in the probe solution was 1 · 10^{−3} mol dm^{−3}. Probe solution pH was measured using a pH meter with a glass electrode and adjusted by addition of NaOH up to pH 7.4. Blank solution was prepared without addition of enzyme and WPA.

2.3. ³¹P NMR spectroscopy

NMR experiments were carried out on Apollo upgrade (Tecmag, USA) Bruker, MSL 400 spectrometer, at 161.978 MHz, with 2048 scans, 9.0 μs pulse and 500 ms repetition time, at 25 °C. ³¹P NMR spectra of control solution (ATP, enzyme), and probe solution containing WPA were recorded in different time intervals: immediately, 4 h, and 4 days after addition of ATP. The duration of spectra recordings was 20 min. In the meantime solutions were kept at 4 °C. 85% H₃PO₄ at 0 ppm was used as external standard for the chemical shift estimation.

2.4. Structural searches

2.4.1. Cambridge Structural Data base (CSD)

CSD was searched for compound containing WPA anion and retrieved depending on the oxygen type O1 and O2 (see supporting information, Table S1). The searches were restricted to entries with: a) error-free coordinate sets in CSD check procedures; b) no crystallographic disorder; c) no polymeric connections and d) crystallographic R factor lower than 0.10. For each interaction, D–H...O distance (D as donor atom) and D–H...O angle using Mercury® software [57] are shorter than the sum of their van der Waals radii.

2.4.2. Crystallographic Open Database (COD)

COD [47] was searched for compound containing WPA anion and retrieved depending on the oxygen type O1 and O2 (see Supporting information, Table S2). The searches were restricted to entries with: a) no crystallographic disorder; b) no polymeric connections and c) crystallographic R factor lower than 0.10. For each interaction, D–H...O distance (D as donor atom) and D–H...O angle using Mercury® software [57] are shorter than the sum of their van der Waals radii.

2.4.3. Inorganic Crystal Structure Database (ICSD)

ICSD was searched for compound containing WPA anion. A similar methodology to those explained in Sections 2.4 and 2.5 has been used to determine the geometry of the structures found (see Supporting information, Table S3).

2.4.4. Protein Data Bank (PDB)

PDB was searched for WPA...H-donor interactions. The enzyme–WPA complexes were found through a PDB search using the “Keggin anion” or “tungstophosphoric” keyword leading to 3 structures (see Supporting information, Table S4). Geometry of intermolecular interactions between the Keggin anion and the protein structure were determined.

2.5. Ab initio computations

All *ab initio* computations have been carried out with Gaussian09 package [58]. These calculations were based on B3LYP hybrid functional, which uses a combination of the Becke exchange functional [59] coupled with the correlational functional proposed by Lee et al. [60,61]. The triple- ζ and polarization type basis set cc-PVTZ [62] was chosen for phosphorus, oxygen, nitrogen, carbon and hydrogen. As for tungsten atom, the effective core potential type basis set LANL2DZ [63] was used to limit computational effort, while the Douglas-Kroll-Hess [64,65] second order scalar relativistic calculation was used to account for relativistic effects at moderate cost. Multi WFN package [66] based on Bader's Atoms in Molecules Theory (AIM) has been used to define atomic basins and their integrated charges. Since an effective core potential was chosen to describe part of W atoms. Non-nuclear attractors [67] were found in the immediate vicinity of W nucleus and need to be back integrated into the nearest W basin contribution.

3. Results and discussion

3.1. Inhibition of ATPase followed by ³¹P NMR spectroscopy

As shown in our earlier study WPA exhibits concentration-dependent inhibitory effect on the activity of rat synaptic plasma membrane Na⁺/K⁺-ATPase and E-NTPDase [31]. The behavior of WPA in solution is important from the aspect of analytical, biomedical, and catalytic applications. Analysis of Fourier transform infrared (FTIR) and Raman spectra have shown that WPA in the incubation medium i.e. in the presence of commercial enzyme and its substrate-ATP, forms monolacunary Keggin anion [PW₁₁O₃₉]^{7−} as the main molecular species in the system under physiological conditions [31,68–69]. This species arises by removal of one WO unit from the Keggin anion and may react with various ligands, including Na/K ATPase, responsible for ATP hydrolysis. In this paper we wanted to follow the changes in molecular structure of heteropoly acid WPA applying ³¹P NMR spectrometry as a common method for analyzing of heteropoly acids of Keggin structure as well as their hydrolysis molecular products. Simultaneously this method enables a direct observation of the enzyme interaction, like the ATPase, with the chemical moieties that actually participate in the reaction [70].

Fig. 2 contains ³¹P NMR spectra of blank (left), control (middle) and probe (right) solutions, recorded at different time intervals: immediately (a), 4 h (b), and 4 days (c) after solution preparation. Assignments of the signals can be readily made on the basis of known ³¹P NMR spectra of ATP and ADP [45]. Three ATP peaks (α - 9.8 ppm, β - 18.2 ppm; and γ - 4.6 ppm) are clearly visible in the ³¹P NMR spectra of the control, and the probe solutions recorded immediately after preparation. However, in the control spectrum recorded 4 h after preparation, two additional small peaks, superimposed on α , and γ ATP peaks are observed at - 9.2 ppm and - 5.0 ppm, originating from α ADP and β ADP respectively. These peaks are indicating the beginning of ATP hydrolysis. The peak of released inorganic phosphate Pi, at + 3.2 ppm is also visible. These changes were more expressed in the spectrum recorded after 4 days. The intensity of Pi signal is considerably enhanced, and a weak peak at + 4.6 ppm is observed at expected position for AMP as a result of ATP hydrolysis and formed ADP [71]. The appearance of the spectra in Fig. 2 (middle) may be explained by irreversible ATP hydrolysis, i.e. the ATP concentration is progressively reduced while the concentration of ADP, AMP and Pi is increased.

On the other hand, no changes are observed in ATP signals when WPA is present (probe solution, Fig. 2, right). Therefore, the signal of β -ATP, as the signal belonging solely to ATP molecule [72] was used for estimation of changes in ATP content. We have compared its normalized area in the blank, control and probe sample in different time intervals. The results are presented in Fig. 3 and indicate that ATP content

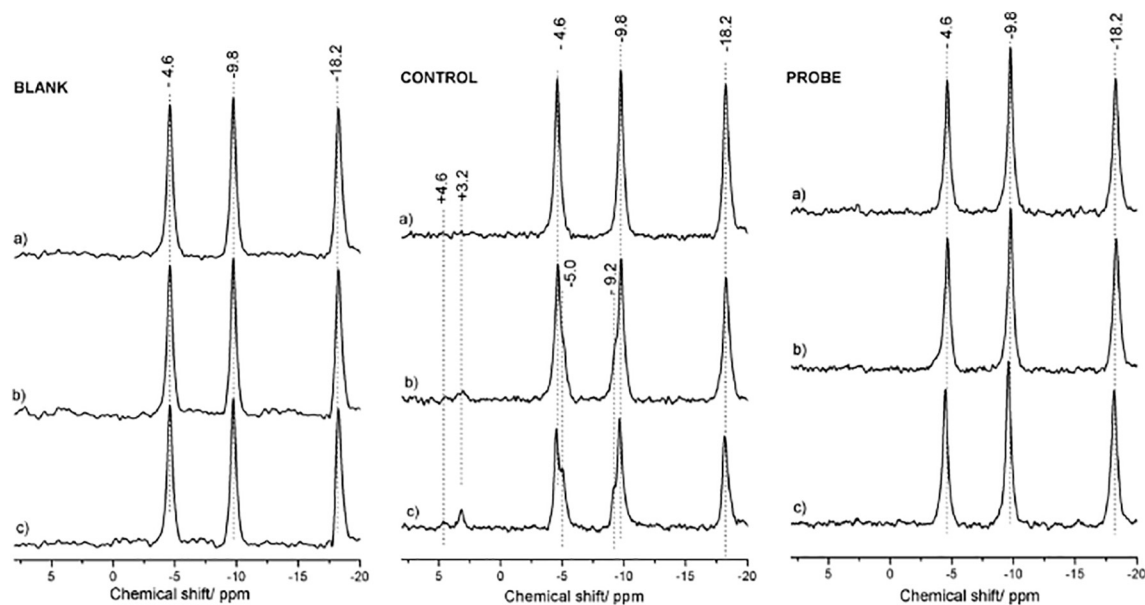


Fig. 2. ^{31}P NMR spectra of blank, control, and probe solution recorded immediately after preparation (a), 4 h (b), and 4 days after preparation of solution (c).

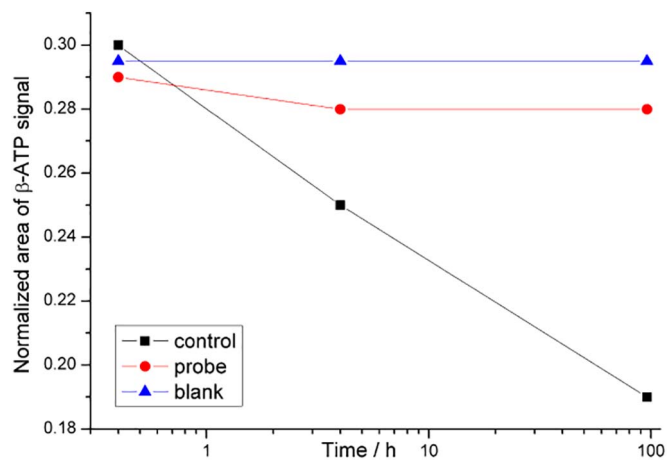


Fig. 3. Influence of WPA on ATP hydrolysis monitored by time changes of β -ATP signal intensity in ^{31}P NMR spectra. The presented values represent normalized area of β -ATP signal (normalization was done on integrated area from +10 to -30 ppm) in blank, control and probe solution.

in control solution was reduced for about 40% four days after preparation of solution. No changes of ATP level was detected in the presence of WPA in the same time interval.

As shown in our earlier study [31], WPA in the presence of commercial enzyme and its substrate-ATP forms monolacunary Keggin anion $[\text{PW}_{11}\text{O}_{39}]^{7-}$, the main molecular species, which is proved to be the active species in aqueous solution at physiological pH. The ^{31}P NMR spectrum of WPA in the incubation medium without ATP and ATPase is presented in Fig. 4a. The dominant peak at about -9.9 ppm, corresponding the monolacunary Keggin anion present under physiological pH [68], is not observed in the spectra presented in Fig. 2 because of low WPA concentration and overlapping of its signal with more intensive peak of α -ATP. Therefore in this way we could not follow the changes in molecular structure of WPA during ATP hydrolysis. However in the experiment where only WPA and enzyme (without ATP) were present under the same experimental conditions, changes in the ^{31}P NMR spectrum (broadening of signal at -9.9 ppm and appearance of shoulder/peak at -9.3 ppm) could be an indication of interaction of enzyme and a monolacunary WPA anion (Fig. 4b).

In order to get further insight about the understanding of the

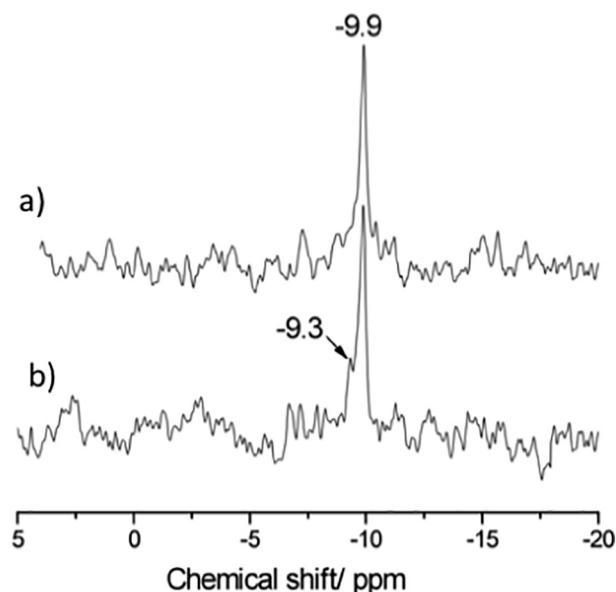


Fig. 4. ^{31}P NMR spectra of WPA in solution: a) WPA in the incubation medium in the absence enzyme and ATP, b) WPA in the incubation medium in the presence of the enzyme (without ATP).

interaction WPA – enzyme, these interactions existing in solution state are studied via a crystallographic statistical study (Sections 3.2 and 3.3) in solid state and via the determination of the atomic net charges, electrostatic potential on the WPA molecular surface in gas state (Section 3.4).

3.2. Geometrical description of WPA interactions with organic moieties in crystalline state

Statistical study on the O–H...O, N–H...O and C–H...O non-covalent interactions for 36 structures containing Keggin anion (WPA) found in CSD [S1], COD [S2], ICSD [S3] and PDB [S4] databases (Table 1), have been performed. 160 contacts have been identified: 23 O–H...O interactions, 2 N–H...O and 135 C–H...O interactions. These interactions were sorted according to the oxygen type of WPA (O1 and O2). Fig. 5 represents D–H...O angles versus H...O distances

Table 1

List of WPA structures used in this paper retrieved from the ICSD, CSD, COD and PDB searches. Structures are ranked in pure inorganic compound, organic – inorganic hybrid or co-crystals compounds and proteins co-crystallized with WPA. Structures with co-ordinates available and R factor < 10% are listed. Code refers to ICSD codes in case of inorganic structures, CSD refcodes or COD numbers in case of organic – inorganic hybrid or co-crystals structures or PDB id in case of protein inorganic co-crystals.

Chemical formula	Code	Reference
Inorganic or hybride organic-inorganic structures retrieved from the ICSD base		
C ₁₂ H ₃₆ Fe O ₄₆ P S ₆ W ₁₂	250528	S3a
C ₉ H ₃₀ N ₃ O ₄₀ P W ₁₂	166878	S3b
C ₆ H ₂₄ N ₃ O ₄₀ P W ₁₂	166877	S3b
C ₂₁ H ₄₉ N ₇ O ₄₇ P Pr W ₁₂	167536	S3c
C ₁₄ H ₄₂ O ₄₇ P S ₇ W ₁₂ Y	167537	S3c
H ₂₁ Mg O ₅₀ P W ₁₂	416173	S3d
H ₁₅ O ₄₆ P W ₁₂	95621	S3e
H ₁₅ O ₄₆ P W ₁₂	95622	S3e
H _{4.5} D _{10.5} O ₄₆ P W ₁₂	95625	S3e
H ₁₅ O ₄₆ P W ₁₂	95624	S3e
H ₄₅ O ₆₁ P W ₁₂	1534	S3f
H ₁₅ O ₄₆ P W ₁₂	904	S3g
H ₁₅ O ₄₆ P W ₁₂	908	S3g
Organic – inorganic hybrid compounds or organic – inorganic co-crystals retrieved from CSD or COD base		
C ₂₄ H ₃₅ N ₄ O ₄₉ P W ₁₂	JUVZUX	S1a
C ₆ H ₁₈ N ₃ O ₄₄ P W ₁₂	OQOFOR	S1b
C ₃₀ H _{56.94} Bi ₃ N ₆ O ₇₂ P Na W ₁₂	EQOFEX	S1c
C ₂₄ H ₄₆ Cl Cu ₂ N ₄ O ₅₆ P W ₁₂	UJAVAE	S1d
C ₆₀ H ₆₃ N ₃ O ₅₂ P W ₁₂	IXUWIJ	S3
C ₂₄ H ₄₅ N ₆ O ₄₀ P W ₁₂	CSLGXY	S1e
C ₂₆ H ₄₀ Cl Cu ₄ N ₃₂ O ₄₀ P S ₈ W ₁₂	JOFKAS	S1f
C ₄₀ H ₃₀ Cl Cu ₂ N ₁₂ O ₄₃ P S ₄ W ₁₂	NOKTIS	S1g
C ₃₀ H ₂₄ Ag ₂ N ₆ O ₄₀ P W ₁₂	FOKKIB	S1h
C ₂₄ H ₄₅ N ₆ O ₄₀ P W ₁₂	HIDGEI	S1i
C ₃₆ H ₃₃ Cu ₅ N ₃₀ O ₄₅ P W ₁₂	LIBKAK	S1j
C ₂₄ H ₂₈ N ₄ O ₅₀ P W ₁₂	KIVPIQ	S1k
C ₁₆ H ₂₅ Ag ₄ N ₁₂ O ₄₀ P W ₁₂	DEZNED	S1l
C ₈ H ₂₇ N ₆ O ₄₆ P W ₁₂	DEZNAS	S1l
C ₂₄ H ₃₉ Ni ₂ N ₄ O ₆₀ P W ₁₂	LIQFOI	S1m
C ₆₀ H ₆₀ Ag ₃ N ₁₀ O ₄₀ P W ₁₂	BIQOQJ	S1n
C ₄₈ H ₃₂ Cl ₃ Cu ₁₂ N ₄₀ O ₄₀ P W ₁₂	DAWWAB	S1o
C ₃₆ H ₃₃ Cu ₆ N ₃₀ O ₄₅ P W ₁₂	DAWVUU	S1o
C ₂₈ H ₄₀ Ag ₅ N ₂₄ O ₄₀ P W ₁₂	VAYWEZ	S1p
C ₉₆ H ₂₀₄ N ₃ O ₄₀ P W ₁₂	ABIJIG	S1q
C ₁₉ H ₂₄ N ₅ O ₄₀ P W ₁₂	AXORUB	S1r
C ₉₀ H ₇₂ Cu _{4.5} N ₁₈ O ₄₀ P W ₁₂	ETAYEE	S1s
C ₁₂ H ₁₂ Cu ₃ N ₆ O ₄₀ P W ₁₂	SEHSEE	S1t
C ₁₈ H ₂₄ Cu ₃ N ₆ P W ₁₂ O ₄₀	SEHRIH	S1t
C ₁₅ H ₂₁ Cu ₂ N ₅ P W ₁₂ O ₄₀	SEHRON	S1t
C ₁₂ H ₁₃ Ag ₃ N ₆ P W ₁₂ O _{40.5}	SEHSAA	S1t
C ₁₄₄ H ₁₂₀ Au ₉ P ₈ O ₄₀ P W ₁₂	WEVZIH	S1u
C ₆₆ H ₈₁ N O ₅₈ P Na ₃ W ₁₂	LEBREQ	S1v
C ₁₂₈ H ₁₀₃ N ₁₆ O ₄₂ P W ₁₂	QAJKOC	S1w
C ₁₃ H ₄₁ Ba N O ₄₉ P S ₄ W ₁₂	AVUWIX	S1x
C ₆₄ H ₁₄₄ N ₄ O ₄₀ P W ₁₂	BIGLIN	S1y
C ₆₈ H ₅₆ Cu ₃ N ₁₄ O ₄₀ P W ₁₂	EDORIY	S1z
C ₆₅ H ₆₈ Ni _{2.5} N ₁₃ O _{41.5} P W ₁₂	WIXSIF	S1α
C ₁₉ H ₇₃ N ₁₂ O _{113.50} P ₂ W ₂₄	2,226,573	S2a

Protein name	PDB id	Reference
Human CTD small phosphatase-like protein	2HHL	S4a
Human extracellular domain of the LDL-receptor	1N7D	S4b
<i>Saccharomyces cerevisiae</i>	5SUQ	S4c

distribution containing inorganic compound or hybride organic-inorganic compound retrieved from ICSD, when D...O distances are < 3.5 Å. The O...H distances show an accumulation between 1.7 and 2.4 Å while the O–H...O angle exhibits values between 125 and 175° (Fig. 5, squares). One can observe two accumulations of O–H...O interactions: a strong one (from 1.7 to 2.0 Å, at higher angles) and a weaker one (from 2.1 to 2.5 Å, at smaller angles). Geometry of 24 C–H...O interactions is analyzed using interactions from 13 crystal structures (triangles) from ICSD database and 111 interactions from 37

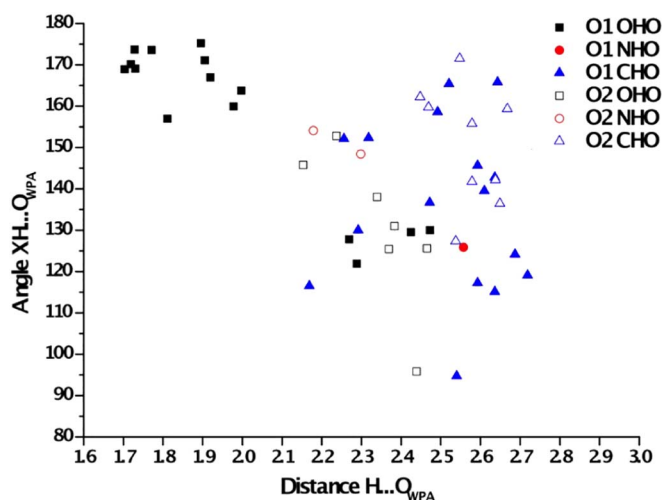


Fig. 5. Distribution of the D–H...O angle (in °) versus the H...O distances (in Å) according to the oxygen atom type for each donor type obtained from the ICSD database search. (O–H...O squares, N–H...O, circles and C–H...O triangles).

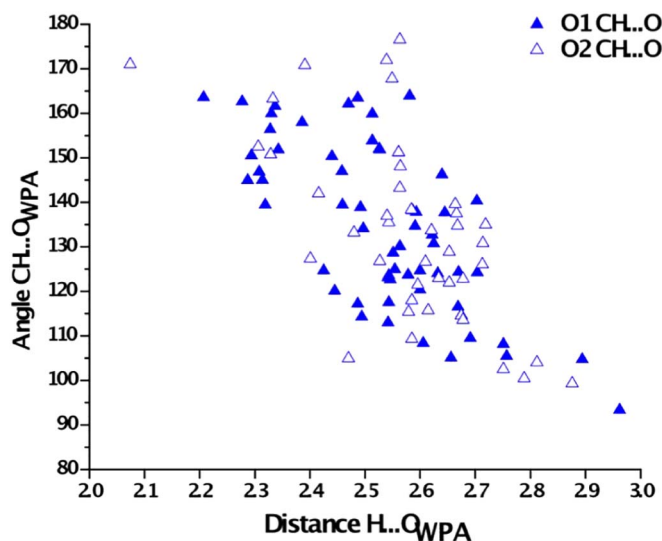


Fig. 6. Distribution of the value of the H...O distances (in Å) and C–H...O angle (in °) interactions according to the oxygen atom type obtained from the CSD database search.

structures from CSD database (Fig. 5, triangles and Fig. 6, triangles). All these interactions follow the trend expected for hydrogen bonds, namely for C–H...O angle opens up as the distance between donor and acceptor increases. C–H...O interactions are mainly at long distance (2.4 to 2.8 Å) and the angles range from 110 to 160°. In terms of angularity, all these interactions follow the trend expected for hydrogen bonds [73]. O–H...O non-covalent interactions (Fig. 6) for the oxygen O1 are mainly at a short distances (1.7 to 2.0 Å) and high angles (155 to 175°) whereas for O2 the interactions are at longer distances (2.1 to 2.5 Å) and smaller angles (90 to 150°). O1 oxygen atoms build the C–H...O interactions from 2.3 to 2.7 Å. For O2 these interactions are at longer distances (2.5 to 2.8 Å). It is therefore clear, that the directionality of the non-covalent interactions depends on the oxygen atom type. O1 oxygen atoms induce strong directionality for O–H...O interactions with short distances and high angle and O1 build stronger C–H...O interactions. O2 can form O–H...O but usually with very long distances (2.1–2.5 Å) and with smaller angles (100 to 140°). In consequence, summation of all the interactions expressed by the 34 structures containing WPA anion clearly indicated that O1 atoms build significant more interactions than oxygen atoms O2 (129 interactions for O1 versus 83 for O2, Fig. 7). Furthermore the distribution median is very slightly

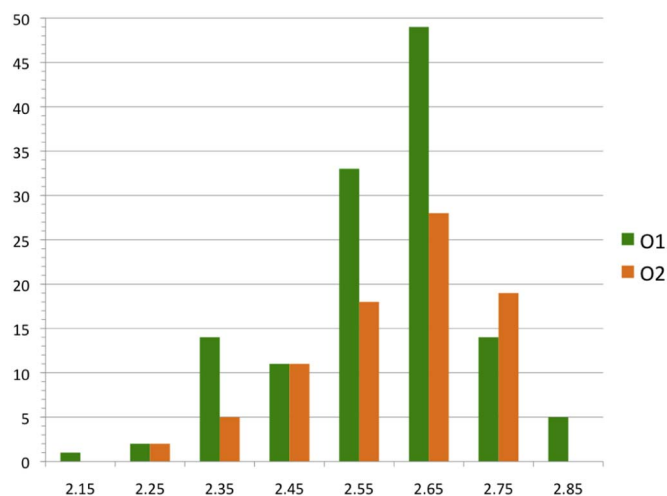


Fig. 7. Number of C–H...O interactions as a functions of the H...O distances (in Å), according to the oxygen atom type (ICSD and CSD databases searches).

greater for O2 atom (2.574 Å) than for O1 atom (2.558 Å) indicating than the CH...O_{WPA} interactions with O1 atom could appear slightly stronger than the interactions with O2 atom.

3.3. Keggin anion binding with proteins

Čolović et al. [31] have clearly demonstrated that WPA exhibits an inhibitory effect on the activity of rat synaptic plasma membrane Na⁺/K⁺-ATPase and the ecto-nucleoside triphosphate diphosphohydrolase (E-NTPDase). Bijelić et al. [10] have shown that almost all POMs are located at positively charged protein regions due to their negative charge and to their ability to form charge–charge interactions and hydrogen bonds. The relatively high content of polar residues indicates a high contribution of hydrogen bonds in POM-binding since almost all polar uncharged side chains have one hydrogen donor atom [10]. Biological activities could be related to ionic size and shape, electron- and proton- transfer ability, reservoir properties (*i.e.* inhibition of biological electron transfer) and stability at micromolar concentration and physiological pH [10]. PDB database was searched for protein structures with Keggin anion, in order to investigate their interactions with WPA and possible impact on the protein structure, which might have influenced the crystallization process. Therefore, the ligand search engine from the PDB was utilized and we searched for commonly used transition metals that were reported to act as addenda atoms in POMs (Mo, V and W). Three Keggin structures, for which the coordinates are available, have been retrieved from PDB (as of January 2017), Table 1: low-density lipoprotein receptor (1n7d) [S4a], protein phosphatase (2hhl) [S4b] and *Saccharomyces cerevisiae* (5suq) [S4c]. Table 2 summarizes the intermolecular interactions between Keggin anion and the rest of the structure, in these three proteins. WPA is bound with serine, arginine molecules and asparagine in (1n7d). The contact O1...O_{Arg} with the distance O...O about 2.44 Å is the shortest contact, and can be assumed as a hydrogen bond. Keggin anion in (2hhl) is bound to lysine, histidine, serine and phenylalanine *via* hydrogen bond. Three different Keggin anions are linked to aspartic acid, threonine, lysine, arginine, asparagine in (5suq) *via* hydrogen bond. In these three structures hydrogen bonds are formed between Keggin anion and polar (serine, asparagine, threonine), positive charged amino acid (arginine, lysine, histidine), negative charged amino acid (aspartic acid) and uncharged acid like (alanine, phenylalanine). In all structures, a large number of interactions take place on the most reactive oxygen O1 atoms (22 interactions for O1 *versus* 9 for O2) leading to almost 70% of hydrogen bonds are formed with O1 atoms. The results show that WPAs bind with the protein in the active site region with positively charged protein regions *via* hydrogen bonds. Therefore, these results

show that the WPA non-covalent behavior deduced from the crystallographic statistical study based on WPA in interaction with organic molecules, remains the same when the anion is bounded to a protein.

3.4. *Ab initio* determination of the net atomic charges and the electrostatic potential

Different theoretical calculations using various approximations involving WPA³⁻ have been reported in the literature. Acidity of WPA was the goal of several studies [3,35,39–41,74–76]. The most energetically favorable site for the acidic proton in anhydrous heteropolyacids was determined by quantum chemical calculations to be a bridging oxygen atom [39]. The bridging oxygen atom between tungsten atoms that share a central oxygen atom (edge-sharing, O2) is the favored site for the addition of the first proton to the WPA³⁻ core [40]. Acidic protons are localized on both bridging (O2) and terminal (O1) oxygen atoms of the Keggin unit [41].

Ab initio calculations were used to ascertain the reactivity of oxygen atoms through the determination of the net atomic charge and the EP values on the molecular surface [54,55]. EP can be used as a tool for predicting chemical reactivity, especially for non-covalent interactions. Guan et al. [77] suggest that the preferred proton site corresponds to a bridging atom (O2) and terminal oxygen (O1) after an observation of the EP mapped on the molecular surface in WPA³⁻. Additionally *ab initio* determination of spectroscopic data [78–79], molecular dynamics [80] or docking studies [81,82] have been performed with WPA as the target compound.

DFT functional types have been extensively studied by Wu et al. [83]. The B3LYP functional chosen in this work gives satisfactory results according to the study of Wang et al. [83]. Results of *ab initio* determination of the Bader net atomic charges are given in Table 3. The average value is used for atom W and O (12 W, 4 O_{inner}, 12 O₁ and 24 O₂ in WPA³⁻). These values are compared to those determined in the literature. This work constitutes the first determination of Bader charges on polyoxotungstate compound. As usually observed [84], Bader charges have greater amplitudes than those from a Mulliken scheme or the natural charges [36,77,78,81]. In a previous work, we have experimentally determined the Bader charges of the polyoxovanadate [V₁₀O₂₈]⁶⁻ [84] and compared to those determined by Henry et al. [85] (PACHA charges) and Kempf et al. [86] (Mulliken charges). It is interesting to notice that the difference (Δ) between the average charges of the bridged O2 atoms and the charge of the terminal O1 atom is approximately -0.2 (-0.23 for WPA³⁻ and -0.17 for [V₁₀O₂₈]⁶⁻) (Table 3, last line). The ChelpG atomic net charges obtained by Lopez et al. [34] has not been used for the determination of this average difference due to the great difference with the other values. These results clearly indicate that the bridged O2 atoms are more acidic or are more reactive than the terminal O1 oxygen. These theoretical results are in agreement with the conclusions obtained by Bardin et al. [40], Janik et al. [41] and Yang et al. [44] from theoretical studies based on other parameters than atomic charges.

Fig. 8 represents three orientations the EP of WPA³⁻ mapped onto an 0.001 a.u. electron probability isodensity surface. EP values are the most negative (red) in the vicinity of bridged O2 atoms. This corresponds to the most nucleophilic regions, while the blue part (positive) is concentrated in the vicinity of the tungsten atoms and represents the most electrophilic regions. Vicinity of the O1 atoms are indicated by black circles while O2 atoms are located with two different colors (white circles for Ob and grey circles for Oc). EP is around -0.485 e.Å⁻¹ (green color) for all the atom of the anion, while EP at the molecular surface takes different values for O2 from -0.537 e.Å⁻¹ (red color, in the vicinity of Ob) to -0.485 e.Å⁻¹ (green color, in the vicinity of Oc). The EP value at the molecular surface seems sensitive to the two bridging oxygen atom types (Ob and Oc) position, while the absolute difference is small (0.05 e.Å⁻¹). Lopez et al. [34] has shown that the most effectively solvated site by H₂O molecules is the terminal

Table 2

Hydrogen bonds between Keggin anion and protein from **2hh1**, **1n7d** and **5suq** structures. Distances $d(D \cdots O) \leq 3.50$ Å have been reported. ARG-arginine, ASN-asparagine, ASP-aspartic acid, LYS-lysine, ARG-arginine, HIS-Histidine, PHE-phenylalanine, SER-serine, THR-threonine.

	1n7d			2hh1			5suq		
	Oxygen type	Amino acid	$d(D \cdots O)$ (Å)	Oxygen type	Amino acid	$d(D \cdots O)$ (Å)	Oxygen type	Amino acid	$d(D \cdots O)$ (Å)
OHO	O1	ASN	3.37				O1	THR	3.0
	O1	SER	3.05				O1	ASP	3.0
	O1	ARG	2.44						
NH \cdots O				O2	HIS	2.46	O2	LYS	1.7
				O2	LYS	2.93	O1	ARG	1.7
				O1	PHE	3.25	O1	ASN	2.4
							O1	ASN	2.7
							O1	ARG	2.9
							O2	ARG	3.0
CH \cdots O	O1	ARG	2.86	O1	PHE	2.52	O1	ARG	3.0
	O2	ARG	2.51	O1	SER	2.85	O1	ARG	3.0
	O1	ARG	3.08	O1	LYS	2.93	O1	ARG	3.3
	O2	ARG	3.26	O2	HIS	3.06	O1	ARG	3.3
	O2	ARG	3.48	O1	PHE	3.06	O1	ARG	3.3
				O2	LYS	3.08			
				O1	PHE	3.22			
				O1	PHE	3.25			
				O1	PHE	3.12			
				O2	LYS	3.32			

oxygen (O1) because, although it carries the lowest negative charge, it is the most external. On the other hand, the bridging oxygens Ob, the most internal ones, are poorly solvated [34]. Chen et al. [87] have very earlier determined the theoretical EP of WPA^{3-} anion and published it in a 2D representation but the quality does not allow a significant comparison. Additionally, these results can be compared to those obtained for two other POM compounds $[V_{10}O_{28}]^{6-}$ [84,86] and functionalized hexavanadate [88]. In all cases the bridged atoms are more reactive than the terminal one. The two other studies where the EP values is mapped on a molecular surface for $[\{Zr(O_2)(\alpha-SiW_{11}O_{39})\}_2]^{12-}$ [89] and for $[HPTi(O_2)W_{11}O_{39}]$ [90], do not allow a discrimination between the different oxygen atoms.

One have to noticed than, due to the precision of the classical X-ray structures, we have decided not to discriminate between the two types of O2 oxygen atoms. However, the sensibility of the theoretical calculations allows us to see a difference in term of electrostatic potential. An analysis of the MEP indicates that, on one hand, the bridging O sites should be the most favorable for a protonation and, on the other, that the terminal oxygen is not a good position for protonation. But, the terminal oxygen (O1), although it carries the lowest negative charge, is the most external and interacts strongly via hydrogen bonds with organic moieties. Similarly, analysis of interactions in solid state show that Keggin anion interacts very strongly with positively charged

proteins via hydrogen bonds and that both O1 and O2 atoms are involved in non-covalent interactions. However O1 atom builds the strongest interactions. Therefore this study shows that the negatively charged Keggin anion interact very strongly with positively charged protein. Biological activities and reactivity mechanism is a competition between charges and accessibility. Reactivity of Keggin anion with proteins offers unique insight into their exact binding mode at the molecular level and may advance the application of POMs as a new class of proteases. This interesting reactivity has been illustrated and demonstrated through the following by NMR of Na + /K + -ATPase inhibition. We found indication of the enzyme interaction with a monolacunary WPA anion by ^{31}P NMR spectrometry as presented in Fig. 4b. Therefore statistical crystallographic analysis and theoretical of various interactions of WPA, has been provided (PDB, EP and DFT), with an emphasis on the changes of bonding nature depending on the oxygen position in the molecules of WPA (O1 or O2).

4. Conclusion

The obtained results of ^{31}P NMR spectroscopy confirm that WPA exhibits inhibitory effect on the activity of Na + /K + -ATPase. Electrostatic effect and hydrogen bond interactions contribute to the enzyme (ATPase) – inhibitor (WPA) complex formation. In the solid

Table 3

Theoretical average atomic charge of WPA^{3-} : Bader charges (this work, column #3), Mulliken charges [34,36,75] *, natural charges [78], net charges, unprecised method [81], CHelpG [34]**. Experimental charges on $[V_{10}O_{28}]^{6-}$: [84] and theoretical charges on $[V_{10}O_{28}]^{6-}$: PACHA charges [85], Mulliken charges [86] and Bader [87]. All charges in (in e). Δ corresponds to the difference between the charges of the bridged O2 atoms minus the charge of the terminal O1 atom.

Atom	Atomic charge	Bader charge	[35]	[82]	[80]	[85]	[91]*	[91]**	[88]	[89]	[90]	[93]
			$[PW_{12}O_{40}]^{3-}$				$[V_{10}O_{28}]^{6-}$					
W	70.82	3.18	2.70	2.23		2.37	2.49	3.81				
P	11.06	3.94		2.71			2.43	1.51				
O _{inner}	9.56	−1.56		−1.17								
O1	8.94	−0.94	−0.74	−0.60	−0.69	−0.69	−0.72	−0.85	< −0.64 >	< −0.558 >	< −0.64 >	< −0.899 >
O2	9.15	−1.158	−1.00	−0.87	−0.90	−0.90	−0.93	−1.37	< −0.811 >	< −0.675 >	< −0.90 >	< −1.040 >
		−1.143	−1.07	−0.84			−0.94	−1.55				
PO ₄		−2.3		−1.97	−1.66	−1.66						
V									< 1.561 ≥	< 1.759 >	< 2.06 >	< 2.272 >
Δ		−0.21	−0.26	−0.27	−0.21	−0.21	−0.21	−0.61	−0.171	−0.117	−0.26	−0.141

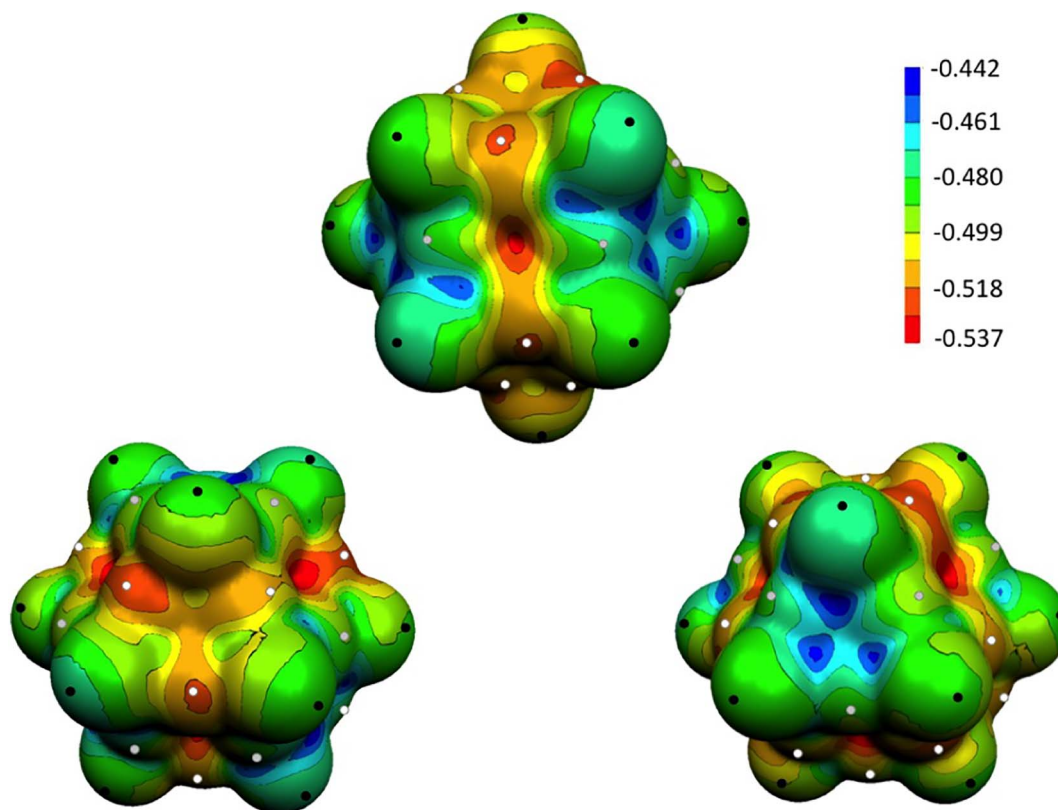


Fig. 8. Theoretical electrostatic potential ($\text{e.}\text{\AA}^{-1}$) of WPA^{3-} mapped on isodensity surface ($0.007 \text{ e.}\text{\AA}^{-3}$) in three orientations of the structure. Black circles in the vicinity of O1. For O2, two colors are used: white circles in the vicinity of Ob and grey circles in the vicinity of Oc.

state, the systematic description and interpretation of non-covalent interactions show that WPA interacts very strongly with protein via hydrogen bonds. Both O1 and O2 atoms are involved in non-covalent interactions but O1 atom builds the strongest interactions. The data retrieved from PDB showed that WPA interacts with the positively charged protein regions via hydrogen bonds. We confirm from *ab initio* calculations (Bader charges and EP on the molecular surface of WPA) that bridging oxygen (O2) are generally more basic than terminal oxygen. As a result, WPA via hydrogen bond should form relative stable complex with protein receptors.

Abbreviations

ADP	adenosine diphosphate
AIM	Atoms in Molecules
AMP	adenosine monophosphate
ATP	adenosine triphosphate
COD	Crystallographic Open Database
CSD	Cambridge Structural Database
DFT	density functional theory
E-NTPDase	ecto-nucleoside triphosphate diphosphohydrolase
EP	Electrostatic potential
FTIR	Fourier Transform Infra Red spectroscopy
HIV	Human immunodeficiency virus
ICSD	Inorganic Crystal Structure Database
NMR	Nuclear magnetic resonance
PDB	Protein Data Bank
Pi	inorganic phosphate
POMs	Polyoxometalates
REDOR	Rotational Echo Double Resonance
WPA	12-tungstophosphoric acid $\text{H}_3\text{PW}_{12}\text{O}_{40}$

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Appendix A. Supplementary data

References of the structures retrieved from the four different bases are given as supporting information. Supplementary data associated with this article can be found in the online version, at <http://dx.doi.org/10.1016/j.jinorgbio.2017.08.014>.

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